Spring 2013

Evaluating Alternatives for Augmented Water Quality Improvement Utilizing Oyster Restoration as Best Management Practice (BMP)

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Recommended Citation

Long, Stephanie R.. "Evaluating Alternatives for Augmented Water Quality Improvement Utilizing Oyster Restoration as Best Management Practice (BMP)" (2013). Master of Science (MS), Thesis, Civil & Environmental Engineering, Old Dominion University, DOI: 10.25777/mh94-wm09
https://digitalcommons.odu.edu/cee_etds/78

EVALUATING ALTERNATIVES FOR AUGMENTED WATER QUALITY IMPROVEMENT UTILIZING OYSTER RESTORATION AS BEST MANAGEMENT PRACTICE (BMP)

by

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A Thesis Submitted to the Faculty of
Old Dominion University in Partial Fulfillment of the
Requirements for the Degree of

MASTER OF SCIENCE

ENVIRONMENTAL ENGINEERING

OLD DOMINION UNIVERSITY
May 2013

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ABSTRACT

EVALUATING ALTERNATIVES FOR AUGMENTED WATER QUALITY IMPROVEMENT UTILIZING OYSTER RESTORATION AS BEST MANAGEMENT PRACTICE (BMP)

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Due to several anthropogenic influences, the Chesapeake Bay has experienced a marked decrease in water quality since the colonists arrived at the Jamestown settlement in Virginia during the 1600s. Higher concentrations of nitrogen and phosphorus have enriched the estuaries and coastal waters via point sources (sewage treatment plants and industrial wastes), nonpoint sources (agricultural run-off and septic tank discharges) and the atmosphere (Newell *et al.*, 2005). Restoring oyster beds is considered a Best Management Practice (BMP) to improve water quality as well as provide physical habitat for aquatic species and a healthier estuarine system (USACE Native Oyster Restoration Master Plan, 2012). Efforts to assist water quality improvement in conjunction with the fisheries include declaring sanctuaries for brood-stocks, supplementing hard substrate on the bottom and aiding natural populations with the addition of hatchery-reared and disease-resistant stocks in most of the coastal states in United States (Coen & Luckenbach, 2000). An economic assessment of oyster reefs suggests that restoring the ecological functions will improve water quality, stabilize shorelines, reduce predation (Grabowski, 2004) and establish a habitat for breeding grounds that outweighs the importance of harvestable oyster production (Luckenbach *et al.*, 2005). Statistical models to investigate factorial multicolinearities between water quality and oyster restoration activities were developed in this research to evaluate productivity levels of oyster restoration on multiple substrates, as well as the physical, chemical, hydrological and biological site characteristics, so that the greatest contributing factors were systematically identified. Findings from the factorial models were then further utilized to propose and develop a number of in situ water quality improvement design in forms of Total Maximum Daily Loads (TMDLs) and Best Management Practices (BMPs). A factorial model evaluates the relationship among the dependent variable, oyster biomass, and treatment levels of temperature (which includes seasonal variability), as well as salinity, TSS (total suspended solids), *Escherichia coli/Enterococcus* bacterial counts, depth, dissolved oxygen levels (DO) and nutrients such as nitrogen, phosphorus and chlorophyll a, and the block levels designated for the model such as alternative substrates (oyster shells versus riprap, granite, cement, cinder blocks, limestone marl or combinations). The different scenarios are analyzed utilizing the Factorial Model along with a Multiple Means Comparison (MMC) to compare the production rates and evaluate which combination of variables produces the highest biomass of oysters. Once the variables of greatest impact are identified, BMPs and TMDLs will be identified to aid in lowering the existing levels and develop future plans for maintaining them. In summary, this model is being developed for maximizing the likelihood of successful oyster reef restoration in an effort to establish a healthier ecosystem and to improve overall estuarine water quality in the Chesapeake Bay estuaries.

KEY WORDS: Water quality, TMDL, BMP, Factorial model, Multi-colinearity, Oyster restoration

This thesis is dedicated to my family
and Dr. Jaewan Yoon for all the
patience and support that they
have shown me during my studies

ACKNOWLEDGEMENTS

There are many people who have contributed to the successful completion of this thesis. I would like to thank all the committee members for their time and patience in reviewing this manuscript. I would also like to recognize Dr. Yoon for all the time that he has spent with me on this project since its first conception. Also, Dr. Burke has been generous in allowing me to utilize his data from his own oyster research in this statistical project and has spent hours answering all of my questions. I feel truly blessed to have worked with these two men and I appreciate all of their contributions to my education.

I also would like to recognize Kristi Britt at DEQ for her efforts in pulling Database information on water quality parameters for this study several times. In addition, I would like to thank Daniel Powell from DSS who also pulled data reports on fecal coliform counts for me. Mac Sisson from VIMS contributed his database information as well. Karen Forget with Lynnhaven River Now was a wealth of information on existing projects occurring in the Lynnhaven as was Steve McLaughlin with the City of Virginia Beach – Stormwater Management.

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CHAPTER 1

INTRODUCTION

1.1 Background

Two segments within the Lynnhaven, Broad and Linkhorn Bays have been identified as impaired waterways on the State of Virginia's 303 (d) list of impaired waters (Lynnhaven Bay, Broad Bay and Linkhorn Bay Watersheds Total Maximum Daily Load (TMDL) Report for Shellfish Areas Listed Due to Bacteria Contamination-Virginia Department of Environmental Quality - March 2004). These are considered shellfish areas and have been closed due to excessive levels of fecal coliform bacteria. For the remainder of this document, the TMDL study will be referenced as TMDL 2004.

Water quality standards are developed in order to protect human health and aquatic life and TMDLs are required for any waters included on the impaired waters list. All of the shellfish sites in this study are included in these impaired waterways.

Oysters are considered an important part of overall strategies to improve water quality in eutrophic estuaries, since they have top-down control of phytoplankton abundance due to their filtering properties. Oyster populations are efficient in filtering phytoplankton, pollutants, bacteria toxins and suspended sediments from the water column. A healthy adult oyster may filter 25 to 60 plus gallons of water per day. Based on historical Eastern oyster densities of *Crassostrea virginica*, Newell (1988) calculated that the entire volume of Chesapeake Bay could be filtered in 3 days prior to 1870. A century later with reduced populations, the filtration process took 325 days.

A large, healthy oyster population may improve the water quality and also provide a valuable habitat for benthic organisms and multiple species of fish. While constructing their habitats with calcium deposits, oysters build refuges, nesting sites and foraging access for a variety of species (over 300 species of invertebrates such as shrimp, crabs, clams, snails and worms, as well as many species of fish such as snook, grouper, redfish, black drum and more). Many adult fish species on the offshore reefs spend the juvenile phase of their life on oyster reefs (Barnes *et al.*,2010).

The structural relief of the oyster reef can dissipate wave energy, acting as a breakwater, stabilizing bottom sediments and reducing erosion. Clearer water allows for more sunlight penetration which can lead to expansion of seagrass beds (Orth *et al.*, 2006). Moreover, oyster reefs also work as a carbon sink, improving the Bay's capacity to absorb excess carbon dioxide from the atmosphere (Henderson *et al.*, 2003). The Chesapeake Bay has seen a radical decline in oyster populations due to years of poor resource management of live oysters as well as shell. One main cause of mortality is disease by the parasites, Dermo (*Perkinsus marinus*) and MSX (*Haplosporidium nelsoni*) (Andrews, 1996; Burreson, 2000). Other influential causes include increased sedimentation of the water bodies (Newell *et al.*, 2006).

Decades of poor water quality, overharvesting, habitat destruction, and disease have reduced the population of oysters in the Chesapeake Bay to less than one percent of its historic levels. These natural, renewing habitats are the focus of many restoration efforts throughout the Bay in order to improve water quality and increase aquatic populations. Today there are over 100 man-made oyster reefs in Virginia and more under construction. The shortage of oyster shell has prompted examination of alternative substrates for reef construction (Nestlerode *et al.*, 2007).

1.2 Problem Statement

Recent studies of Virginia's waterways identified multiple locations where water quality standards were not being met. Due to the natural filtration assets of the oyster and their efficiency in filtering phytoplankton, pollutants, bacteria toxins and suspended sediments from the water column, restoration work of oyster beds at a higher pace appeared to be a viable alternative to be included as a Best Management Practice. Evaluating substrates for oyster restoration as well as site locations via water quality parameter measurements in order to improve reproduction and survivability rates of restored oyster beds is critical for assessing and establishing future plans for TMDLs. Building statistical models to evaluate the environmental characteristics along with several of the tested substrates was the next logical step to be taken. The Factorial Model in this study will compare multiple variables that impact successful reproduction rates and rank the success rates in order to come to a resolution of which combination gives the highest probability of success with the ultimate goal of improving water quality in the process of implementable, scalable BMPs and TMDL subsets.

1.3 Objectives

- Assess existing TMDL data and BMPs in conjunction with water quality issues and oyster restoration in the Lynnhaven River System
- Collect ambient water quality data on oyster restoration sites
- State criteria for pre-site and site selection for restoration beds
- Define post-audit monitoring procedures to evaluate changes in water quality
- Develop statistical models relating oyster (*Crassostrea virginica*) biomass production in the Lynnhaven River System to different block- and treatment-level factor characteristics, and compare restoration effectiveness of natural reefs to constructed reefs
- Review existing TMDLs and BMPs for additions to and revisions on water quality management strategy based on results of model estimates and summarize revised recommendations

1.4 TMDL and Best Management Practices (BMPs)

Based on the latest 2012 State of the River Report published by Lynnhaven River Now, only 42% of the Lynnhaven River meets the shellfish standard. However, 90.4% of the river meets the swimmable/fishable standard (Grade C+). The goal is that the river meets 100% of the shellfish standard. In addition, the nitrogen and phosphorus levels (Grade D) are too high for sea-grass beds to survive and the goal is to meet the necessary requirements for the sea-grass beds to return. At this point, there are 7.9 impaired square miles (approximately 90% of the river) in Lynnhaven River based on the latest DO (dissolved oxygen) levels (Grade D). The goal is to have 0 impaired square miles. Needless to say, the sediment and algae levels are also too high which is impacting the water clarity as well (Grade F).

Some of the controls that have been put into place in the City of Virginia Beach to improve the water quality have been the No Discharge Zone implemented in 2007, sanitary sewer maintenance and improvement projects and stormwater improvement projects. In addition, four living shoreline projects were completed in 2012 as well as an additional 104 acres added to open space areas in order to increase the infiltration area for rainwaters. Stormwater runoff after rain events is the main carrier of pollutants through storm drains that dump directly into the river (Personal communication with Karen Forget, Lynnhaven River Now and Steve McLaughlin, City of Virginia Beach – Stormwater Management).

The No Discharge Zone for boaters has been in effect in the Lynnhaven River System for six years. In the summer of 2012, 2300 gallons were pumped out and this was a 62% increase over 2011. Since the beginning of the program, 8800 gallons of waste has been pumped out. Based on a study done by the Army Corps of Engineers, boat wastes registered Biochemical Oxygen Demand (BOD(5)) levels of 3200 mg/L, Chemical Oxygen Demand (COD) levels of 11,100 mg/L , 1660 mg/L of nitrogen and 117 mg/L of phosphorus. Each tank pumped equates to 30 to 50 gallons of waste. Assuming a 30-gallon tank was pumped out, this would equate to 188.5 grams of nitrogen and 13.3 grams of phosphorus removed each time. The City of Virginia Beach is pursuing the avenue of getting credit towards their Watershed Implementation Plan (WIP) for the annual removal of these boat wastes. The original Chesapeake Bay Watershed Implementation Plan was issued in January 2012. Appendix Q in this watershed plan details the requirements for each area (Personal communication with Steve McLaughlin, City of Virginia Beach – Stormwater Management).

Virginia Beach has also been working on replacing as many septic tank systems as possible, as well as expanding and improving sanitary sewer systems. Sixty projects were completed in 2012 with a total cost of $6.9 million. There were four sanitary sewer overflows during 2012 that equated to 4175 gallons (comparable to 2011). The next steps to be implemented are to continue with upgrading and expanding sanitary sewer systems and to insure that all pump stations have adequate back-up power (Personal communication with Steve McLaughlin – City of Virginia Beach – Stormwater Management).

By continually monitoring the bacterial levels in the Lynnhaven River System, it became apparent that the bacterial levels started rising again once the oyster beds were opened to harvest in 2007. This increase has continued and the action plan being put in place is to close these oyster beds again effective April 12th (2013) by an Executive Order. The criteria will be if 1 ½ inches of rain fall within a 24-hour period in the previous week, the area will be closed for the following 10 days and will re-open after bacteria testing is completed and has met an acceptable level. During May or June, this may be amended since the oyster harvesting season is at a peak level in this time frame (Personal communication with Steve McLaughlin – City of Virginia Beach – Stormwater Management).

Today in Virginia Beach, only 20% of stormwater is treated or retained before being dumped into the river. Three million dollars is being allocated annually in order to continue to do upgrades for stormwater treatment and retention ponds in this area. The State and Federal stormwater requirements are becoming more stringent, which is critical. Also, property owners may contribute to solving this problem by installing rain barrels, rain gardens, riparian buffers along the edge of their properties, as well as living shorelines. Educational programs have been implemented in the city in order to reach the community and make them aware of these options (Personal communication with Karen Forget – Lynnhaven River Now).

Since stormwater treatment is cost-prohibitive, a test site has been selected by the City at Milldam Creek due to extreme bacterial counts running in the ten thousand range and above. The goal is to reduce the nitrogen and phosphorus levels by placing a clarifier that will utilize flocculating agents in the stream and collect the sediments in a sedimentation chamber. The projected cost for this one site at an outfall is $700,000. It is hoped that this might correct the huge bacterial problem in this area (Personal communication with Steve McLaughlin – City of Virginia Beach – Stormwater Management).

Another project underway is some renovation work at the outfall locations in Virginia Beach. There is a total of 1050 outfalls in the Lynnhaven, 250 outfalls in Eastern Branch and 100 in the Little Creek area for a grand total of 1400 in the Lynnhaven River watershed. At this time, there is a substantial vertical drop from these outfalls in several locations and the water lands directly on a sediment base and scours out high volumes of sediments. This adds to the turbidity and TSS in the Lynnhaven River System and the plans are to have a concrete bottom placed at the outfalls in order to eliminate this problem. Since these areas are considered tidal waters that are under the jurisdiction of the United States, permits will be required in order to do this work. The plan is to continue and do this work in conjunction with developing goals for the WIP in this area.

Funding has also been allocated for 110 additional acres of sanctuary oyster reef construction within the Lynnhaven River System at an approximate cost of $125,000 per acre (Lynnhaven River Now, USACE Native Oyster Restoration Master Plan – March 2004). From past projects, 65 acres of sanctuary reef have already been placed in the Lynnhaven River System and this Native Oyster Restoration plan states that it will be necessary to continue to declare these areas as sanctuary reefs. It has been difficult to find a large enough area in the Lynnhaven due to the number of leases that have already been issued to commercial oystermen and landowners. Some of these legalities and permits may need to be researched in order to continue to expand these beds. There are also several narrow channels throughout the Lynnhaven River System that have been dredged by the Army Corps of Engineers and oyster restoration is prohibited in these areas. Other viable alternatives in these areas are living shorelines or floating reefs on homeowners' docks with their permission.

In order to evaluate the impact of oyster restoration, the City of Virginia Beach is working with the Army Corps of Engineers to coordinate a study that will determine how much TSS per acre is removed per oyster reef. This will be needed in order to determine the impact for inclusion in the final WIP plans for this area. This past year in the Long Creek area, *Spartina* grasses were planted and additional shell was added to build up an existing oyster bed. Also, an oyster castle reef has been placed in this area and has already experienced a high spat set (Lynnhaven River Now project). Oyster castles have also been showing success on the Eastern Shore in the Tidewater area. These are hopeful projects for inclusion in the plans for the final WIP.

Living shorelines appear to be one of the strongest possibilities to lower the high phosphorus and nitrogen counts in the Lynnhaven River System. They aid in protecting tidal shorelines from erosion by planting native wetland plants and grasses as well as shrubs and trees along the tidal water line. Bio-engineered materials such as manmade coconut-fiber rolls may be used to protect vegetation and soils. Where viable, oysters or riprap may also be included. These living shorelines improve water quality by settling sediments and filtering pollutants and toxins. They also help in re-establishing the natural shoreline around marsh areas that have been broken and separated by housing development and bulkheads being placed. This also cuts down and/or eliminates high dredging costs that are required in several of the narrow channels in the Lynnhaven River System (Personal communication with Steve McLaughlin – City of Virginia Beach – Stormwater Management).

Another natural innovation being tested by Virginia Tech as well as the Virginia Beach area are floating wetlands. Constructed of post-consumer polymer fibers, these floating wetlands are planted with native plants that act as a natural wetland to purify water. They have been shown to aid in the removal of total nitrogen, ammonia, phosphorus, BOD and TSS, all water quality parameters of concern. In the locations tested at Virginia Beach, birds and muskrats infested the floating systems and the muskrats destroyed the plants by consuming them. Additional sites are planned for trial since other areas of the country have experienced success with these systems (Personal communication with Steve McLaughlin – City Of Virginia Beach – Stormwater Management).

In other applications, these floating wetlands have been an enormous aid in locations experiencing high populations of waterfowl. Waterfowl populations in the Broad Bay area of the Lynnhaven are high and the sand sediments have reflected very high bacterial counts from these waterfowl. The 2004 TMDL also reflected that the waterfowl contributed 29% of the additional nutrients added to the Lynnhaven from the bacterial source tracking studies. Since this city is on the Inter-coastal Waterway along migration routes, it is not an option to taper down the waterfowl population. These floating wetlands are an option since they have been shown to act as a nesting area and have aided in biodegrading the waterfowl excrements before they enter the waterways.

Since some of the areas in the Lynnhaven River System have been experiencing phosphorus concentration readings as high as 1 to 2 mg/L , the City is also planning on implementing a fertilizer ban this year on any fertilizer containing phosphorus or any derivatives. Another plan being implemented this year to aid in nutrient removal is utilizing *Phragmites australis*, an invasive species to this area. It is a common large perennial grass found in wetlands since it tolerates brackish water. It grows 15 feet tall and has extremely deep roots as long as 15 to 20 feet deep which aid in combating soil erosion. It also naturally removes nitrogen and phosphorus from the soil. Thirty-three acres have been allocated to plant these grasses and it is anticipated to remove over 10,800 lbs of nitrogen (will decrease nitrogen input by approximately 10% - WIP goal is to reach removal rate of 126,300 lbs by 2017)) and 800 lbs (will decrease phosphorus input by 39% - WIP goal is to reach removal rate of 2220 lbs by 2017) of phosphorus by harvesting these grasses (Analysis of Harvested Wetlands Potential in Virginia Beach – URS Company – December 2012). The Environmental Protection Agency has a model that is run to determine the nitrogen and phosphorus load removal requirements for each area and it is scheduled to be re-run in 2017.

WIPs are the next step in progressing toward a restored Lynnhaven River watershed. These plans consider ecological restoration such as riparian buffers and living shorelines as well as promoting accountability for improved performance and sustaining previously attained levels of improvement. These WIPs are being developed in order to progress towards goals that will be finalized in a Federal TMDL in 2017. This TMDL will require annual reductions in nitrogen, phosphorus and sediment in each of the Bay's tidal segments, tributaries and embayments listed as impaired under 303(d) of the Clean Water Act.

CHAPTER 2

LITERATURE REVIEW

2.1 Total Maximum Daily Loads (TMDLs)

States are required to develop Total Maximum Daily Loads (TMDLs) for water bodies exceeding water quality standards. TMDLs quantify the total pollutant loading that a water body may receive without violating these standards. For this study, the most recent TMDL report for the Lynnhaven Bay watershed was obtained from the Virginia Department of Environmental Quality (VDEQ). The Lynnhaven River System has sections identified on the state's list of impaired waters. Restricted shellfish harvest areas that include the oyster beds in this study have been delineated and bacteria TMDLs established due to excessive levels of bacteria in these waters which are the main culprit for the water quality violations. In addition, the harvesting for market has been closed in order to protect human health. For the Lynnhaven, Broad and Linkhorn Bays, the Virginia Department of Health, Division of Shellfish Sanitation (VDH-DSS) describes these restricted areas in Notice and Description of Shellfish Condemnation Area 25, Lynnhaven River, Broad Creek and Linkhorn Bay (Effective 10 April 1998). The condemned areas (Figure 2-1) include all of the oyster bed locations included in this study – Long Creek, Linkhorn Bay and Eastern Branch.

First, the TMDL study determines the amount of pollutant reduction necessary to achieve water quality standards. Next, an implementation plan is developed to identify specific controls to aid in achieving the reductions. Included in these plans are timelines and cost estimates as well as potential funding sources. Finally, the plan is implemented, usually in steps, along with a monitoring program to review progress in the pollutant reduction. While in progress, changes may be identified in order to make continual improvements in the water quality. This is a form of adaptive management.

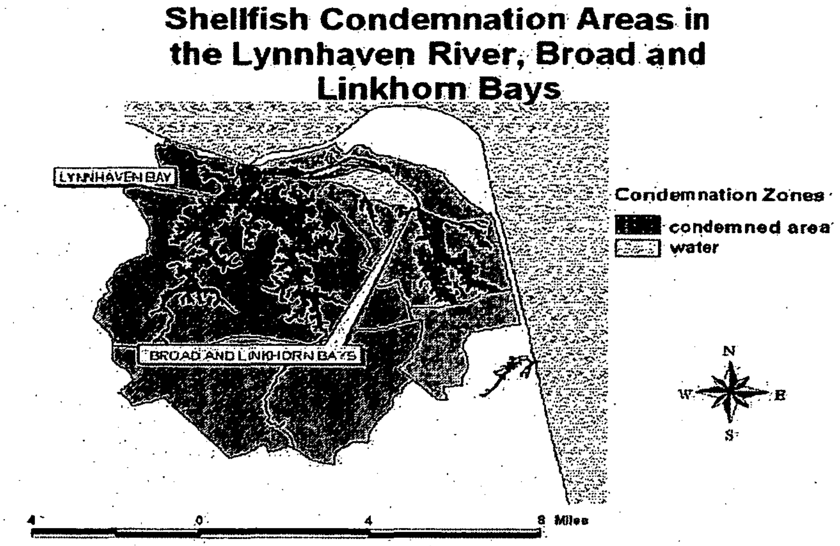

Figure 2-1. Shellfish Condemnation Areas in the Lynnhaven River System

Source – TMDL 2004

Several agencies (DEQ, VDH-DSS, Department of Conservation and Recreation (DCR), U.S. Geological Survey, U.S. Environmental Protection Agency (EPA) and state agencies) have worked together in developing a methodology for TMDLs in impaired shellfish waters. This method utilizes bacteria source tracking (BST) data to determine potential sources of fecal coliform in the water. This BST data provides information to aid in identification of bacterial pollution sources to target. For the Lynnhaven Bay, Broad and Linkhorn Bay area, the human contribution averaged 25%, with additional sources of 29% from birds, 17% from wildlife, 15% from livestock and 14% from pets. In addition to this BST data, VDH-DSS coordinates monthly monitoring and sanitary shoreline surveys (TMDL 2004).

While developing an overall TMDL process, seasonal and annual variations in precipitation, flow, land-use and pollutant contributions are taken into account. This ensures that violations do not occur under a wide variety of scenarios that impact bacterial loading in the waterway. In order to insure the health of human consumption of Virginia shellfish, VDH-DSS collects monthly samples at over 2,000 stations in shellfish growing areas of Virginia. Every 6 months the data are evaluated to see if water quality standards are being met. If exceeded, the shellfish area is closed to harvest for market and a shoreline survey is completed by DSS. Fecal coliform concentrations in water samples collected in the immediate vicinity of the shellfish beds aid in defining the borders between approved and condemned waters.

The shoreline survey is accomplished via a property-by-property inspection of on-site sanitary waste disposal facilities, un-sewered sections of the watershed, wastewater treatment plants (WWTP), marinas, livestock operations, landfills, etc. A written report is compiled and distributed to various state agencies that are responsible for correcting the identified concerns. There were some deficiencies noted as possible pollution areas in the Linkhorn Bay and Eastern Branch areas as well as some locations noted near Long Creek where there were no facilities and there was direct access to Lynnhaven Bay. The oyster bed locations in this study are close to these designated areas. The latest survey conducted prior to the TMDL was in February 1997 and identified 26 sanitary sewage deficiencies, 7 industrial waste, 1 solid waste dumpsite, 7 boating related sources, 2 sites with a potential for pollution and 3 animal waste sources. The shoreline survey is the primary source for indications of non-point sources of pollution in the watershed. Non-point source contributions to bacterial levels in Lynnhaven Bay from human sources generally arise from failing septic systems and associated drain fields, moored or marina vessel discharges, stormwater management facilities and pump station failures. The largest concentration of septic systems and drain fields for water treatment in a suburban home area in Lynnhaven Bay is at Little Neck Point (TMDL 2004).

In addition to the shoreline survey, DSS also collects water samples in the oyster bed areas. The most recent 30 samples collected randomly with respect to weather are utilized to assess each sampling location. In Virginia, there is a two-part standard for fecal coliforms in water near direct shellfish harvest for market – (1) a geometric mean no greater than 14 MPN (Most Probable Number) fecal coliforms/100 ml and (2) an estimated 90th percentile no greater than 49 MPN/100 ml. Exceeding either requirement requires closure in Virginia. Most of the high fecal coliform counts in this state are due to runoff from development, agriculture and livestock operations, or from wildlife (Lynnhaven Bay, Broad Bay and Linkhorn Bay Watersheds Total Maximum Daily Load (TMDL) Report for Shellfish Areas Listed Due to Bacteria Contamination, VDEQ March 2004). In the time frame of this study, the data reflected that the bacterial levels were above the 90th percentile for all of the shellfish condemnation areas in the Lynnhaven Bay watershed.

Most of the coastal areas along the Atlantic Ocean have experienced a high level of development and the Lynnhaven Bay, Broad Bay and Linkhorn Bay watersheds are no exception. The TMDL 2004 sampling completed in these areas reflected bacterial levels above the 90th percentile in all collection sites in the Lynnhaven and the majority of sites in Broad Bay and Linkhorn Bay. All of the bacterial readings exceeding the criteria are reflected in bold print (Table 2-1).

Table 2-1. Lynnhaven, Broad & Linkhorn Bay Bacterial Water Quality Data Summary January 2001 to February 2003

Station Lynnhaven	90th Percentile Preceeding 30 Months	Water Quality Standard	Station Meets Standard?	Geometric Mean Preceeding 30 Months	Geometric Mean Standard	Station Meets Standard?	Current Condemnation
225A-1	**68.4**	49	No	11.4	14	Yes	Yes
25A-2*	**111.7**		No	**16.8**		No	Yes
25A-2Z	**103.0**		No	13.6		Yes	Yes
225A-3*	**259.0**		No	**27.2**		No	Yes
25A4	**190.1**		No	**24.7**		No	Yes
25A-4_3	**258.0**		No	**31.6**		No	Yes
25A-4_9	**164.1**		No	**14.7**		Yes	Yes
25A-5	**143.3**		No	**19.2**		No	Yes
25A-7*	**209.7**		No	**21.0**		No	Yes
25A-8	**332.7**		No	**27.1**		No	Yes
25A-9*	**306.8**		No	**30.5**		No	Yes
25A-10*	**368.0**		No	**30.2**		No	Yes
25A-11*	**182.9**		No	**27.1**		No	Yes
25A-12*	**569.1**		No	**41.7**		No	Yes
25A-15	**116.6**		No	**14.5**		Yes	Yes
25A-16*	**195.1**		No	**18.7**		No	Yes
25A-17	**230.0**		No	**20.4**		No	Yes
25A-18	**265.7**		No	**20.2**		No	Yes
25A-24*	**445.0**		No	**36.3**		No	Yes
25A-25*	**760.7**		No	**52.6**		No	Yes
Average	**264.0**			**25.0**			

*Bacterial Source Tracking Stations; Source – TMDL 2004

Table 2-1. Lynnhaven, Broad & Linkhorn Bay Bacterial Water Quality Data Summary January 2001 to February 2003 (Continued)

Station Broad Bay & Linkhorn Bay	90th Percentile Preceeding 30 Months	Water Quality Standard	Station Meets Standard?	Geometric Mean Preceding 30 Months	Geometric Mean Standard	Station Meets Standard?	Current Condemnation
25B-1*	**54.8**	49	No	10.2	14	Yes	Yes
25B-1_6	**51.9**		No	10.5		Yes	Yes
25B-2	**52.7**		No	9.6		Yes	Yes
25B-3	**66.1**		No	10.2		Yes	Yes
25B-3Z	37.2		Yes	7.9		Yes	No
25B-4	**62.4**		No	8.0		Yes	Yes
25B-4A	**209.4**		No	**22.0**		No	Yes
25B-4B	**443.9**		No	**30.9**		No	Yes
25B-4C	**287.0**		No	**24.3**		No	Yes
25B-4U	**187.2**		No	10.2		Yes	Yes
25B-4V	23.8		Yes	5.8		Yes	No
25B-4W	32.7		Yes	7.4		Yes	No
25B-4X	13.4		Yes	4.0		Yes	No
25B-4Y	**61.1**		No	12.3		Yes	Yes
25B-4Z	34.4		Yes	8.6		Yes	No
25B-5	44.7		Yes	7.8		Yes	No
25B-5Z	29.1		Yes	5.7		Yes	No
25B-6	46.3		Yes	7.6		Yes	No
25B-7	**59.9**		No	8.6		Yes	Yes
25B-8	36.7		Yes	7.5		Yes	No
25B-9	**72.2**		No	9.8		Yes	Yes
Average	**90.17**			10.9			

*Bacterial Source Tracking Stations; Source – TMDL 2004

The Lynnhaven watershed was chosen for this study due to its high success rate historically with oyster production (Chipman, 1948) and the fact that collocated oyster beds utilizing various alternative substrates had been tested in this area (Burke, 2010). This watershed is characterized as highly urbanized and densely populated. Population density ranges from 0 to 38 persons per hectare (2.2 acres). Less than 25% of the watershed comprises undeveloped land such as forest, wetland, urban grassland or water. Approximately 75% is developed as residential areas, streets, commercial and office space or military use (Table 2-2).

Table 2-2. Land use in the Lynnhaven, Broad & Linkhorn Bay Watershed

Land Use Category	Area (acres)	Area (%)
Single Family/Duplex	15078	37%
Town House	768	2%
Multi-family	1551	4%
Commercial	1806	4%
Office	652	2%
Industrial	457	1%
Military	2393	6%
Streets	5178	13%
Public/Semi-public	2662	7%
Park	2876	7%
Agriculture-cropland	1717	4%
Agriculture-pasture	248	1%
Marsh/wetland	1711	4%
Approved f/development	6	0%
Undeveloped	3580	9%
Total Area	40683	100%

Source: Virginia Beach Department of Public Works (Included in TMDL 2004)

The drainage area encompasses approximately 40,683 acres or 64 square miles and the nearest climate station is located at Cape Henry in Virginia Beach (2 miles east of study area). The 30-year average annual rainfall recorded at Cape Henry is 41.32 inches (Table 2-3).

Table 2-3. Climate Data for Cape Henry City Virginia Beach, Virginia (441362)

	Jan	Feb	Mar	Apr	May	Jun	Jul	Aug	Sep	Oct	Nov	Dec	Annual
Avg Max Temp	48.3	49.1	55.1	65.3	72.7	80.5	85.0	83.7	77.8	68.0	59.6	50.4	66.4
Avg Min Temp	35.0	35.0	40.3	49.4	58.0	66.5	71.2	70.9	66.6	56.8	46.4	37.0	52.8
Avg Tot Precip(in)	2.81	3.17	3.04	2.67	3.26	3.84	4.65	5.68	3.54	3.04	2.54	3.05	41.32
Avg Tot Snowfall(in)	2.1	1.2	0.5	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.9	4.8

Source: Southeast Regional Climate Center, ***sercc@dnrstatesc.us***
(Included in TMDL 2004)

2.2 TMDL Development

Several agencies (including EPA, Virginia DEQ, Virginia Department of Conservation & Recreation (DCR), Maryland Department of the Environment (MDE), Virginia DSS, Virginia Institute of Marine Sciences (VIMS), United States Geological Survey, Virginia Polytechnic University, James Madison University and Tetra Tech) composed the shellfish TMDL group and developed a procedure for developing TMDLs using a simplified approach. The initial step was to utilize BST data along with shoreline surveys and other information such as water quality data to determine the sources of fecal coliform violations and the needed load reductions to reach the established criteria.

The source of loading from all anthropogenic sources is called Waste Load Allocation (WLA) and is regulated by the Clean Water Act and the Department of Environmental Quality (DEQ). The formula utilized for the relationship between Total Load Allocation (TLA) and Load Allocation (LA) is:

Total Load Allocation = Waste Load Allocation (WLA) + 5% Margin of Safety (MOS)
+ Load Allocation (LA)

In an urbanized setting such as Virginia Beach, an averaging approach is utilized based upon land-use and average impervious area by land use type. This was the approach adopted for this TMDL metric.

Figures were recently updated in the '2012 State of the River Report' published by Lynnhaven River Now (Table 2-4). The impervious areas (rooftops, driveways, parking lots, roadways) comprises approximately 38%. In addition, 30% is managed turf, which only leaves 32% of the watershed with optimal rainwater filtration.

Table 2-4. Average Impervious Area in Lynnhaven, Broad & Linkhorn Bay Watershed

Land Use Type	Acres	Percent of Land Area	Percent Impervious
Single Family/Duplex	15078	37%	20%
Town House	768	2%	50%
Multi-family	1551	4%	70%
Commercial	1806	4%	70%
Office	652	2%	70%
Industrial	457	1%	65%
Military	2393	6%	50%
Streets	5178	13%	90%
Public/Semi-public	2662	7%	8%
Park	2876	7%	2%
Agriculture-cropland	1717	4%	2%
Agriculture-pasture	248	1%	2%
Marsh/wetland	1711	4%	2%
Approved f/development	6	0%	2%
Undeveloped	3580	9%	2%
Total Area	40683	100%	
Avg. Impervious %			34%

Source: Virginia Beach Department of Public Works (Included in TMDL 2004)

2.3 Best Management Practices (BMPs)

The U.S. Army Corps of Engineers (USACE) along with its partners has evaluated 8 sites in Virginia for their potential to support large-scale oyster restoration utilizing salinity, dissolved oxygen, water depth and hydrodynamic criteria in their Native Oyster Restoration Master Plan (March 2012). Tier 1 tributaries were the highest priority and demonstrated the historical, physical and biological attributes necessary to provide the highest potential to develop self-sustaining oyster populations. The Lynnhaven River System was one of these identified target areas. A Best Management Practice recommended in this document is to establish these restoration areas as long-term sanctuaries in order to enable long-term growth and an increase in size of the oysters to facilitate developing disease resistance. Additionally, the USACE supported efforts to establish harvest reserves within proximity of sanctuaries to provide support to the seafood industry via expansions in aquaculture operations. Subsequently, a temporary harvest moratorium on native oysters would be put in place.

Due to the perceived lack of a sufficient supply of oyster shell for oyster restoration, the USACE recognized that alternative substrates would need to be a part of large-scale restoration. It was also recognized that poor land management and further declines in water quality would only jeopardize any future gains accrued via oyster restoration. The nutrient reduction goals established in the Lynnhaven Bay TMDL will be critical in addressing water quality issues. Historically, the oyster served as Chesapeake Bay's primary filter-feeding organism. The loss of its filtering capacity coupled with ongoing anthropogenic pollution has had a profound negative effect on the entire Chesapeake Bay ecosystem (USACE Native Oyster Restoration Master Plan – March 2012; Hargis and Haven, 1999).

2.4 Study Sites

This study utilized data that were shared from a previous dissertation on "Alternate Substrates as a Native Oyster (*Crassostrea virginica)* Reef Restoration Strategy in Chesapeake Bay" (Burke, 2010). In addition to the oyster data compiled from this previous study, water quality data and the latest TMDL study (Lynnhaven Bay, Broad Bay and Linkhorn Bay Watersheds Total Maximum Daily Load (TMDL) Report for Shellfish Areas Listed Due to Bacteria Contamination – Virginia Department of Environmental Quality (VDEQ) – March 2004) was obtained from VDEQ and bacterial counts from DSS (Virginia Department of Health – Division of Shellfish Sanitation). The actual locations utilized for these alternative substrate sites were at Long Creek, Eastern Branch and Linkhorn Bay (Figure 2-2). Based on the TMDL data, all of these shellfish beds are in the areas that have been condemned (Figure 2-1).

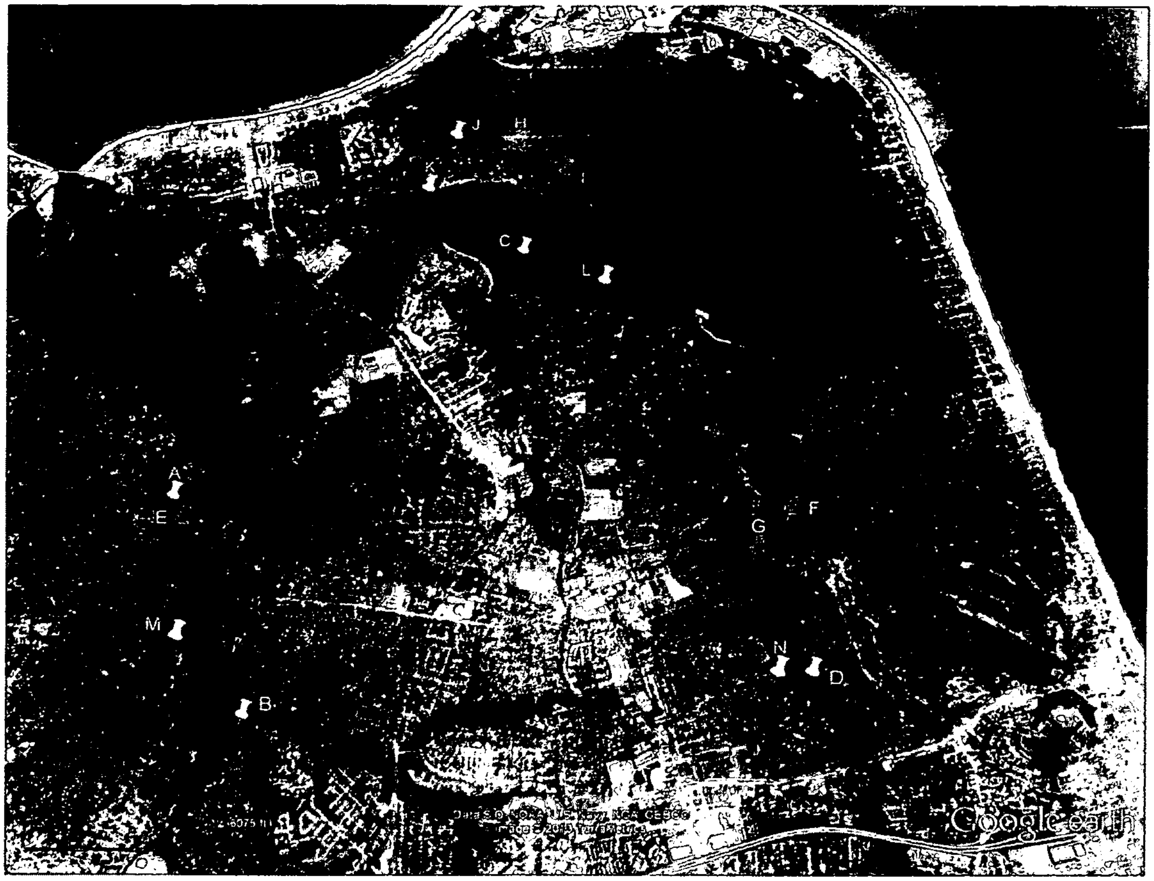

Figure 2-2. Locations of Reefs (Red), DEQ Stations (Yellow), DSS Stations (Green)

Map ID	Location	Station Number	Longitude	Latitude
A	Eastern Branch DEQ	7-EBL001.15	36.873611	-76.073611
B	Eastern Branch DEQ	7-EBL002.54	36.855556	-76.063889
C	Long Creek DEQ	7-BBY002.88	36.897500	-76.037778
D	Linkhorn Bay DEQ	7-LKN002.77	36.858611	-76.009444
E	Eastern Branch DSS	70-25	36.871317	-76.072371
F	Linkhorn Bay DSS	71-9	36.871886	-76.010225
G	Linkhorn Bay DSS	71-10	36.868485	-76.013922
H	Long Creek DSS	71-4Y	36.909376	-76.038541
I	Long Creek DSS	71-4Z	36.906033	-76.033156
J	Long Creek Reef Site		36.91048	-76.04602
K	Long Creek Reef Site		36.90428	-76.04892
L	Long Creek Reef Site		36.89414	-76.02883
M	Eastern Branch		36.86161	-76.07137
N	Linkhorn Bay		36.85850	-76.01278

The Long Creek site included a natural marsh area, an existing oyster reef and two riprap sites. At each of these locations , there were six substrate classes placed in individual trays.

CVS = Small Pieces of Recycled Concrete
GL = Large Granite
GS = Small Granite
LML= Large Limestone Marl
LMS = Small Limestone Marl
OSU = Unconsolidated Loose Oyster Shell

Each location contained three replicates of each substrate. In order to evaluate the impact of predation on each site, a caged and non-caged option was deployed for each of the replicates for a total of six samples for each substrate.

The Living Shoreline sites were located at homeowners' shorelines – one in Eastern Branch and the other in Linkhorn Bay. Nine reef structures were erected at each site in July 2006. It included three oyster shell, three riprap and three concrete modules. Instead of the caged option tested at Long Creek, these sites compared seeded and unseeded alternatives. At Linkhorn Bay, cinder blocks were later included as an additional incidental substrate. Additionally, six reefballs were added late (September 2006) in the project at both Linkhorn Bay and Eastern Branch. Unfortunately, the reefballs had to be destructively sampled in order to count the live and dead shells and this was only done at the end of the experiment. With only a single sampling period at the end of the experiment, these data did not meet the modeling criteria and were removed from the modeling component of this study.

CHAPTER 3

OYSTER RESTORATION AS WATER QUALITY IMPROVEMENT

3.1 Desired Conditions for Oyster Restoration

Oyster reef restoration is being initiated in order to replace or maintain critical ecosystem functions and communities, and to improve water quality. Local, state and federal government agencies as well as volunteer groups and universities have developed restoration plans. In order to design a successful plan, biological (habitat), physical (topography, sediment type, tides, turbidity), chemical (salinity and dissolved oxygen) and hydrological (water flow) characteristics that influence the survivability of the oyster need to be monitored to ensure conditions are favorable for successful restoration. State public health departments monitor potential shellfish growing waters in order to insure safe consumption by the public. If high bacterial levels (*Escherichia coli* or *Vibrio vulnificus*) or specific toxins are detected, then the waters are restricted from harvesting (Coen and Luckenbach, 2000).

Considering the desired conditions, the Eastern oyster (*Crassostrea virginica)* initiates spawning at temperatures between 20 to 25 degrees Celsius or salinity cues > 10 practical salinity units (psu). This typically happens between June and October in lower Chesapeake Bay. Reduced initial settlement of oysters may result from physical processes such as turbulence and water flow (Kennedy *et al.*, 1996). In addition, oyster shell reefs with larger interstitial spaces may be more accessible to fish and crab predators. However, the larger predators prey on smaller, intermediate predators of the oyster and actually create a safe haven in the reef for the young oysters. Decapods such as blue crabs (*Callinectes sapidus*) and mud crabs (*Panopeus herbstii*, etc.) are major predators of the oyster and can cause high levels of mortality in juvenile oyster populations. Crabs usually chip the valve margins to gain access. Overall, the complexity of the reef reduces the predator's efficiency as well as the encounter rate

(Grabowski, 2005). Additionally, utilizing reef balls to surround existing oyster reefs aids in reducing predator access especially to the older oyster population at the base of the reef and also places roadblocks to poachers for access to the reef (Personal communication Tommy Leggett – Chesapeake Bay Foundation). Some of the major triggers for improving oyster survivability and water quality are detailed below.

3.1.1 Habitat

Oyster reefs are formed as individual oysters stack and form layers of multiple generations that create a complex interstitial three-dimensional structure in intertidal or subtidal zones, and fringing or patch reefs that vary in size from 10 to 1000 square meters. The reef size continues to increase as multiple classes of oysters accumulate and form micro-habitats for multiple species. Restoration has depended on the natural development of biofilms which induces the settlement of the oyster larvae, however, utilizing extracts or synthetic peptides may be an avenue for enhancing larval settlement in future restoration projects (Coen and Luckenbach, 2000).

Additionally, the interaction among several species in the oyster reef environment is also critical. Barnacles appear to improve the attachment rate of oysters by increasing the surface roughness as well as excreting a chemical cue that attracts oysters to their location. In addition, they have a fanlike mechanism for feeding that brings food particles closer to the immobilized oyster. Yet, barnacles compete for food and surface space on the oyster shell (Barnes *et al.*, 2010). Oysters are a large part of the blue crab's diet and the presence of blue crabs definitely increases the mortality rates on these reefs. Also, mussels out-compete the oysters for substrate space. Blue crabs and mud crabs are the natural predators for mollusks and juvenile oysters whose shells are still fragile (<15 mm shell height) (Nestlerode *et al.*, 2007). It would be best to select a site with lower quantities of blue crabs and mussels, if possible.

3.1.2 Temperature

Extreme exposure to high temperatures is likely to have profound effects on oysters, particularly in regard to reproduction, disease susceptibility, and responses to anthropogenic stressors. Elevated temperatures have been shown to increase oyster susceptibility to the two major oyster diseases, Dermo and MSX (Andrews, 1996). Both diseases infect oysters during their first year and cause high mortality rates. This particularly occurs during drought or low flow years (Stroupe and Lynn, 1963). Additionally, subtidal rather than intertidal (> 2m) oysters may be more adversely affected by such extreme environmental fluctuations due to anoxic condition (Restoration Monitoring of Oyster Reefs).

Finally, water filtration and other oyster physiological processes are highly dependent on water temperature. Summer rates of filtration are substantially higher than the rest of the year (Newell and Langdon, 1996). Temperature measurements between 20 to 25 degrees Celsius are usually the most favorable environment for oysters.

3.1.3 Salinity

Oyster reefs may be found in a wide salinity range (12 psu to 28 psu). Extreme fluctuations may affect survival, growth and distribution of oysters as well as associated macro-invertebrates. Dermo disease increases during periods of high salinity (>15 psupsu).

This usually happens in an estuary during the summer when severe storms are frequent or during periods of low rainfall (Andrews, 1996. Simulations on environmental impacts to the Eastern oyster, *Crassostrea virginica*, revealed that salinity is the primary factor controlling the spatial degree of oyster distribution. Salinity plays an important role during oyster spat development and needs to be closely monitored during restoration activities (Restoration Monitoring of Oyster Reefs).

Also, the salinity may vary substantially from the mouth of the river to upstream locations. It is anticipated that upstream flow rates would tend to be slower and the salinity would increase towards the Bay.

3.1.4 Dissolved Oxygen (DO)

Dissolved oxygen is an important parameter in assessing water quality and a certain level needs to be maintained for most aquatic organisms to survive. Oxygen is utilized for respiration and for the cycling and recycling of organic carbon. The concentration of DO is considered a key indicator of the health of an estuary. When DO concentrations are too low, organisms become stressed and may be unable to grow, feed or reproduce properly. DO concentrations above 5 mg/L are considered suitable to sustain healthy communities. However, concentrations below 2.8 mg/L are considered hypoxic (low in oxygen) and usually create stress on the oyster (Cerco *et al.*, 2005).

3.1.5 Total Suspended Solids (TSS)

Due to the natural variability in physical characteristics, total suspended solids must be determined for each differing body of water and is site-specific. The amount of suspended material in the water column may indicate potential silt problems and/or food availability (phytoplankton). Though oysters filter water and improve its quality, an increase in turbidity can negatively influence oyster reef growth and survival. Sediment increase in the water column caused by high energy tides can smother oyster larvae as well as disturb the filter feeding process of oysters. Sources that increase sediments and turbidity are agriculture, forestry, mining, road construction and urban activities. Additionally, oyster reef communities are negatively impacted by excess nutrients from runoff, which promotes algae growth and again increases turbidity. Algal blooms deplete oxygen and limit sunlight for other vegetative species near the oyster reefs (Restoration Monitoring of Oyster Reefs).

3.1.6 Density

Oyster density (number of live oysters per unit area) is a common measurement utilized to assess reef restoration success. Usually a sample of known dimensions is excavated (10 to 15 cm) using a quadrat or a core. Then, all the live and/or dead oysters are counted. Samples are collected from different reef elevations (reef crest, slope and base). Size frequency distributions as well as survival and mortality rates may be derived from these same density samples (Cerco *et al.*, 2005). In studies of the native Eastern oyster in the James River (Mann *et al.*, 2009), the following equations were utilized for survival and mortality in cohorts with more than two successive years.

$$\text{Survivorship} = \#\text{Live}_{(\text{time}+1)}/\#\text{Live}_{(\text{time})}$$

$$\text{Mortality} = [\#\text{Live}_{(\text{time})} - \#\text{Live}_{(\text{time}+1)}]/\#\text{Live}_{(\text{time})}$$

A possible error inherent in this approach is classifying oysters in an incorrect year class based on an age to length relationship. This would cascade through each year class.

3.1.7 Depth

Oyster restoration appears to be more successful in shallow regions with limited circulation rather than areas of greater depth, larger water volume and greater spatial extent. Reefs in shallow, semi-enclosed regions appear to reflect greater benefits. Most of the planned restoration areas occur in water depths ranging from 3 to 5 feet in the intertidal range (Oyster Reef Restoration). An exception recently has been the sub-tidal reefs rejuvenated in the Great Wicomico River in Virginia. Juvenile recruitment was higher and oyster density was four-fold greater on high-relief reefs. This re-established meta-population was the largest of any native oyster world-wide and validates continuing oyster restoration. With better site selection in a hydrodynamically restricted area and construction methods utilizing significantly more shell substrate per unit area of bottom, the higher relief reef (as high as 45 cm) allowed for enhanced recruitment, reduced sedimentation and higher survival of recruits (Schulte *et al.*, 2009).

3.1.8 Reef Size

Reef area is important for oyster production and its associated communities. The perimeter of intertidal reefs may be measured by walking the edge of the reef with surveying equipment. Sub-tidal reefs may be mapped by digital side-scan sonar, towed video and diver sampled quadrats. Images may be processed to reflect the percent of coverage by oyster clusters and shells. Data may be integrated into a Geographical Information System (GIS) and changes in reef size may be followed over time (Hargis and Haven, 1999).

Originally, scientists assumed that the larger reef would provide higher production levels. Now it appears that, with the dispersion capabilities of spat, high production levels may be reached by grouping smaller reefs together allowing for high spat production and dispersion to the surrounding reefs as well as the shoreline (USACE Native Oyster Restoration Master Plan, 2012).

Additionally, reducing the reef height impacts water flow by decreasing speeds. Due to this reduction, sedimentation increases and reduces the quality of suspended food for oysters which impacts their health and mortality rates. Oyster reefs improve water quality by filtering suspended solids and nutrients in addition to altering hydrology patterns that also assist in removing particulate and organic material (Hargis and Haven, 1999). Lenihan and Peterson (1998) created sub-tidal reefs that varied in morphology, water depth and location on the Neuse River in North Carolina. It demonstrated that the oyster's survival varied with reef height, position and depth in relation to flow velocity, sedimentation rate and dissolved oxygen levels. This indicated that prior knowledge of hydrographic conditions (sedimentation, current velocities, temperature and density stratification, and oxygen levels) was a critical requirement.

3.1.9 Population/ Class Size

Oyster population size is determined by measuring the shell length of each oyster shell within a collected sample. Typically these are the same samples utilized to determine oyster density. The individual lengths are then grouped into size classes and used to estimate size class (age) changes over time (Oyster Reef Restoration).

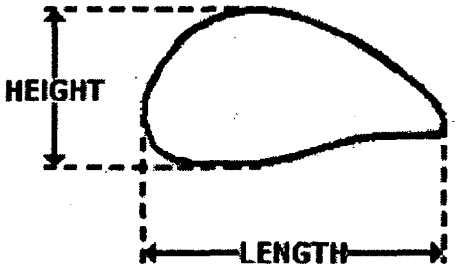

Figure 3-1: Measuring an Oyster

Juvenile oysters typically have a shell height less than 30 mm, while young oysters are typically less than 15 mm. Oysters larger than 30 mm are considered adult oysters. Oyster shell height is measured from the hinge to the ventral shell margin (Nestlerode *et al.*, 2007). A newer approach to evaluating the population size is utilizing a ratio of the shell length to shell width (Harding et al., 2008) which gives a truer indication of the shell size and the oyster body dimensions.

Additionally, in previous studies (Coen & Luckenbach, 2000 and Walters & Coen, 2006), concurrent samples were collected from adjacent natural and experimental reefs on various substrates in order to compute sample variance estimates between sites. This design allowed an evaluation of convergence (or divergence) of the natural and experimental reefs over time. Oyster densities taken over 3 years on experimental reefs only reached 23% (averaged across replicate reefs) of the adjacent natural reefs. Maximum shell heights reached 70 to 98 mm on experimental reefs versus 103 to 136 mm on the natural reefs.

3.1.10 *E. coli*

Specific guidelines have been issued in the state of Virginia for evaluating water quality in shellfish bed areas. The most recent 30 samples, collected randomly by DSS with respect to weather, are utilized to assess each sampling location. In Virginia, there is a two-part standard for fecal coliforms in water near direct shellfish harvest for market – (1) a geometric mean no greater than 14 MPN (Most Probable Number) fecal coliforms/100 ml and (2) an estimated 90th percentile no greater than 49 MPN/100 ml. Exceeding either requirement requires closure in Virginia. Most of the high fecal coliform counts in this state are due to runoff from development, agriculture and livestock operations, or from wildlife. Based on the BST studies conducted for Lynnhaven Bay, Broad and Linkhorn Bay area, the human contribution averaged 25%, with additional sources of 29% from birds, 17% from wildlife, 15% from livestock and 14% from pets. In 2007, new guidelines were issued for saline waters to utilize *Enterococci* counts instead of *Escherichia coli.* For this study, both *Escherichia coli* and *Enterococci* counts were included in the model.

3.2 Substrates

For this project, the alternative substrates being reviewed include concrete, granite, limestone marl, cinder blocks and rip-rap in combination with oyster shell. The most desirable material utilized in oyster reef construction in the past is empty *Crassostrea* *virginica* shell obtained from local shucking operations, restaurants or historic deposits of oyster shell reefs. When piled in mounds, these shells form an interstitial matrix of voids that provide a settlement habitat as well as a refuge from predation (Nestlerode *et al.*, 2007). Since the British Petroleum Gulf oil spill, shortages of oyster shell have prompted examining suitable alternative substrates. The results are relevant to future design strategies in oyster reef restoration. Through the oysters' natural filtering processes and a number of important coastal system ecological roles, the water body and the surrounding habitat is rejuvenated.

Previously, one material commonly used as an alternative was Surf clamshell (*Spisula solidissima*). The main disadvantage was that the shells easily fractured either from deliberate crushing to compact the material or unintentionally through repeated handling. These crushed pieces packed together tightly and offered limited surface area and interstitial space. In Nestlerode's study, a reef was constructed at Goodwin's Island of Surf clamshell and a second reef at Fisherman's Island with oyster shell. Oysters were consistently more abundant on the oyster shell than on the clamshell reef. In addition, the oysters were smaller and few survived to sizes larger than 30 mm. Usually the base of an oyster reef becomes encrusted with a continuous veneer of oysters which never formed on the clamshell reef (Nestlerode *et al.*, 2007).

Some successful alternative substrates utilized have been buoys and floating oyster reefs used in an aquaculture environment as well as castles, reef balls and limestone marl in sub-tidal and intertidal areas. By attaching netting, with oysters and spat, to a buoy, the oysters reproduced and utilized the buoy as a substrate. This has been utilized in Korea as well as the United States.

One of the best man-made substrates is oyster castles which are multi-surfaced building blocks composed of a mixture of concrete, crushed shell and lime. In a project on Eastern Shore in an intertidal zone, these castles are typically covered with oyster shell within three years (Personal Communication with Barry Truitt - The Nature Conservancy). An additional man-made structure, the reef balls, have been placed at project locations in 59 countries and have planned projects in another 11 countries. High reproductive rates have been experienced in Florida on reef-ball reefs (Reef Ball Foundation). Recently, this past summer, an established oyster shell reef in the

Piankatank River (Chesapeake Bay region) was partially encircled with 150 reef-balls and will be completely encircled with 300 by the end of this summer. Another new reef location is in the planning stages and will be placed in the Elizabeth River.

Reef balls are constructed hollow domes with holes that are installed on the ocean bottom in order to create a reef habitat. These balls provide a hard surface for attachment and decrease the amount of natural shell required to create the reef. Reef balls assist in reducing oyster poaching, which is still an issue on oyster reefs designated as sanctuaries (Reef Ball Foundation). Reef ball modules are constructed using a fiberglass mold and a special concrete mix which reduces the concrete pH to that of natural seawater. Approximately 180 kilograms (400 lbs) of biomass are produced annually on each module. The textured surface of the ball and the pH modification enhances oyster larvae and other marine life attachment. Reef balls can also be used together to create submerged breakwaters in addition to re- establishing oyster reefs, coral reefs and mangrove trees (Harris, 2009; Reef Ball Foundation).

The oyster farmer's use of floating oyster reefs as a form of oyster aquaculture is increasing and preferred over the standard substrate reefs located on the water body. The method includes connecting mesh bags to flotation devices which remain just below the water surface. The positioning in the water column created by the floats increases the sunlight and algae surrounding the oysters. Additionally, suspending the oysters reduces their susceptibility of contracting Dermo and MSX and decreases their predation by crabs and other bottom dwellers. In terms of growing area, the floating reef significantly decreases the amount of area required. Pacanowsky states that these floating reefs increase production from the "Chesapeake Bay average of 12 ½ oysters per acre to 1,000 oysters in only 30 square feet" (Pacanowsky, 2009). Although, research at Virginia Tech is ongoing, it is anticipated that each float containing approximately 1500 three inch oysters is able to filter approximately 1.77 pounds of nitrogen and 1.43 pounds of phosphorus (Pacanowsky, 2009). Currents and waves increase the flushing impact by supporting dissolved oxygen and nutrient levels (Forrest *et al.*, 2009).

A new Best Management Practice is being considered in order to maintain natural oyster reefs as declared sanctuaries. Oystermen may possibly be trained on aquaculture and the floating reefs used as a food source rather than continuing to harvest from the natural ones (USACE Native Oyster Restoration Plan, 2012).

Limestone marl, a combination of limestone and fractured pieces of shell, was utilized to build mounds for oyster restoration at Ocracoke in 2005. The oyster recruitment was so successful that the individual pieces of marl are no longer distinguishable. Due to this success, a new project is underway at Belhaven, North Carolina. The $5 million federal economic stimulus grant is being funded by the National Oceanic and Atmospheric Administration (NOAA). The plans are to utilize the limestone marl along with shell plantings to build as well as monitor approximately 47 acres of oyster reefs in Pamlico Sound (Miller, 2009).

CHAPTER 4

METHODOLOGY

4.1 Procedures/Methodology

4.1.1 Pre-Site Survey

The Initial Step-Site Selection: Most project organizers have a general idea where the reef will be placed. It is best to start the study with a mariner's chart (http://www.navquest.com). In addition, Google Earth ™ provides satellite images of various details anywhere on earth and the government has developed Geographical Information System (GIS) databases that are helpful. Other critical information includes currents, wave heights and tidal ranges. Tides play a significant role in delivering nutrients as well as acting as a flushing system. Oyster reef survival is highest in areas where bottom currents transport feces and bio-deposits away from the reef. Additionally, tides promote oyster settlement and growth by transporting oyster larvae great distances (Restoration Monitoring of Oyster Reefs). Questioning local people who spend time on the water, such as fishermen and boat captains, may also reveal some of the variable, seasonal and site specific data that might be an aid for the project. Were there oyster beds in this area previously? If so, what caused their demise? Were there any previous cases of diseases (such as Dermo or MSX) or any problems with water quality? Historical data about the area would be invaluable. After completing this initial evaluation, utilize a map and block out any areas that may be eliminated upfront (Reef Ball Foundation).

Also, the Environmental Protection Agency (EPA) has compiled a list of additional areas that need to be excluded:

1. Shipping lanes
2. Restricted military areas
3. Areas of poor water quality (low dissolved oxygen, dredged material disposal sites, sewer outfalls, river drainage, and other point sources of pollution)

4. Traditional trawling grounds
5. Unstable bottoms
6. Areas with extreme currents or high wave energy
7. Existing right-of-ways (Oil and gas pipelines and telecommunication cables)
8. Sites with purposes incompatible with reef development (such as aquaculture)

Any marginal areas should also be eliminated. Local restrictions and designated marine reserves need to be investigated since they may require special permits, which could be difficult or impossible to obtain. In addition, it is best to avoid areas of existing healthy reefs or sea grass beds, especially downstream from new aquaculture sites due to the heavy excrement load (Hargis and Haven, 1999).

4.1.2 Site Survey

The next site survey step includes a visual survey from a boat along the shoreline in order to verify the substrate quality (rip-rap, bulkheads, oyster shell, sand, marsh) for possible oyster attachment. This would also be the time to survey the physical characteristics and water quality in the area of the site. Preferably, surface water samples and species samples (with nets or benthic grab samplers) would be taken at sporadic locations along the coastline to be evaluated. A Dataflow might be utilized to collect water parameter data. Readings will be taken on water temperature, salinity, dissolved oxygen levels (DO), chlorophyll a and pH at ebb tide and at different depths. Surface water samples for chlorophyll analysis will also be taken to duplicate the results seen with the Dataflow equipment. Nitrogen, phosphorus and ammonium levels will be tracked to see if there is a trend in conjunction with the health of the phytoplankton blooms and the benthic communities. Sediment cores may be taken at the water sample sites and analyzed for metal and hydrocarbon contaminants known to be effluents from point sources (such as refineries and sewage treatment plants, etc). These especially need to be performed for locations near a known Superfund site or oil refinery. Finer sediments tend to retain higher pollutant concentrations than coarse sediments. Oil pollution increases oyster mortality, disrupts reproduction and reduces growth and resistance to parasites (Lorio and Malone, 1994). It is an important step to assess the sediments at a site being considered for restoration.

Turbidity is another critical factor since heavy sediment loads are not conducive to oyster growth or water quality. Turbidity can be measured using a Secchi disk, a Secchi tube or turbidity meter at the water sample locations. Listed below are the physical site criteria previously discussed and some of their optimum conditions.

Physical Site Criteria for Oysters

1. Temperature (20 to 25 degrees Celsius) due to seasons (June to October)*
2. Salinity > 10 psu* (Chesapeake Bay & tributaries – range of 12 to 28 psu)
3. DO > 5 mg/L & not less than 2.8 mg/L
4. Turbidity (Secchi disk, turbidity meter, secchi tube) converted to TSS based on site
5. Composition of sediment – sandy composition or other? (shoreline & sea bed)
6. Depth
7. Sub tidal/intertidal- mudflats, salt marsh or sea grass area
8. Nitrogen/Phosphorus levels (water quality)
9. Chlorophyll a (algal blooms)
10. Species diversity/predators

*(Values are summarized for spawning of *Crassostrea virginica* in the Chesapeake Bay by Nestlerode *et al.*, 2007)

In oyster restoration site surveys previously made by Virginia Institute of Marine Science (VIMS) and Chesapeake Bay Foundation (CBF), oyster strings (10 oysters strung on a wire) have been located on docks and wharfs owned by residents along the coastline for a minimum of 60 to 90 days in order to evaluate the attachment rates of the spat. In a recent study, for the Elizabeth River, cages containing 50 oyster shells were tied to wharfs along the coastline at 60 volunteer sites from early June to mid October. These were collected and the number of spat counted on each shell to identify which sites were more successful. Some cages contained blue crabs and toadfish and several of the oyster shells were covered with barnacles and mussels. This also gives clues about the nutrient levels based on the size of the newly attached oysters to the shells and about species diversity by the cages' content (Chesapeake Bay Foundation – *Unpublished Volunteer Data*).

For this study, the pre-site/site surveys had been conducted by the USACE along with partners in prioritizing the watersheds into Tiers for large-scale oyster restoration. The main criteria utilized in this study were salinity, dissolved oxygen levels, water depth and hydrodynamic criteria (USACE Native Oyster Restoration Master Plan – March 2012).

4.1.3 Pre-Established Reef Surveys (First Year)

After the reef's new location has been established, bi-monthly surveys should be conducted. Rotating sample sites may be selected on the top of the mound, midway and sides, and at the bottom of the reef in order to minimize sampling identical locations. Then the numbers of dead and live oysters on the shells as well as the attached spat are counted. Any holes that may have been drilled by worms or caused by crabs are noted in order to speculate the cause of mortality (Nestlerode *et al.*, 2007). Usually, a certain transect size is selected and then extrapolated based on the reef size in order to calculate survival/mortality rates. If there are high mortality rates, the species and water samples will help to differentiate whether it occurred due to predation or due to a lack of nutrients or water quality. These were the main procedures followed in the oyster data collection in the Burke study (Burke, 2010).

The oyster abundance and size are the main survey criteria for the first three quarters. Oyster abundance will be evaluated by population density through transect sampling from the top, middle, sides and bottom of the reef bi-monthly for the first year and quarterly for the second year, and bi-annually for subsequent years (Luckenbach *et al.*, 2005) . Care will be taken not to disturb or damage the main structure of the reef. Utilizing meter quadrats for designating an area to be counted or nets will minimize damage to the reef. Tongs may be used when shell samples need to be physically removed from the reef (e-mail communication with CBF Restoration Analyst, Jackie Harmon).

At the end of the year, one would anticipate seeing an excreted biofilm forming with attached oysters around the base of the reef. This is a positive sign that the reef production is at a healthy level. Also, seeing a dense population of oysters that have multiple shells attaching to the old shells, that built the reef, is reflective of high reproduction and survival rates (Nestlerode *et al.*, 2007). Net samples of the benthic community will establish whether diverse species are flourishing in this new environment.

4.1.4 Post-Audit Surveys (Second Year)

Even in the most conducive environment, it usually takes at least six years for a reef to become established. Post-audit surveys need to continue at least through the second year on a quarterly basis and a biannual basis thereafter. However, typically funding is limited on restoration projects and post audits are rarely conducted past the two year window, unless radical changes are seen (such as high mortality rates or high reproduction rates). When radical changes are noted, post audit surveys are warranted (e-mail communication with Dr. Mark Luckenbach - VIMS). Listed below are the recommendations for these surveys. Again due to funding restrictions, items #1 through #5 are usually the ones conducted. The sampling requires equipment, ship time, labor and extensive lab work.

Post-Audit Surveys

1. Oyster abundance (transect samples top, middle, sides and bottom of reef)
2. Shell length/density/stacking
3. Oyster size (>35 mm marketable, desired >75 mm)
4. Excretion film around base of oyster reef (strong indicator)
5. Survival/mortality rates
6. Net samples or grabs for species diversity/predators
7. Water samples (Water quality measures – DO, Turbidity, Depth, nitrogen, phosphorus, ammonia, chlorophyll A

Evaluation Methods

Oyster shell size is a strong indicator of the reef's survival. Oysters with a shell length greater than 35 mm are considered marketable and greater than 75 mm are an outstanding level (Kennedy *et al.,* 1996). An additional positive indicator is the beginning of new multiple oysters growing on the same shell and a multi-layer stack being formed. This initiates a three-sided layering effect that forms the interstitial matrix of the reef that is critical for the hiding and nesting places of oyster larvae and other species. In addition, an excreted film begins to form around the base of a healthy oyster reef at the end of the first year or beginning of the second year. This is a definite indicator that the reef is growing in a conducive environment (Nestlerode *et al.*, 2007). The biofilm is an organic-inorganic hybrid material which differs from the shell and is not found in other shellfish. The film contains an increased protein level as well as an alternate calcium carbonate crystalline form (Burkett *et al.*, 2010).

4.1.5 Cost/Restoration Benefits

Restoration costs need to be weighed against the restoration benefits. Rarely will the restoration efforts be cost effective. They are long-term evaluations, require expensive equipment and are labor intensive. Some of the labor cost may be minimized by utilizing volunteers; however, it does not outweigh all of the initial costs required for the reef placement and the maintenance and monitoring costs.

In comparison to other high marginal ecological benefit restorations (such as marsh or sea grass restoration), oyster reefs have been shown to have a relatively low marginal cost. The interest in oyster harvesting usually brings local stakeholders and sponsors to assist. An analysis of constructed reefs in Maryland and Virginia showed a 5-year recovery rate of costs versus a 14-year recovery rate of costs, respectively. The Virginia reefs were constructed with oyster shell as a base at a cost of $10,000 per acre. The Maryland reefs had a similar construction; however, they were also seeded with broodstock. Therefore, their initial construction ran approximately $20,000 per acre. It was found that the addition of maintenance broodstock by Maryland increased productivity to an average of 100 bushels/acre/year while Virginia's reefs produced less than 20 bushels /acre/year. It was also found that harvesting damages the reef and prevents the aging of the oyster populations. The maintenance of the reefs and the lack of disturbance increased the lifespan and created greater habitat diversity (Henderson *et al.*, 2003).

For the Lynnhaven River System, funding has been allocated for 110 additional acres of sanctuary oyster reef to be placed at an approximate cost of $125,000 per acre (Lynnhaven River Now, USACE Native Oyster Restoration Plan – March 2012).

4.2 Statistical Models for Evaluating Factorial Multi-colinearities

Initially for this study, a Tree Diagram was built with all of the different data points available from the Burke study (Burke, 2010). This schematic helped to evaluate which variable was dependent on another and which variables inevitably led to the final biomass production. Once a final diagram was completed, all of these variables were loaded into a spreadsheet in Excel for future use to be downloaded into SAS for evaluation of a final model reflecting the variables with the highest impact.

For this spreadsheet, oyster data was compiled from the Burke study (Burke, 2010) and combined with water quality parameter data from DEQ and bacterial counts from DSS. Due to Tropical Storm Gabrielle in September 2007, several of the collection stations in the Lynnhaven area were down from September 2007 through March 2008. This impacted the data package that was compiled since there were several missing data points for certain collection periods. If there were multiple missing data points, that sample was removed from the data. Also, any substrates that did not have at least two years of data to be analyzed were eliminated from the study.

In this statistical analysis, a Factorial design was utilized. A Factorial design is based on a statistical method known as ANOVA, or analysis of variance to compare central tendency among different groups on a quantitative level. It evaluates a series of test of hypotheses (THs) whether the different groups have equal mean scores. It is an important method to determine the effects of multiple variables on a response. Additionally, Factorial design can be used to find both main effects on the dependent variable versus individual variables as well as any interaction effects or multicolinearity among multiple independent variables.

Factorial design is especially valuable in environmental studies due to their ability to evaluate the 'synergy effect' of multiple factors interacting. Another advantage is the fact that it tests all possible combinations. This type of evaluation works well when there are strong interactions between variables and every variable is assumed to contribute significantly toward the dependent variable. That is the case in evaluating the different substrates utilized in conjunction with oyster restoration and the impact of all of the environmental conditions affecting it.

Utilizing Multiple Mean Comparison (MMC) method along with the Factorial design allows for comparing all the different combinations of pairs of treatments in order to give a clear assessment of which have the largest or smallest impact on the dependent variable. There are several MMC methods and in this study, Duncan's Multiple Range Test (MRT) (Duncan, 1955) was used since it is considered to be the most conservative procedure compared to other MMC techniques such as Tukey (Tukey,1951), Scheffe (Scheffe, 1959), Student Newman-Keuls (Keuls, 1952) and Dunnett's (Dunnett, 1955) tests. Once the variables with the largest impact to the dependent variable are identified, a Stepwise Selection Regression Method (Efroymson, 1960) may be utilized to narrow it down to the most significant independent variables to be considered in the final statistical model.

The main objective in this statistical analysis is to identify the major factors influencing the reproduction of the oyster (*Crassostrea virginica*) in the Lynnhaven to the greatest degree. In addition, this model is being constructed with the intent of evaluating alternative substrates on an equivalent level and providing a comparison between the natural reefs and the living shoreline. Both were constructed with alternative substrates in order to evaluate if there is a convergence or divergence of the abundance of oysters in these different scenarios. In previous studies (Coen and Luckenbach, 2000; Walters and Coen, 2006), concurrent samples were collected from adjacent natural and experimental reefs on various substrates in order to compute sample variance estimates between sites. This design allowed an evaluation of convergence (or divergence) of the natural and experimental reefs over time.

This statistical model when utilized will establish if a relationship is present between the dependent variable, biomass production, and treatment levels of temperature (which includes seasonal variability), salinity (includes water flow rate), TSS (total suspended solids), depth, dissolved oxygen levels (DO) and nutrient levels for nitrogen, phosphorus, and chlorophyll a as well as *Escherichia coli/Enterococci* counts. The block levels chosen for this model were the alternative substrates - cement, granite, limestone marl, oyster shell, cinder blocks, concrete modules and combinations. The bi-monthly data values for all of the block and treatment levels were obtained from databases maintained by DEQ and DSS. Sampling stations were chosen that were closest to the oyster bed locations. The bacterial counts will also be critical in establishing recommendations for TMDLs and/or Best Management Practices to impact water quality parameters based on results from this study.

4.2.1 Assumptions

In order to evaluate the impact of predators in this experiment, data were accumulated on various substrates utilizing caged and uncaged scenarios at the Long Creek site. The openings in the cages were sized in order to keep out blue crabs and fish. This alternative at Long Creek was evaluated on the marsh area, an established oyster reef and rip rap areas. In addition, some concrete and granite sites were placed. Cages were not used at the living shoreline sites in Eastern Branch and Linkhorn Bay. At these locations, each substrate was tested with seeded and non-seeded alternatives.

In establishing criteria for measuring the health of the oyster reef, the survival rate would be weighted heavier than the biomass for the first year since the spat are very sensitive and are more susceptible to disease and predation. For the second year, the evaluation criteria would change to the formation of multiple stacking arrangements, area of the reef and biomass as the oyster matures.

The data included reef-balls as a substrate on the living shoreline; however, in order to count the number of live and dead oysters, the reef-balls were destructively sampled at the end of the experiment for a final count. Since there was only one final year of data, these counts were not included in the calculations. At least two years would be needed for it to be considered statistically valid.

For the initial computer runs, one of the data points included in the spreadsheet was AFDM (Ash-free dry tissue mass). This was used in the Burke study in the calculation for the final biomass. The initial outputs were only showing a relationship between these two criteria. Once the AFDM values were removed from the dataset, SAS was able to construct a model.

Once a final model was run for Long Creek, Eastern Branch and Linkhorn Bay living shorelines and a composite, these models were re-input along with the same data file and re-run.

4.2.2 Test of Hypothesis

The null hypothesis for this statistical analysis states that all of the independent variables (Temperature, salinity, TSS, *E. coli/Enterococcus*, alternative substrates, depth, DO, nitrogen, phosphorus and chlorophyll a) are equal in impact to the oyster's biomass production, the dependent variable. The alternate hypothesis states that at least one or a combination of the independent variables does affect the biomass production. The Factorial Model along with a Multiple Means Comparison (MMC) was utilized to evaluate which combinations of blocks and treatments provided the most conducive environment for total oyster biomass production. The Stepwise Selection Method was used to narrow the field to the ones with the largest impact for the final model.

4.2.3 Factorial Model

Y (Reproduction Rate Dependent Variable)$_{ijk}$ =
μ (Population Mean) + $\tau_i + \beta_j + \tau_{k1}$ (Treatment- Temperature) | τ_{k2}
(Treatment-Salinity) | τ_{k3} (Treatment-TSS) | τ_{k4} (Treatment-*E. coli*) | τ_{k5} (Depth)
| τ_{k6} (DO) | τ_{k7} (Nitrogen) | τ_{k8} (Phosphorus) | τ_{k9} (Chlorophyll a) | β_{k1}
(Alternative Substrates – Cement, Granite, Limestone Marl, Oyster Shell, Cinder
blocks, Concrete Modules) + ε (Random Error)$_{ijk}$

Note: Bar| denotes all factorial combinations of treatments and blocks are evaluated, and $\varepsilon \sim NID(0,\sigma^2)$ under the Gaussian-Markov Theorem

Where:

Y = Oyster reproduction response to the independent variables (Temperature, Salinity, TSS, *E. Coli/Enterococcus*, Alternative Substrates, Depth, DO, Nitrogen, Phosphorus and Chlorophyll a)

μ = Population mean

τ = Treatment effect from Temperature (Degree C), Salinity (psu), TSS (mg/L), *E. coli/Enterococcus* (MPN/100ml), Depth (m), DO (mg/L), Nitrogen (mg/L), Phosphorus (mg/L) and Chlorophyll a(mg/L)

β = Block effects of Independent Variables Alternative Substrates (Cement, Granite, Limestone Marl, Oyster Shell, Cinder blocks, Concrete Modules)

ε = Random error, $\varepsilon \sim NID(0,\sigma^2)$

Test of Hypotheses

(a) Test of Treatment effects:

H_0 : $\tau_1 = \tau_2 = \tau_3 = \tau_4 = \tau_5 = 0$ (Levels of Temperature, Salinity, TSS, Depth (m), DO (mg/L), Nitrogen (mg/L), Phosphorus (mg/L), Chlorophyll a(mg/L) and *E. coli/Enterococcus*) have equivalent impact on oyster biomass production)

H_a : At least one or more $\tau_i \neq 0$ (At least one or more may have significant impact on oyster biomass production)

(b) Test of Block effects:

H_0 : $\beta_1 = \beta_2 = \beta_3 = \beta_4 = \beta_5 = \beta_6 = 0$ (Alternative Substrates Cement, Granite, Limestone Marl, Oyster Shell, Cinder blocks, Concrete Modules) have equivalent impact on Oyster reproduction rate)

H_a : At least one or more $\beta_i \neq 0$ (At least one or more may have significant impact on Oyster biomass production)

For the Multiple Mean Comparison (MMC), Duncan's Multiple Range Test (MRT) was utilized after Stepwise Selection Regression analysis was used to identify any significant effects to differentiate which levels of these variables had the largest and smallest effects. In addition, the health of the oyster reef may be evaluated by the following equations:

Reef Age Less Than 1 Year

C.T. (survival rate) x 70% + C.T. (biomass) x 30%

Survival Rate = # Live Shell / # Total Live & Dead Shell x 100

Biomass = Reef Areas or Dried Weight (AFDM/square meter)

Reef Age Greater Than 1 Year

%(stacking) x 30% + %(biofilm) x 40% %(biomass) x 30%

Primary Criteria

Central Tendency (C.T. biomass) = AFDM/square meter

Central Tendency (C.T. survival rate) = # Live Shell / # Total Live & Dead Shell x 100

Secondary Criteria

% (Bio) = layering/stacking

Escherichia coli/Enterococci bacterial counts

Environmental water quality indicators at each site

CHAPTER 5

RESULTS AND DISCUSSION

5.1 Statistical Evaluation

5.1.1 Long Creek Site

In evaluating each indicator individually as well as paired with Duncan's Multiple Range Test (MRT) at the Long Creek site, the actual site location, the cage control and year over year comparison of biomass production were the items individually that reflected the most significant impacts. The mean of biomass production was not significantly different between the fall and spring seasons, indicating no siginificant temporal variability in the magnitude of the dependent variable, biomass.

Duncan Grouping	Mean	N	season
A	82.243	252	Fall
A			
A	76.744	288	Spring

Note: Means with the same letter are not significantly different in this analysis. N denotes the number of samples included in the analysis.

However, there was a significant difference in looking at biomass production year over year. The mean increased each year and also was classified in a separate grouping denoting a significant statistical difference between each level in terms of system level reproducibility – a positive sign of a productive reef.

Duncan Grouping	Mean	N	period
A	171.27	72	2008
B	101.24	216	2007
C	38.99	216	2006
D	5.73	36	2005

In addition, the Duncan analysis concluded that the marsh site had the highest productivity followed by riprap and oyster shell and that there was a significant difference between each of these locations.

Duncan Grouping	Mean	N	site
A	147.618	180	Marsh
B	63.699	180	Riprap
C	26.614	180	Oyster Reef

In comparing caged versus uncaged at Long Creek, the uncaged in a natural environment with the predators actually produced significantly more oyster biomass.

Duncan Grouping	Mean	N	c-control
A	88.363	270	Uncaged
B	70.258	270	Caged

In evaluating the alternative substrates at Long Creek, the Duncan MRT reflected a significant difference in biomass production with the granite substrate-both large and small. The limestone marl was the least effective substrate. Looking at individual substrate locations, all of the groupings overlapped, such as OSU and CVS for example, which means that they were all considered to be statistically equivalent in biomass production.

Duncan Grouping	Mean	N	substrate
A	140.756	90	GL
B	114.125	90	GS
C	71.305	90	OSU
C			
C	65.790	90	CVS
D	45.732	90	LML
D			
D	38.154	90	LMS

At Long Creek, the temperature with the highest production level was actually in a lower range than anticipated (Mean – 12.86 degrees Celsius) and the second most productive was in a high range (Mean – 27.94 degrees Celsius) – both contradictory with past results reflecting a temperature range between 20 to 25 degrees Celsius as the most conducive for growth.

Duncan Grouping	Mean	N	temperature
A	171.27	72	12.86
B	128.41	108	27.94
C	74.07	108	13.69
C			
C	61.58	108	23.81
D	16.41	108	20.81
D			
D	5.73	36	11.01

The salinity was also in the low range (Mean - 18.89 psu) for the highest biomass production and there was very little difference in salinity at the highest and lowest production levels (Mean – 18.8 to 17.82 psu at lowest level). In general, river discharge has a large impact on salinity and is important when modeling data. Unfortunately, this researcher was unable to obtain data for these sites.

Duncan Grouping	Mean	N	salinity
A	171.27	72	18.89
B	128.41	108	21.45
C	74.07	108	21.01
C			
C	61.58	108	22.61
D	16.41	108	18.8
D			
D	5.73	18	17.92
D			
D	5.72	18	17.82

The maximum biomass production occurred at a DO level of 7 mg/L which is well above the 5 mg/L criteria. Surprisingly, the lowest production occurred at the highest oxygen level of 12 mg/L. Resulting DO level of 7 mg/L provides an important target criteria for subsequent TMDL and BMP recommendations.

Duncan Grouping	Mean	N	doxy
A	128.41	108	7
B	78.35	180	6.5
B			
B	74.07	108	7.12
B			
B	61.58	108	7.8
C	5.73	36	12

Total Suspended Solids (TSS) were at a very high level (Mean – 30 mg/L) when the biomass production was at the highest, indicative of the symbiotic nature of filtering and feeding oyster and filtered TSS relationship.

Duncan Grouping	Mean	N	tss
A	171.27	72	30
B	128.41	108	32
C	74.07	108	16.093
C			
C	61.58	108	11.053
D	16.41	108	31
D			
D	5.73	36	7

Kjiedahl nitrogen maintained a narrow range of change between the highest and lowest production levels (Mean – 1.2 and 1.1), providing the optimal target management range for organic nitrification process and nitrogen availability in the water.

Duncan Grouping	Mean	N	ktn
A	171.268	72	1.2
B	128.411	108	0.8
C	74.066	108	0.6
C			
C	61.580	108	1.338
D	13.736	144	1.1

Phosphorus measurement levels were fairly low at this location and the highest biomass production occurred at the highest phosphorus level, implying mesotrophic and eutrophic composition of phytoplankton mass ratio in TSS in response to available phosphorous in the water.

Duncan Grouping	Mean	N	tp
A	171.27	72	0.09
B	74.07	108	0.035
B			
B	72.41	216	0.07
B			
B	61.58	108	0.054
C	5.73	36	0.04

The chlorophyll a levels correlated with the TSS levels which does lead to the conclusion that both the highs and lows experienced an algal bloom. The highest biomass production occurred when the oxygen level was stable and above 5 mg/L.

Duncan Grouping	Mean	N	chl_a
A	171.27	72	15.51
B	128.41	108	7.87
C	74.07	108	2.866
C			
C	61.58	108	7.267
D	16.41	108	8.58
D			
D	5.73	36	15.47

Escherichia coli's lowest counts occurred when the biomass production was at its highest, which implies rate of filtration of *E. coli* is proportional to the biomass increase.

Duncan Grouping	Mean	N	e_coli
A	171.27	72	3.16
B	128.41	108	2.45

C	74.07	108	0
C			
C	61.58	108	8.45
D	16.41	108	7.35
D			
D	5.73	36	21.8

The combination of water quality parameters (in bold) shown below reflected the highest biomass mean and largest standard deviation

Level of temperature	Level of doxy	Level of tss	Level of ktn	Level of tp	Level of chl_a	Level of e_coli	Level of f_entrococci	N	---biomass-- Mean
11.01	12	7	1.1	0.04	15.47	21.8	25	36	5.726667
12.86	**6.5**	**30**	**1.2**	**0.09**	**15.51**	**3.16**	**25**	**72**	**171.268486**
13.69	7.12	16.093	0.6	0.035	2.866	0	25	108	74.066167
20.81	6.5	31	1.1	0.07	8.58	7.35	25	108	16.405796
23.81	7.	11.053	1.338	0.054	7.267	8.45	25	108	61.580472
27.94	7	32	0.8	0.07	7.87	2.45	25	108	128.411120

Level of temperature	Level of doxy	Level of tss	Level of ktn	Level of tp	Level of chl_a	Level of e_coli	Level of f_entrococci	N	---biomass-- Std Dev
11.01	12	7	1.1	0.04	15.47	21.8	25	36	7.658328
12.86	**6.5**	**30**	**1.2**	**0.09**	**15.51**	**3.16**	**25**	**72**	**145.420192**
13.69	7.12	16.093	0.6	0.035	2.866	0	25	108	84.025220
20.81	6.5	31	1.1	0.07	8.58	7.35	25	108	26.952188
23.81	7.8	11.053	1.338	0.054	7.267	8.45	25	108	74.032969
27.94	7	32	0.8	0.07	7.87	2.45	25	108	114.694896

In summary, after iterative Stepwise Selection minimization, only water quality variables remained in the model that reflected the largest impact at Long Creek. These are summarized below. All of the variables that prevailed are significant at the 0.1500 level in Stepwise selection minimization procedure. Magnitude of contribution by the substrates were all considered statistically equivalent and insignificantly different in biomass production. The only other significant differences reflected at this site were the uncaged scenario, the marsh location and the year over year comparison of biomass production. All of these options reflected a significantly higher level of biomass production.

```
Summary of Stepwise Selection

        Variable     Variable   Number  Partial    Model
Step    Entered      Removed    Vars In R-Square   R-Square  C(p)     F Value   Pr > F

1        tp                       1      0.4094    0.4094  134.766   373.66  <.0001
2        e_coli                   2      0.0453    0.4547   85.1671   44.69  <.0001
3        chl_a                    3      0.0226    0.4773   61.4139   23.23  <.0001
4        temperature              4      0.0467    0.5241   10.1619   52.65  <.0001
5        ktn                      5      0.0072    0.5313    3.9255    8.25  0.0042
```

5.1.2 Living Shoreline Locations

At the living shoreline the combination of site, seeded vs. unseeded and *Escherichia coli* made a significant impact. First, looking at the individual indicators, the fall and spring seasons did show a significant difference in biomass production at the living shoreline locations.

Duncan Grouping	Mean	N	season
A	498.13	57	Fall
B	119.66	18	Summer

These locations also showed a significant difference in year over year biomass production.

Duncan Grouping	Mean	N	period
A	609.83	39	2008

B	187.88	36	2007

Linkhorn Bay site reflected a much higher biomass productivity level than Eastern Branch.

Duncan Grouping	Mean	N	site
A	488.92	41	LB
B	308.87	34	EB

The seeded sites also produced at a significantly higher level than the un-seeded locations. This may be due to the fact that sterile triploid oysters were used for the initial seeding and wild diploid for subsequent spat sets. Triploid oysters tend to grow larger in a shorter time frame than the diploid. All of the unseeded sites were diploid oysters.

Duncan Grouping	Mean	N	control
A	855.89	18	Seeded
B	265.63	57	Unseeded

The alternative substrates on the living shorelines also showed a significant difference in production with cinder block reflecting the highest followed by the oysters, riprap and finally concrete module. The footprint area of the cinder block was much smaller than the oyster reef area and may have impacted these results. A factor to consider with the riprap and concrete substrates is that no pre-conditioning was done and this may have hindered their success rate.

Duncan Grouping	Mean	N	substrate
A	853.88	6	CB
B	680.31	22	OS
C	261.88	23	RR
D	184.74	24	CM

In addition, most of the individual substrate locations overlapped on the living shorelines as the Long Creek site with one exception. The oyster reefs at both Eastern Branch (CS.OR2) and Linkhorn Bay (HS.OR2) were significantly higher than the other substrates.

The biomass production on the living shorelines was also at the highest level when the *E. coli* bacterial counts were at one of their lowest. This could possibly be the result of low river discharge during a time frame of relative drought conditions.

Duncan Grouping	Mean	N	e_coli
A	766.57	23	2.45
B	384.53	16	40.91
C	261.06	9	7.42
C			
C	251.13	9	2.83
C			
C	222.16	9	407.93
D	17.17	9	0

The most productive oxygen level on the living shorelines was 9.6 – higher than Long Creek at 7 – however, still in the medium range of the readings at these locations.

Duncan Grouping	Mean	N	doxy
A	766.57	23	9.6
B	384.53	16	8.3
C	261.06	9	9.2
C			
C	251.13	9	11.4
C			
C	222.16	9	5.5
D	17.17	9	7

These locations also performed better with the lowest total phosphate count.

Duncan Grouping	Mean	N	tp
A	621.60	32	0.05
B	384.53	16	0.06
C	261.06	9	0.14
C			
C	222.16	9	0.09
D	17.17	9	0.07

After iterative Stepwise Selection minimization, variables that remained in the model for the living shoreline locations in Eastern Branch and Linkhorn Bay are summarized below – again only water quality parameters that impacted the biomass production to the largest extent. All variables left in the model are significant at the 0.1500 level.

Summary of Stepwise Selection

```
     Variable   Variable  Number  Partial   Model
Step Entered    Removed   Vars In R-Square  R-Square  C(p)    F Value Pr > F

 1   doxy                    1    0.4614    0.4614   21.1967  63.40  <.0001
 2   tp                      2    0.0223    0.4837   19.3027   3.15  0.0802
```

5.1.3 Composite of Long Creek and Living Shoreline Locations

For the final comparison, all of the data are combined to see if there were any significant changes when all of the sites within the selected Lynnhaven watersheds were evaluated together. Again, a lower temperature than the previously published ranges showed the highest biomass production. Seasonal peaks in phytoplankton occur in the spring when water temperatures are lower and have not risen to summer levels.

Duncan Grouping	Mean	N	temperature
A	766.57	23	16
B	384.53	16	15.9
C	261.06	9	11.7
C			

	C		251.13	9	7.9
	C				
D	C		222.16	9	26.5
D	C				
D	C	E	171.27	72	12.86
D		E			
D	F	E	128.41	108	27.94
	F	E			
G	F	E	74.07	108	13.69
G	F	E			
G	F	E	61.58	108	23.81
G	F				
G	F		17.17	9	25.7
G	F				
G	F		16.41	108	20.81
G					
G			5.73	36	11.01

Now with the sites combined, the salinity value fell more into line with published figures. The highest biomass was produced at 22.4 psu salinity and this was significantly higher than the other Duncan groupings.

Duncan Grouping		Mean	N	salinity
	A	624.39	32	22.4
	B	384.53	16	24.8
	C	251.13	9	19.1
	C			
D	C	171.27	72	18.89
D				
D	E	128.41	108	21.45
D	E			
D	E	119.66	18	20.7
	E			
F	E	74.07	108	21.01
F	E			
F	E	61.58	108	22.61
F				
F		16.41	108	18.8
F				
F		5.73	18	17.92
F				
F		5.72	18	17.82

The lower Total Suspended Solids (TSS) counts also produced the highest biomass mean.

```
Duncan Grouping      Mean     N   tss
            A       624.39   32   6

            B       384.53   16   13

            C       251.13    9   4
            C
        D   C       222.16    9   40
        D   C
        D   C   E    171.27   72   30
        D       E
        D   F   E   128.41   108   32
            F   E
        G   F   E    74.07   108   16.093
        G   F
        G   F        61.58   108   11.053
        G
        G            17.17     9   18
        G
        G            16.41   108   31
        G
        G             5.73    36    7
```

With the combined grouping, a higher *E. coli count* produces the highest biomass, however, it is still below the required level of 49.

```
Duncan Grouping      Mean     N   e_coli
            A    384.53   16   40.91

            B    261.06    9    7.42
            B
            B    251.13    9    2.83
            B
            B    240.45   131   2.45
            B
            B    222.16    9   407.93
            B
            B    171.27   72   3.16
```

C	69.69	117	0
C			
C	61.58	108	8.45
C			
C	16.41	108	7.35
C			
C	5.73	36	21.8

With the combined locations, the DO level is still maintaining a middle range for the highest biomass productivity.

Duncan Grouping	Mean	N	doxy
A	766.57	23	9.6
B	384.53	16	8.3
C	261.06	9	9.2
C			
C	251.13	9	11.4
C			
C	222.16	9	5.5
D	119.85	117	7
D			
E D	78.35	180	6.5
E D			
E D	74.07	108	7.12
E D			
E D	61.58	108	7.8
E			
E	5.73	36	12

The phosphorus at a low level still produced the highest biomass with combining all the sites. Possibly, the phytoplankton are using the phosphorus for growth and the oysters are then utilizing the phytoplankton for their nutrients.

Duncan Grouping	Mean	N	tp
A	621.60	32	0.05

B	384.53	16	0.06
C	261.06	9	0.14
D	176.92	81	0.09
E	74.07	108	0.035
E			
E	70.20	225	0.07
E			
E	61.58	108	0.054
E			
E	5.73	36	0.04

After transitioning through Eight Stepwise Selections, these are the variables that remained in the composite model for all locations in Lynnhaven River in this study – Long Creek, Eastern Branch and Linkhorn Bay. The ktn (Kjiedahl nitrogen) is eliminated due to the high variance (0.3414 > 0.05) in the eighth step. Since the depth for all of the samples were taken at 1 meter, this was also eliminated – leaving salinity, temperature, total phosphorus, DO (dissolved oxygen) and TSS (Total Suspended Solids) for the composite model in Lynnhaven River. Only water quality parameters remained and all variables left in the model are significant at the 0.1500 level.

Summary of Stepwise Selection

Step	Variable Entered	Variable Removed	Number Vars In	Partial R-Square	Model R-Square	C(p)	F Value	Pr > F
1	salinity		1	0.2450	0.2450	150.171	199.24	<.0001
2	ktn		2	0.0382	0.2832	113.532	32.69	<.0001
3	temperature		3	0.0162	0.2994	99.1541	14.15	0.0002
4	depth		4	0.0195	0.3189	81.4692	17.47	<.0001
5	tp		5	0.0379	0.3568	45.1940	35.91	<.0001
6	doxy		6	0.0191	0.3759	27.8638	18.66	<.0001
7	tss		7	0.0232	0.3991	6.4475	23.44	<.0001
8		ktn	6	0.0009	0.3982	5.3531	0.91	0.3414

In summary, the Long Creek site did not show a significant difference in biomass production between the fall and spring seasons. However, the living shorelines in Eastern Branch and Linkhorn Bay did reflect a significant difference between the fall and summer seasons. All of the locations reflected a significant difference in year over year production and this is a positive sign of productive reefs.

At the Long Creek site, the Duncan analysis concluded that the marsh site had the highest productivity level followed by riprap and oyster shell and there was a significant difference between these locations. In comparing caged versus uncaged at this site, the uncaged option actually produced significantly more. The seeded substrates at Linkhorn Bay and Eastern Branch also produced significantly higher biomass.

In evaluating substrates, the Duncan analysis reflected the highest biomass production with the granite and the lowest with the limestone marl at Long Creek. Eastern Branch and Linkhorn Bay produced the highest biomass on cinder blocks with oyster shell substrate running second. The area of the cinder block footprint was much smaller than the oyster reef and this may have impacted the results. Also, the riprap and concrete models produced at the lowest level and this may be due to the fact that no conditioning of these substrates was done prior to deployment. Overall, the site at Linkhorn Bay had significantly higher biomass production than Eastern Branch.

Considering the water quality parameters at Long Creek, the highest biomass production occurred at a low temperature (12.86 degrees Celsius), a medium range salinity (18.89 psu), a medium range DO level(7 mg/L), a very high level TSS (30 mg/L), low Kjiedahl nitrogen and low phosphorus levels (1.2 and 0.09 mg/L, respectively), a high chlorophyll a count (15.51 mg/L) and one of the lowest *E. coli* counts (3.16 mg/MPN) in the study years. It would be expected to produce a higher biomass at a lower temperature and salinity since the advent of disease would be less probable. Also, a medium level for DO would also be a positive setting instead of lower levels below 2.8 mg/L at anoxic levels. In addition, a low *E. coli* count would only add to this positive scenario. The high TSS and high chlorophyll a measurements reflect the possibility of an algal bloom occurrence which would provide plenty of nutrients for the oysters. Possibly, the high chlorophyll a count with low nutrient levels may also be reflecting the fact that the phytoplankton are consuming the nutrients to grow. Overall, this appeared to be a positive environment for biomass production to occur.

At Linkhorn Bay and Eastern Branch, several of the datapoints were lost for nitrogen levels and these were excluded from the study. Considering the remaining water quality parameters, *E. coli* counts were at their lowest in the study when the highest biomass level occurred. The DO level was at 9.6 mg/L, which again fell in the medium range. Finally, total phosphorus was at its lowest level in the study years at 0.05 mg/L.

The composite run of all three sites revealed some of the same trends. The temperature was in a low range (16 degrees Celsius), however, the salinity actually registered a higher level and fell in the range of previous documentation (22.4 psu). For the composite model with the highest overall biomass, the TSS values were very low (6 mg/L) and the *E. coli* count was higher (40.91 MPN/L). Both the DO levels and the total phosphorus stayed in their ranges (9.6 mg/L and 0.05 mg/L, respectively).

All three of the statistical models that were calculated after the Regression analysis along with the Stepwise Selection method reflected the fact that the water quality parameters had the highest impact on the oyster biomass production. At Long Creek, the parameters that had the strongest influence were temperature, Kjiedahl nitrogen, total phosphorus, chlorophyll a and *E. coli* counts. For Linkhorn Bay and Eastern Branch, the DO levels and total phosphorus had the largest impact. After combining all of the sites' data together to get an overall picture for the Lynnhaven River, the composite model reflected influences of temperature, salinity, DO levels, TSS, total phosphorus and fecal *Enterococci* counts. It is obvious that these impacts are site specific and that water quality parameters are the driving force.

5.2 TMDL and Best Management Practices Impact

Based on the statistical analysis, the water quality variables in the final composite model that will be impacted the most by the TMDLs and BMPs are total phosphorus, DO (dissolved oxygen), TSS (Total Suspended Solids) and bacterial counts. Utilizing the narrow ranges reflected in the model output for phosphorus, DO levels and other treatments will be a first step in setting realistic TMDL goals. The next step is developing the details for WIPs in order to restore the Lynnhaven watershed. The initial WIP was issued in January 2012 and Appendix Q details the requirements for each area. These plans consider ecological restoration such as riparian buffers and living shorelines as well as promoting accountability for improved performance and sustaining previously attained levels of improvement. These WIPs are being developed in order to progress towards goals that will be finalized in a Federal TMDL in 2017. This TMDL will require annual reductions in nitrogen, phosphorus and sediment in each of the Bay's tidal segments, tributaries and embayments listed as impaired under 303 (d) of the Clean Water Act.

In summation, to meet the WIP annual goal of removal rates of 126,300 lbs of nitrogen and 2220 lbs of phosphorus by 2017, there will need to be multiple avenues pursued for the Lynnhaven. Listed below are the strongest candidates to be pursued in this environmentalist's estimation:

- Allocate annual funding for septic tank eliminations as well as sewer and stormwater enhancements.
- Set goals to increase No Discharge Zone pump-outs by at least 20 to 50% year over year by educating the community on the negative impacts. Also, increase the number of stations available.
- Continue to monitor bacteria levels and increase frequency in areas that are known to have high counts historically. Implement the Executive Order to close oyster bed harvesting without hesitation in that area if the counts are above the standards.
- Educate the community on the advantages of rain barrels, rain gardens, riparian buffers and living shorelines. Include the public as volunteers in oyster gardening and shell recovery.
- Allocate annual funding in the City of Virginia Beach for living shorelines and floating wetlands as well as planting vegetation along streams and creeks and continuing to increase open areas.
- Institute new program in City of Virginia Beach for bulkhead replacement with riprap or living shoreline where applicable in order to rejoin marsh areas to coastline.
- Pursue several facets of oyster restoration via re-building existing oyster beds, placing oyster castles and reefballs or any other substrate with a high success level.

- Implement plans to go forward with additional 110 acre expansion of oyster beds in Lynnhaven.
- Obtain permits for outfall renovations and budget annual funds for decreasing TSS via other innovative projects.

(Personal communication with Karen Forget – Lynnhaven River Now and Steve McLaughlin – City of Virginia Beach - Stormwater Management)

CHAPTER 6

CONCLUSIONS AND RECOMMENDATIONS

6.1 Brief Overview

Today, the Lynnhaven River is still maintaining high levels of TSS, nitrogen and phosphorus as well as high *Escherichia coli* counts in some areas. It is impacting the water quality as well as the aquatic animal and plant survivability even with all of the Best Management Practices and TMDLS that have been in place for years in the Lynnhaven River watershed. There has been improvement in some areas, however, continued vigilance will be required for the future in order to make an impact and save our natural treasure – coastal estuaries.

Oyster restoration will need to play a part in this as well as innovative designs for riparian buffers, living shorelines, floating wetlands, enlarged open spaces, renovated outfalls and stormwater systems. Citizen participation will be required in utilizing boat pumping stations, organic bio-degradable fertilizers, rain barrels and by placing riparian buffers to aid in natural nutrient filtration after rainstorms. The community's participation will also be welcomed in shell conservation and oyster gardening.

6.2 Statistical Summation

Based on the statistical runs made in this study, the results reflected that the water quality parameters were the driving force for a high level of biomass production by the oyster. It also indicated that the parameters fluctuated from location to location and were site specific. It is apparent that time spent in evaluating future locations is imperative. General guidelines for site evaluation have been addressed in this study and the Army Corps of Engineers have done extensive work in Virginia and Maryland evaluating hydrodynamics, salinity, DO levels and water depths in order to select their Tier 1 tributaries with the highest potential to develop self-sustaining oyster populations. The Lynnhaven River was one of these identified target areas. In their Native Oyster Restoration Plan of 2012, it is stated that oyster restoration is considered a Best

Management Practice in lowering nitrogen, phosphorus and TSS levels in Chesapeake Bay.

From the statistical analysis runs for the Long Creek site, it was determined that both the fall and spring seasons reflected significant biomass production. In addition, the site in the marsh area had the highest productivity level and the oyster reef the lowest. It was also significant to find out that the uncaged option for the predator analysis showed the highest biomass levels. After the model producing the highest biomass levels was developed for this location, it was apparent that the temperature, Kjiedahl nitrogen, total phosphorus, chlorophyll a and *E. coli* counts had the largest impact in this area.

The sites at Eastern Branch and Linkhorn Bay revealed a different picture. The living shorelines did reflect a significant difference in their biomass production between the fall and summer seasons. These two locations, as well as Long Creek, showed significant differences year over year and this is a positive sign of productive reefs. At the living shoreline sites, seeded substrates were tested and they did reflect a significant increase in biomass over the un-seeded substrates. This may be due to the fact that sterile triploid oysters were used for the initial seeding and wild diploid for subsequent spat sets. Triploid oysters tend to grow larger in a shorter time frame than the diploid. All of the unseeded sites utilized diploid oysters.

Evaluating substrates, the Duncan analysis reflected the highest biomass with the granite and the lowest with the limestone marl at Long Creek. Again, at different sites, a different result occurred. The highest biomass levels at Eastern Branch and Linkhorn Bay were on the cinder blocks with the oyster shell substrate running second. The footprint area of the cinder block was much smaller than the oyster reef area and may have impacted these results. The riprap and concrete modules produced the lowest amounts. A factor to consider with the riprap and concrete substrates is that no pre-conditioning was done and this may have hindered their success rate.

Overall, the Linkhorn Bay site had a higher production level than Eastern Branch. Again, this can be attributed to the water quality parameters. The model for Eastern Branch and Linkhorn Bay reflected that DO levels and total phosphorus levels had the largest impact.

In order to produce a complete picture for the Lynnhaven River, all of the data from the three sites were combined for a composite model. This composite view reflected temperature, salinity, DO levels, TSS, total phosphorus and fecal *Enterococci* counts as the largest impact areas. There is no doubt that the water quality parameters are the driving force in the Lynnhaven River and need to be addressed through TMDLs and Best Management Practices being implemented and tracked on success rates.

6.3 TMDL and BMPs Summation

The water quality parameters in the final composite model that will be impacted the most by TMDLs and BMPs are total phosphorus, DO (dissolved oxygen), TSS (Total Suspended Solids) and bacterial counts. Some of the controls that have been put into place in the City of Virginia Beach are the No Discharge Zone implemented in 2007 and a new phosphorus fertilizer ban that is being implemented this year. Funds have also been allocated on an annual basis to replace old septic tank systems, renovate sewer systems and upgrade stormwater systems.

With the advent of a continual rise in bacterial counts in the Eastern Branch, an Executive Order is going into effect on April 12th to close down oyster harvesting when the bacterial counts are not meeting the criteria. If more than 1½ inches of rain falls within a 24 hour period in the previous week, the oyster beds will be closed to harvest for the following 10 days and will re-open only after bacteria testing is completed and meets the state criteria.

In order to impact TSS, another project is underway to upgrade outfall locations. There is a total of 1050 outfalls in the Lynnhaven River System, 250 outfalls in the Eastern Branch and 100 in Little Creek area for a grand total of 1400 in the Lynnhaven River watershed for this area. These outfalls have a vast descent in several locations and the water lands directly on a sediment base and scours out high amounts of sediments. The plan is to place a concrete bottom at selected outfalls to eliminate the problem.

Funding has also been allocated for 110 additional acres of sanctuary oyster reef to be placed in Lynnhaven at an approximate cost of $125,000 per acre. It has been difficult to find a large enough area in the Lynnhaven due to the number of permits that have already been issued to commercial oystermen and landowners. The legalities may need to be researched on some of these permits in order to continue expanding the oyster reefs in this area. To evaluate the impact of oyster restoration, the City of Virginia Beach is co-ordinating a study with the Army Corps of Engineers to determine how much TSS per acre will be removed by an oyster reef. This is being done in order to include this as a goal in the final WIP plans for this area.

Natural alternatives that are conducive to the Tidewater area are living shorelines, floating wetlands and planting additional vegetation along creeks and streams.
This is a clean solution that will definitely aid in protecting tidal shorelines from erosion. Where possible, oysters or riprap may also be included in the project. The living shorelines improve water quality by settling sediments and filtering toxins. They also help to re-establish the natural shoreline around marsh areas that have been broken by housing development and bulkheads being placed. The floating wetlands may be the answer to the high waterfowl populations in this area and their high production of fecal matter that impacts the water quality. In the TMDL 2004, the BST studies reflected a 29% contribution by the waterfowl to the Lynnhaven. This was higher than the human fecal contribution of 25%. These wetlands aid in the removal of total nitrogen, ammonia, phosphorus, BOD and TSS, all of the water parameters of concern.

Water quality is a major concern to all of us. Continued vigilance on establishing goals for TMDLs and Best Management Practices and tracking results will ultimately reflect positive impact in this arena. Public education on boating impacts and daily routine items that affect water quality will also aid in making a difference and in saving this valuable watershed for the future generations.

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APPENDICES

Appendix I Observed Measurements from Oyster Restoration Sites

Living Shoreline (LSE)

Locations: Linkhorn Bay - Chalmers, Eastern Branch - Handeland

Sampling Period	Site	Cage Control	Substrate	Substrate #	Temp	Salinity	DO	Depth	TSS
Summer 2007	LB	Unseeded	OS	CU-OR1	25.7	20.7	7	1	18
Summer 2007	LB	Unseeded	OS	CU-OR2	25.7	20.7	7	1	18
Summer 2007	LB	Unseeded	OS	CU-OR3	25.7	20.7	7	1	18
Summer 2007	LB	Unseeded	RR	CU-RR1	25.7	20.7	7	1	18
Summer 2007	LB	Unseeded	RR	CU-RR2	25.7	20.7	7	1	18
Summer 2007	LB	Unseeded	RR	CU-RR3	25.7	20.7	7	1	18
Summer 2007	LB	Unseeded	CM	CU-CM1	25.7	20.7	7	1	18
Summer 2007	LB	Unseeded	CM	CU-CM2	25.7	20.7	7	1	18
Summer 2007	LB	Unseeded	CM	CU-CM3	25.7	20.7	7	1	18
Summer 2007	LB	Unseeded	CB	CU-CB1	25.7	20.7	7	1	18
Summer 2007	LB	Unseeded	CB	CU-CB2	25.7	20.7	7	1	18
Summer 2007	LB	Unseeded	CB	CU-CB3	25.7	20.7	7	1	18
Summer 2007	LB	Seeded	OS	CS-OR1	25.7	20.7	7	1	18
Summer 2007	LB	Seeded	OS	CS-OR2	25.7	20.7	7	1	18
Summer 2007	LB	Seeded	OS	CS-OR3	25.7	20.7	7	1	18
Summer 2007	LB	Seeded	RR	CS-RR1	25.7	20.7	7	1	18
Summer 2007	LB	Seeded	RR	CS-RR2	25.7	20.7	7	1	18
Summer 2007	LB	Seeded	RR	CS-RR3	25.7	20.7	7	1	18
Summer 2007	LB	Seeded	CM	CS-CM1	25.7	20.7	7	1	18
Summer 2007	LB	Seeded	CM	CS-CM2	25.7	20.7	7	1	18
Summer 2007	LB	Seeded	CM	CS-CM3	25.7	20.7	7	1	18

Living Shoreline (LSE) – Continued

Sampling Period	Site	Cage Control	Substrate	Substrate #	Temp	Salinity	DO	Depth	TSS
Summer 2007	LB	Seeded	CB	CS-CB1	25.7	20.7	7	1	18
Summer 2007	LB	Seeded	CB	CS-CB2	25.7	20.7	7	1	18
Summer 2007	LB	Seeded	CB	CS-CB3	25.7	20.7	7	1	18
Summer 2007	EB	Unseeded	OS	HU-OR1	26.5	20.7	5.5	1	40
Summer 2007	EB	Unseeded	OS	HU-OR2	26.5	20.7	5.5	1	40
Summer 2007	EB	Unseeded	OS	HU-OR3	26.5	20.7	5.5	1	40
Summer 2007	EB	Unseeded	RR	HU-RR1	26.5	20.7	5.5	1	40
Summer 2007	EB	Unseeded	RR	HU-RR2	26.5	20.7	5.5	1	40
Summer 2007	EB	Unseeded	RR	HU-RR3	26.5	20.7	5.5	1	40
Summer 2007	EB	Unseeded	CM	HU-CM1	26.5	20.7	5.5	1	40
Summer 2007	EB	Unseeded	CM	HU-CM2	26.5	20.7	5.5	1	40
Summer 2007	EB	Unseeded	CM	HU-CM3	26.5	20.7	5.5	1	40
Summer 2007	EB	Unseeded	CB	HU-CB1	26.5	20.7	5.5	1	40
Summer 2007	EB	Unseeded	CB	HU-CB2	26.5	20.7	5.5	1	40
Summer 2007	EB	Unseeded	CB	HU-CB3	26.5	20.7	5.5	1	40
Summer 2007	EB	Seeded	OS	HS-OR1	26.5	20.7	5.5	1	40
Summer 2007	EB	Seeded	OS	HS-OR2	26.5	20.7	5.5	1	40
Summer 2007	EB	Seeded	OS	HS-OR3	26.5	20.7	5.5	1	40
Summer 2007	EB	Seeded	RR	HS-RR1	26.5	20.7	5.5	1	40
Summer 2007	EB	Seeded	RR	HS-RR2	26.5	20.7	5.5	1	40
Summer 2007	EB	Seeded	RR	HS-RR3	26.5	20.7	5.5	1	40
Summer 2007	EB	Seeded	CM	HS-CM1	26.5	20.7	5.5	1	40
Summer 2007	EB	Seeded	CM	HS-CM2	26.5	20.7	5.5	1	40

Living Shoreline (LSE) -- Continued

Sampling Period	Site	Cage Control	Substrate	Substrate #	Temp	Salinity	DO	Depth	TSS
Summer 2007	EB	Seeded	CM	HS-CM3	26.5	20.7	5.5	1	40
Summer 2007	EB	Seeded	CB	HS-CB1	26.5	20.7	5.5	1	40
Summer 2007	EB	Seeded	CB	HS-CB2	26.5	20.7	5.5	1	40
Summer 2007	EB	Seeded	CB	HS-CB3	26.5	20.7	5.5	1	40
Fall 2007	LB	Unseeded	OS	CU-OR1	7.9	19.1	11.4	1	4
Fall 2007	LB	Unseeded	OS	CU-OR2	7.9	19.1	11.4	1	4
Fall 2007	LB	Unseeded	OS	CU-OR3	7.9	19.1	11.4	1	4
Fall 2007	LB	Unseeded	RR	CU-RR1	7.9	19.1	11.4	1	4
Fall 2007	LB	Unseeded	RR	CU-RR2	7.9	19.1	11.4	1	4
Fall 2007	LB	Unseeded	RR	CU-RR3	7.9	19.1	11.4	1	4
Fall 2007	LB	Unseeded	CM	CU-CM1	7.9	19.1	11.4	1	4
Fall 2007	LB	Unseeded	CM	CU-CM2	7.9	19.1	11.4	1	4
Fall 2007	LB	Unseeded	CM	CU-CM3	7.9	19.1	11.4	1	4
Fall 2007	LB	Unseeded	CB	CU-CB1	7.9	19.1	11.4	1	4
Fall 2007	LB	Unseeded	CB	CU-CB2	7.9	19.1	11.4	1	4
Fall 2007	LB	Unseeded	CB	CU-CB3	7.9	19.1	11.4	1	4
Fall 2007	LB	Seeded	OS	CS-OR1	7.9	19.1	11.4	1	4
Fall 2007	LB	Seeded	OS	CS-OR2	7.9	19.1	11.4	1	4
Fall 2007	LB	Seeded	OS	CS-OR3	7.9	19.1	11.4	1	4
Fall 2007	LB	Seeded	RR	CS-RR1	7.9	19.1	11.4	1	4
Fall 2007	LB	Seeded	RR	CS-RR2	7.9	19.1	11.4	1	4
Fall 2007	LB	Seeded	RR	CS-RR3	7.9	19.1	11.4	1	4

Living Shoreline (LSE) -- Continued

Sampling Period	Site	Cage Control	Substrate	Substrate #	Temp	Salinity	DO	Depth	TSS
Fall 2007	LB	Seeded	CM	CS-CM1	7.9	19.1	11.4	1	4
Fall 2007	LB	Seeded	CM	CS-CM2	7.9	19.1	11.4	1	4
Fall 2007	LB	Seeded	CM	CS-CM3	7.9	19.1	11.4	1	4
Fall 2007	LB	Seeded	CB	CS-CB1	7.9	19.1	11.4	1	4
Fall 2007	LB	Seeded	CB	CS-CB2	7.9	19.1	11.4	1	4
Fall 2007	LB	Seeded	CB	CS-CB3	7.9	19.1	11.4	1	4
Fall 2007	EB	Unseeded	OS	HU-OR1	11.7	22.4	9.2	1	6
Fall 2007	EB	Unseeded	OS	HU-OR2	11.7	22.4	9.2	1	6
Fall 2007	EB	Unseeded	OS	HU-OR3	11.7	22.4	9.2	1	6
Fall 2007	EB	Unseeded	RR	HU-RR1	11.7	22.4	9.2	1	6
Fall 2007	EB	Unseeded	RR	HU-RR2	11.7	22.4	9.2	1	6
Fall 2007	EB	Unseeded	RR	HU-RR3	11.7	22.4	9.2	1	6
Fall 2007	EB	Unseeded	CM	HU-CM1	11.7	22.4	9.2	1	6
Fall 2007	EB	Unseeded	CM	HU-CM2	11.7	22.4	9.2	1	6
Fall 2007	EB	Unseeded	CM	HU-CM3	11.7	22.4	9.2	1	6
Fall 2007	EB	Unseeded	CB	HU-CB1	11.7	22.4	9.2	1	6
Fall 2007	EB	Unseeded	CB	HU-CB2	11.7	22.4	9.2	1	6
Fall 2007	EB	Unseeded	CB	HU-CB3	11.7	22.4	9.2	1	6
Fall 2007	EB	Seeded	OS	HS-OR1	11.7	22.4	9.2	1	6
Fall 2007	EB	Seeded	OS	HS-OR2	11.7	22.4	9.2	1	6
Fall 2007	EB	Seeded	OS	HS-OR3	11.7	22.4	9.2	1	6
Fall 2007	EB	Seeded	RR	HS-RR1	11.7	22.4	9.2	1	6

Living Shoreline (LSE) -- Continued

Sampling Period	Site	Cage Control	Substrate	Substrate #	Temp	Salinity	DO	Depth	TSS
Fall 2007	EB	Seeded	RR	HS-RR2	11.7	22.4	9.2	1	6
Fall 2007	EB	Seeded	RR	HS-RR3	11.7	22.4	9.2	1	6
Fall 2007	EB	Seeded	CM	HS-CM1	11.7	22.4	9.2	1	6
Fall 2007	EB	Seeded	CM	HS-CM2	11.7	22.4	9.2	1	6
Fall 2007	EB	Seeded	CM	HS-CM3	11.7	22.4	9.2	1	6
Fall 2007	EB	Seeded	CB	HS-CB1	11.7	22.4	9.2	1	6
Fall 2007	EB	Seeded	CB	HS-CB2	11.7	22.4	9.2	1	6
Fall 2007	EB	Seeded	CB	HS-CB3	11.7	22.4	9.2	1	6
Fall 2008	LB	Unseeded	OS	CU-OR1	16.0	22.4	9.6	1	6
Fall 2008	LB	Unseeded	OS	CU-OR2	16.0	22.4	9.6	1	6
Fall 2008	LB	Unseeded	OS	CU-OR3	16.0	22.4	9.6	1	6
Fall 2008	LB	Unseeded	RR	CU-RR1	16.0	22.4	9.6	1	6
Fall 2008	LB	Unseeded	RR	CU-RR2	16.0	22.4	9.6	1	6
Fall 2008	LB	Unseeded	RR	CU-RR3	16.0	22.4	9.6	1	6
Fall 2008	LB	Unseeded	CM	CU-CM1	16.0	22.4	9.6	1	6
Fall 2008	LB	Unseeded	CM	CU-CM2	16.0	22.4	9.6	1	6
Fall 2008	LB	Unseeded	CM	CU-CM3	16.0	22.4	9.6	1	6
Fall 2008	LB	Unseeded	CB	CU-CB1	16.0	22.4	9.6	1	6
Fall 2008	LB	Unseeded	CB	CU-CB2	16.0	22.4	9.6	1	6
Fall 2008	LB	Unseeded	CB	CU-CB3	16.0	22.4	9.6	1	6
Fall 2008	LB	Seeded	OS	CS-OR1	16.0	22.4	9.6	1	6
Fall 2008	LB	Seeded	OS	CS-OR2	16.0	22.4	9.6	1	6

Living Shoreline (LSE) -- Continued

Sampling Period	Site	Cage Control	Substrate	Substrate #	Temp	Salinity	DO	Depth	TSS
Fall 2008	LB	Seeded	OS	CS-OR3	16.0	22.4	9.6	1	6
Fall 2008	LB	Seeded	RR	CS-RR1	16.0	22.4	9.6	1	6
Fall 2008	LB	Seeded	RR	CS-RR2	16.0	22.4	9.6	1	6
Fall 2008	LB	Seeded	RR	CS-RR3	16.0	22.4	9.6	1	6
Fall 2008	LB	Seeded	CM	CS-CM1	16.0	22.4	9.6	1	6
Fall 2008	LB	Seeded	CM	CS-CM2	16.0	22.4	9.6	1	6
Fall 2008	LB	Seeded	CM	CS-CM3	16.0	22.4	9.6	1	6
Fall 2008	LB	Seeded	CB	CS-CB1	16.0	22.4	9.6	1	6
Fall 2008	LB	Seeded	CB	CS-CB2	16.0	22.4	9.6	1	6
Fall 2008	LB	Seeded	CB	CS-CB3	16.0	22.4	9.6	1	6
Fall 2008	EB	Unseeded	OS	HU-OR1	15.9	24.8	8.3	1	13
Fall 2008	EB	Unseeded	OS	HU-OR2	15.9	24.8	8.3	1	13
Fall 2008	EB	Unseeded	OS	HU-OR3	15.9	24.8	8.3	1	13
Fall 2008	EB	Unseeded	RR	HU-RR1	15.9	24.8	8.3	1	13
Fall 2008	EB	Unseeded	RR	HU-RR2	15.9	24.8	8.3	1	13
Fall 2008	EB	Unseeded	RR	HU-RR3	15.9	24.8	8.3	1	13
Fall 2008	EB	Unseeded	CM	HU-CM1	15.9	24.8	8.3	1	13
Fall 2008	EB	Unseeded	CM	HU-CM2	15.9	24.8	8.3	1	13
Fall 2008	EB	Unseeded	CM	HU-CM3	15.9	24.8	8.3	1	13
Fall 2008	EB	Unseeded	CB	HU-CB1	15.9	24.8	8.3	1	13
Fall 2008	EB	Unseeded	CB	HU-CB2	15.9	24.8	8.3	1	13
Fall 2008	EB	Unseeded	CB	HU-CB3	15.9	24.8	8.3	1	13

Living Shoreline (LSE) -- Continued

Sampling Period	Site	Cage Control	Substrate	Substrate #	Temp	Salinity	DO	Depth	TSS
Fall 2008	EB	Seeded	OS	HS-OR1	15.9	24.8	8.3	1	13
Fall 2008	EB	Seeded	OS	HS-OR2	15.9	24.8	8.3	1	13
Fall 2008	EB	Seeded	OS	HS-OR3	15.9	24.8	8.3	1	13
Fall 2008	EB	Seeded	RR	HS-RR1	15.9	24.8	8.3	1	13
Fall 2008	EB	Seeded	RR	HS-RR2	15.9	24.8	8.3	1	13
Fall 2008	EB	Seeded	RR	HS-RR3	15.9	24.8	8.3	1	13
Fall 2008	EB	Seeded	CM	HS-CM1	15.9	24.8	8.3	1	13
Fall 2008	EB	Seeded	CM	HS-CM2	15.9	24.8	8.3	1	13
Fall 2008	EB	Seeded	CM	HS-CM3	15.9	24.8	8.3	1	13
Fall 2008	EB	Seeded	CB	HS-CB1	15.9	24.8	8.3	1	13
Fall 2008	EB	Seeded	CB	HS-CB2	15.9	24.8	8.3	1	13
Fall 2008	EB	Seeded	CB	HS-CB3	15.9	24.8	8.3	1	13

Living Shoreline (LSE) -- Continued

Sampling Period	Site	Cage Control	Substrate	Substrate #	Nitrogen	Kjiedahl Nitrogen	Phosphorus	E coli	Enterococcus
Summer 2007	LB	Unseeded	OS	CU-OR1	-	1.4	0.07	0	25
Summer 2007	LB	Unseeded	OS	CU-OR2	-	1.4	0.07	0	25
Summer 2007	LB	Unseeded	OS	CU-OR3	-	1.4	0.07	0	25
Summer 2007	LB	Unseeded	RR	CU-RR1	-	1.4	0.07	0	25
Summer 2007	LB	Unseeded	RR	CU-RR2	-	1.4	0.07	0	25
Summer 2007	LB	Unseeded	RR	CU-RR3	-	1.4	0.07	0	25
Summer 2007	LB	Unseeded	CM	CU-CM1	-	1.4	0.07	0	25
Summer 2007	LB	Unseeded	CM	CU-CM2	-	1.4	0.07	0	25
Summer 2007	LB	Unseeded	CM	CU-CM3	-	1.4	0.07	0	25
Summer 2007	LB	Unseeded	CB	CU-CB1	-	1.4	0.07	0	25
Summer 2007	LB	Unseeded	CB	CU-CB2	-	1.4	0.07	0	25
Summer 2007	LB	Unseeded	CB	CU-CB3	-	1.4	0.07	0	25
Summer 2007	LB	Seeded	OS	CS-OR1	-	1.4	0.07	0	25
Summer 2007	LB	Seeded	OS	CS-OR2	-	1.4	0.07	0	25
Summer 2007	LB	Seeded	OS	CS-OR3	-	1.4	0.07	0	25
Summer 2007	LB	Seeded	RR	CS-RR1	-	1.4	0.07	0	25
Summer 2007	LB	Seeded	RR	CS-RR2	-	1.4	0.07	0	25
Summer 2007	LB	Seeded	RR	CS-RR3	-	1.4	0.07	0	25
Summer 2007	LB	Seeded	CM	CS-CM1	-	1.4	0.07	0	25
Summer 2007	LB	Seeded	CM	CS-CM2		1.4	0.07	0	25

Living Shoreline (LSE) – Continued

Sampling Period	Site	Cage Control	Substrate	Substrate #	Nitrogen	Kjiedahl Nitrogen	Phosphorus	E coli	Enterococcus
Summer 2007	LB	Seeded	CM	CS-CM3		1.4	0.07	0	25
Summer 2007	LB	Seeded	CB	CS-CB1	-	1.4	0.07	0	25
Summer 2007	LB	Seeded	CB	CS-CB2	-	1.4	0.07	0	25
Summer 2007	LB	Seeded	CB	CS-CB3	-	1.4	0.07	0	25
Summer 2007	EB	Unseeded	OS	HU-OR1	-	0.9	0.09	407.93	25
Summer 2007	EB	Unseeded	OS	HU-OR2	-	0.9	0.09	407.93	25
Summer 2007	EB	Unseeded	OS	HU-OR3	-	0.9	0.09	407.93	25
Summer 2007	EB	Unseeded	RR	HU-RR1	-	0.9	0.09	407.93	25
Summer 2007	EB	Unseeded	RR	HU-RR2	-	0.9	0.09	407.93	25
Summer 2007	EB	Unseeded	RR	HU-RR3	-	0.9	0.09	407.93	25
Summer 2007	EB	Unseeded	CM	HU-CM1	-	0.9	0.09	407.93	25
Summer 2007	EB	Unseeded	CM	HU-CM2	-	0.9	0.09	407.93	25
Summer 2007	EB	Unseeded	CM	HU-CM3	-	0.9	0.09	407.93	25
Summer 2007	EB	Unseeded	CB	HU-CB1	-	0.9	0.09	407.93	25
Summer 2007	EB	Unseeded	CB	HU-CB2	-	0.9	0.09	407.93	25
Summer 2007	EB	Unseeded	CB	HU-CB3	-	0.9	0.09	407.93	25
Summer 2007	EB	Seeded	OS	HS-OR1	-	0.9	0.09	407.93	25
Summer 2007	EB	Seeded	OS	HS-OR2	-	0.9	0.09	407.93	25
Summer 2007	EB	Seeded	OS	HS-OR3	-	0.9	0.09	407.93	25
Summer 2007	EB	Seeded	RR	HS-RR1	-	0.9	0.09	407.93	25

Living Shoreline (LSE) -- Continued

Sampling Period	Site	Cage Control	Substrate	Substrate #	Nitrogen	Kjiedahl Nitrogen	Phosphorus	E coli	Enterococcus
Summer 2007	EB	Seeded	RR	HS-RR2	-	0.9	0.09	407.93	25
Summer 2007	EB	Seeded	RR	HS-RR3	-	0.9	0.09	407.93	25
Summer 2007	EB	Seeded	CM	HS-CM1	-	0.9	0.09	407.93	25
Summer 2007	EB	Seeded	CM	HS-CM2	-	0.9	0.09	407.93	25
Summer 2007	EB	Seeded	CM	HS-CM3	-	0.9	0.09	407.93	25
Summer 2007	EB	Seeded	CB	HS-CB1	-	0.9	0.09	407.93	25
Summer 2007	EB	Seeded	CB	HS-CB2	-	0.9	0.09	407.93	25
Summer 2007	EB	Seeded	CB	HS-CB3	-	0.9	0.09	407.93	25
Fall 2007	LB	Unseeded	OS	CU-OR1	-	1.0	0.05	2.83	25
Fall 2007	LB	Unseeded	OS	CU-OR2	-	1.0	0.05	2.83	25
Fall 2007	LB	Unseeded	OS	CU-OR3	-	1.0	0.05	2.83	25
Fall 2007	LB	Unseeded	RR	CU-RR1	-	1.0	0.05	2.83	25
Fall 2007	LB	Unseeded	RR	CU-RR2	-	1.0	0.05	2.83	25
Fall 2007	LB	Unseeded	RR	CU-RR3	-	1.0	0.05	2.83	25
Fall 2007	LB	Unseeded	CM	CU-CM1	-	1.0	0.05	2.83	25
Fall 2007	LB	Unseeded	CM	CU-CM2	-	1.0	0.05	2.83	25
Fall 2007	LB	Unseeded	CM	CU-CM3	-	1.0	0.05	2.83	25
Fall 2007	LB	Unseeded	CB	CU-CB1	-	1.0	0.05	2.83	25
Fall 2007	LB	Unseeded	CB	CU-CB2	-	1.0	0.05	2.83	25
Fall 2007	LB	Unseeded	CB	CU-CB3	-	1.0	0.05	2.83	25

Living Shoreline (LSE) -- Continued

Sampling Period	Site	Cage Control	Substrate	Substrate #	Nitrogen	Kjiedahl Nitrogen	Phosphorus	E coli	Enterococcus
Fall 2007	LB	Seeded	OS	CS-OR1	-	1.0	0.05	2.83	25
Fall 2007	LB	Seeded	OS	CS-OR2	-	1.0	0.05	2.83	25
Fall 2007	LB	Seeded	OS	CS-OR3	-	1.0	0.05	2.83	25
Fall 2007	LB	Seeded	RR	CS-RR1	-	1.0	0.05	2.83	25
Fall 2007	LB	Seeded	RR	CS-RR2	-	1.0	0.05	2.83	25
Fall 2007	LB	Seeded	RR	CS-RR3	-	1.0	0.05	2.83	25
Fall 2007	LB	Seeded	CM	CS-CM1	-	1.0	0.05	2.83	25
Fall 2007	LB	Seeded	CM	CS-CM2	-	1.0	0.05	2.83	25
Fall 2007	LB	Seeded	CM	CS-CM3	-	1.0	0.05	2.83	25
Fall 2007	LB	Seeded	CB	CS-CB1	-	1.0	0.05	2.83	25
Fall 2007	LB	Seeded	CB	CS-CB2	-	1.0	0.05	2.83	25
Fall 2007	LB	Seeded	CB	CS-CB3	-	1.0	0.05	2.83	25
Fall 2007	EB	Unseeded	OS	HU-OR1	0.3	0.5	0.14	7.42	25
Fall 2007	EB	Unseeded	OS	HU-OR2	0.3	0.5	0.14	7.42	25
Fall 2007	EB	Unseeded	OS	HU-OR3	0.3	0.5	0.14	7.42	25
Fall 2007	EB	Unseeded	RR	HU-RR1	0.3	0.5	0.14	7.42	25
Fall 2007	EB	Unseeded	RR	HU-RR2	0.3	0.5	0.14	7.42	25
Fall 2007	EB	Unseeded	RR	HU-RR3	0.3	0.5	0.14	7.42	25
Fall 2007	EB	Unseeded	CM	HU-CM1	0.3	0.5	0.14	7.42	25
Fall 2007	EB	Unseeded	CM	HU-CM2	0.3	0.5	0.14	7.42	25

Living Shoreline (LSE) -- Continued

Sampling Period	Site	Cage Control	Substrate	Substrate #	Nitrogen	Kjiedahl Nitrogen	Phosphorus	E coli	Enterococcus
Fall 2007	EB	Unseeded	CM	HU-CM3	0.3	0.5	0.14	7.42	25
Fall 2007	EB	Unseeded	CB	HU-CB1	0.3	0.5	0.14	7.42	25
Fall 2007	EB	Unseeded	CB	HU-CB2	0.3	0.5	0.14	7.42	25
Fall 2007	EB	Unseeded	CB	HU-CB3	0.3	0.5	0.14	7.42	25
Fall 2007	EB	Seeded	OS	HS-OR1	0.3	0.5	0.14	7.42	25
Fall 2007	EB	Seeded	OS	HS-OR2	0.3	0.5	0.14	7.42	25
Fall 2007	EB	Seeded	OS	HS-OR3	0.3	0.5	0.14	7.42	25
Fall 2007	EB	Seeded	RR	HS-RR1	0.3	0.5	0.14	7.42	25
Fall 2007	EB	Seeded	RR	HS-RR2	0.3	0.5	0.14	7.42	25
Fall 2007	EB	Seeded	RR	HS-RR3	0.3	0.5	0.14	7.42	25
Fall 2007	EB	Seeded	CM	HS-CM1	0.3	0.5	0.14	7.42	25
Fall 2007	EB	Seeded	CM	HS-CM2	0.3	0.5	0.14	7.42	25
Fall 2007	EB	Seeded	CM	HS-CM3	0.3	0.5	0.14	7.42	25
Fall 2007	EB	Seeded	CB	HS-CB1	0.3	0.5	0.14	7.42	25
Fall 2007	EB	Seeded	CB	HS-CB2	0.3	0.5	0.14	7.42	25
Fall 2007	EB	Seeded	CB	HS-CB3	0.3	0.5	0.14	7.42	25
Fall 2008	LB	Unseeded	OS	CU-OR1	0.55	0.8	0.050	2.45	25
Fall 2008	LB	Unseeded	OS	CU-OR2	0.55	0.8	0.050	2.45	25
Fall 2008	LB	Unseeded	OS	CU-OR3	0.55	0.8	0.050	2,45	25
Fall 2008	LB	Unseeded	RR	CU-RR1	0.55	0.8	0.050	2.45	25

Living Shoreline (LSE) -- Continued

Sampling Period	Site	Cage Control	Substrate	Substrate #	Nitrogen	Kjiedahl Nitrogen	Phosphorus	E coli	Enterococcus
Fall 2008	LB	Unseeded	RR	CU-RR2	0.55	0.8	0.050	2.45	25
Fall 2008	LB	Unseeded	RR	CU-RR3	0.55	0.8	0.050	2.45	25
Fall 2008	LB	Unseeded	CM	CU-CM1	0.55	0.8	0.050	2.45	25
Fall 2008	LB	Unseeded	CM	CU-CM2	0.55	0.8	0.050	2.45	25
Fall 2008	LB	Unseeded	CM	CU-CM3	0.55	0.8	0.050	2.45	25
Fall 2008	LB	Unseeded	CB	CU-CB1	0.55	0.8	0.050	2.45	25
Fall 2008	LB	Unseeded	CB	CU-CB2	0.55	0.8	0.050	2.45	25
Fall 2008	LB	Unseeded	CB	CU-CB3	0.55	0.8	0.050	2.45	25
Fall 2008	LB	Seeded	OS	CS-OR1	0.55	0.8	0.050	2.45	25
Fall 2008	LB	Seeded	OS	CS-OR2	0.55	0.8	0.050	2.45	25
Fall 2008	LB	Seeded	OS	CS-OR3	0.55	0.8	0.050	2,45	25
Fall 2008	LB	Seeded	RR	CS-RR1	0.55	0.8	0.050	2.45	25
Fall 2008	LB	Seeded	RR	CS-RR2	0.55	0.8	0.050	2.45	25
Fall 2008	LB	Seeded	RR	CS-RR3	0.55	0.8	0.050	2.45	25
Fall 2008	LB	Seeded	CM	CS-CM1	0.55	0.8	0.050	2.45	25
Fall 2008	LB	Seeded	CM	CS-CM2	0.55	0.8	0.050	2.45	25
Fall 2008	LB	Seeded	CM	CS-CM3	0.55	0.8	0.050	2.45	25
Fall 2008	LB	Seeded	CB	CS-CB1	0.55	0.8	0.050	2.45	25
Fall 2008	LB	Seeded	CB	CS-CB2	0.55	0.8	0.050	2.45	25
Fall 2008	LB	Seeded	CB	CS-CB3	0.55	0.8	0.050	2.45	25

Living Shoreline (LSE) -- Continued

Sampling Period	Site	Cage Control	Substrate	Substrate #	Nitrogen	Kjiedahl Nitrogen	Phosphorus	E coli	Enterococcus
Fall 2008	EB	Unseeded	OS	HU-OR1	0.43	0.5	0.060	40.91	25
Fall 2008	EB	Unseeded	OS	HU-OR2	0.43	0.5	0.060	40.91	25
Fall 2008	EB	Unseeded	OS	HU-OR3	0.43	0.5	0.060	40.91	25
Fall 2008	EB	Unseeded	RR	HU-RR1	0.43	0.5	0.060	40.91	25
Fall 2008	EB	Unseeded	RR	HU-RR2	0.43	0.5	0.060	40.91	25
Fall 2008	EB	Unseeded	RR	HU-RR3	0.43	0.5	0.060	40.91	25
Fall 2008	EB	Unseeded	CM	HU-CM1	0.43	0.5	0.060	40.91	25
Fall 2008	EB	Unseeded	CM	HU-CM2	0.43	0.5	0.060	40.91	25
Fall 2008	EB	Unseeded	CM	HU-CM3	0.43	0.5	0.060	40.91	25
Fall 2008	EB	Unseeded	CB	HU-CB1	0.43	0.5	0.060	40.91	25
Fall 2008	EB	Unseeded	CB	HU-CB2	0.43	0.5	0.060	40.91	25
Fall 2008	EB	Unseeded	CB	HU-CB3	0.43	0.5	0.060	40.91	25
Fall 2008	EB	Seeded	OS	HS-OR1	0.43	0.5	0.060	40.91	25
Fall 2008	EB	Seeded	OS	HS-OR2	0.43	0.5	0.060	40.91	25
Fall 2008	EB	Seeded	OS	HS-OR3	0.43	0.5	0.060	40.91	25
Fall 2008	EB	Seeded	RR	HS-RR1	0.43	0.5	0.060	40.91	25
Fall 2008	EB	Seeded	RR	HS-RR2	0.43	0.5	0.060	40.91	25
Fall 2008	EB	Seeded	RR	HS-RR3	0.43	0.5	0.060	40.91	25
Fall 2008	EB	Seeded	CM	HS-CM1	0.43	0.5	0.060	40.91	25
Fall 2008	EB	Seeded	CM	HS-CM2	0.43	0.5	0.060	40.91	25

Living Shoreline (LSE) -- Continued

Sampling Period	Site	Cage Control	Substrate	Substrate #	Nitrogen	Kjiedahl Nitrogen	Phosphorus	E coli	Enterococcu
Fall 2008	EB	Seeded	CM	HS-CM3	0.43	0.5	0.060	40.91	25
Fall 2008	EB	Seeded	CB	HS-CB1	0.43	0.5	0.060	40.91	25
Fall 2008	EB	Seeded	CB	HS-CB2	0.43	0.5	0.060	40.91	25
Fall 2008	EB	Seeded	CB	HS-CB3	0.43	0.5	0.060	40.91	25

Living Shoreline (LSE) -- Continued

Sampling Period	Site	Cage Control	Substrate	Substrate #	Total Set	Total Live	Total Dead	Live Density	Total Density (#/m2)
Summer 2007	LB	Unseeded	OS	CU-OR1	50	41	9	249.7	304.6
Summer 2007	LB	Unseeded	OS	CU-OR2	35	32	3	194.9	213.2
Summer 2007	LB	Unseeded	OS	CU-OR3	29	28	1	170.6	176.6
Summer 2007	LB	Unseeded	RR	CU-RR1	11	5	6	30.5	67.0
Summer 2007	LB	Unseeded	RR	CU-RR2	8	4	3	24.4	48.7
Summer 2007	LB	Unseeded	RR	CU-RR3	8	7	1	42.6	48.7
Summer 2007	LB	Unseeded	CM	CU-CM1	8	7	1	25.1	28.7
Summer 2007	LB	Unseeded	CM	CU-CM2	9	9	0	32.3	32.3
Summer 2007	LB	Unseeded	CM	CU-CM3	4	4	0	14.4	14.4
Summer 2007	LB	Unseeded	CB	CU-CB1	-	-	-	-	-
Summer 2007	LB	Unseeded	CB	CU-CB2	-	-	-	-	-
Summer 2007	LB	Unseeded	CB	CU-CB3	-	-	-	-	-
Summer 2007	LB	Seeded	OS	CS-OR1	669	622	47		
Summer 2007	LB	Seeded	OS	CS-OR2	-	-	-	-	-
Summer 2007	LB	Seeded	OS	CS-OR3	-	-	-	-	-
Summer 2007	LB	Seeded	RR	CS-RR1	22	22	0	-	-
Summer 2007	LB	Seeded	RR	CS-RR2	20	15	5	-	-
Summer 2007	LB	Seeded	RR	CS-RR3	43	43	0	-	-
Summer 2007	LB	Seeded	CM	CS-CM1	49	48	1	131.4	-
Summer 2007	LB	Seeded	CM	CS-CM2	91	88	3	253.2	-

Living Shoreline (LSE) -- Continued

Sampling Period	Site	Cage Control	Substrate	Substrate #	Total Set	Total Live	Total Dead	Live Density	Total Density (#/m2)
Summer 2007	LB	Seeded	CM	CS-CM3	28	28	0	76.9	-
Summer 2007	LB	Seeded	CB	CS-CB1	-	-	-	-	-
Summer 2007	LB	Seeded	CB	CS-CB2	-	-	-	-	-
Summer 2007	LB	Seeded	CB	CS-CB3	-	-	-	-	-
Summer 2007	EB	Unseeded	OS	HU-OR1	325	265	60	1614.1	1979.6
Summer 2007	EB	Unseeded	OS	HU-OR2	248	195	53	1187.8	1510.6
Summer 2007	EB	Unseeded	OS	HU-OR3	267	187	80	1139.0	1626.3
Summer 2007	EB	Unseeded	RR	HU-RR1	74	58	16	353.3	450.7
Summer 2007	EB	Unseeded	RR	HU-RR2	44	27	17	164.5	268.0
Summer 2007	EB	Unseeded	RR	HU-RR3	13	10	3	60.9	79.2
Summer 2007	EB	Unseeded	CM	HU-CM1	37	36	1	129.2	132.8
Summer 2007	EB	Unseeded	CM	HU-CM2	10	8	4	21.5	35.9
Summer 2007	EB	Unseeded	CM	HU-CM3	22	20	2	71.8	78.9
Summer 2007	EB	Unseeded	CB	HU-CB1	-	-	-	-	-
Summer 2007	EB	Unseeded	CB	HU-CB2	-	-	-	-	-
Summer 2007	EB	Unseeded	CB	HU-CB3	-	-	-	-	-
Summer 2007	EB	Seeded	OS	HS-OR1	226	184	42		
Summer 2007	EB	Seeded	OS	HS-OR2	-	-	-	-	-
Summer 2007	EB	Seeded	OS	HS-OR3	-	-	-	-	-
Summer 2007	EB	Seeded	RR	HS-RR1	12	9	3	-	-

Living Shoreline (LSE) -- Continued

Sampling Period	Site	Cage Control	Substrate	Substrate #	Total Set	Total Live	Total Dead	Live Density	Total Density (#/m2)
Summer 2007	EB	Seeded	RR	HS-RR2	10				
Summer 2007	EB	Seeded	RR	HS-RR3	29				
Summer 2007	EB	Seeded	CM	HS-CM1	47				
Summer 2007	EB	Seeded	CM	HS-CM2	14				
Summer 2007	EB	Seeded	CM	HS-CM3	31				
Summer 2007	EB	Seeded	CB	HS-CB1	-				
Summer 2007	EB	Seeded	CB	HS-CB2	-				
Summer 2007	EB	Seeded	CB	HS-CB3	-				
Fall 2007	LB	Unseeded	OS	CU-OR1	682				
Fall 2007	LB	Unseeded	OS	CU-OR2	532				
Fall 2007	LB	Unseeded	OS	CU-OR3	422				
Fall 2007	LB	Unseeded	RR	CU-RR1	127				
Fall 2007	LB	Unseeded	RR	CU-RR2	251				
Fall 2007	LB	Unseeded	RR	CU-RR3	77				
Fall 2007	LB	Unseeded	CM	CU-CM1	90				
Fall 2007	LB	Unseeded	CM	CU-CM2	61				
Fall 2007	LB	Unseeded	CM	CU-CM3	100				
Fall 2007	LB	Unseeded	CB	CU-CB1	-				
Fall 2007	LB	Unseeded	CB	CU-CB2	-				
Fall 2007	LB	Unseeded	CB	CU-CB3	-				
Fall 2007	LB	Seeded	OS	CS-OR1	671				

Living Shoreline (LSE) -- Continued

Sampling Period	Site	Cage Control	Substrate	Substrate #	Total Set	Total Live	Total Dead	Live Density	Total Density (#/m2)
Fall 2007	LB	Seeded	OS	CS-OR2	-		-	-	-
Fall 2007	LB	Seeded	OS	CS-OR3	-		-	-	-
Fall 2007	LB	Seeded	RR	CS-RR1	163		10	-	-
Fall 2007	LB	Seeded	RR	CS-RR2	74		5	-	-
Fall 2007	LB	Seeded	RR	CS-RR3	103		3	-	-
Fall 2007	LB	Seeded	CM	CS-CM1	-		-	592.9	-
Fall 2007	LB	Seeded	CM	CS-CM2	-		-	814.1	-
Fall 2007	LB	Seeded	CM	CS-CM3	-		-	134.6	-
Fall 2007	LB	Seeded	CB	CS-CB1	113		22	1181.8	-
Fall 2007	LB	Seeded	CB	CS-CB2	117		8	1415.6	-
Fall 2007	LB	Seeded	CB	CS-CB3	128		5	1597.4	-
Fall 2007	EB	Unseeded	OS	HU-OR1	455		73	1308.2	1558.2
Fall 2007	EB	Unseeded	OS	HU-OR2	602		153	1537.7	2061.6
Fall 2007	EB	Unseeded	OS	HU-OR3	531		168	1243.2	1818.5
Fall 2007	EB	Unseeded	RR	HU-RR1	141		42	603.0	858.8
Fall 2007	EB	Unseeded	RR	HU-RR2	142		33	663.9	864.9
Fall 2007	EB	Unseeded	RR	HU-RR3	138		44	572.6	840.6
Fall 2007	EB	Unseeded	CM	HU-CM1	65		9	477.4	-
Fall 2007	EB	Unseeded	CM	HU-CM2	19		0	162.0	-
Fall 2007	EB	Unseeded	CM	HU-CM3	6		0	51.2	-
Fall 2007	EB	Unseeded	CB	HU-CB1	-		-	-	-

Living Shoreline (LSE) -- Continued

Sampling Period	Site	Cage Control	Substrate	Substrate #	Total Set	Total Live	Total Dead	Live Density	Total Density (#/m2)
Fall 2007	EB	Unseeded	CB	HU-CB2	-		-	-	-
Fall 2007	EB	Unseeded	CB	HU-CB3	-		-	-	-
Fall 2007	EB	Seeded	OS	HS-OR1	539		133	-	-
Fall 2007	EB	Seeded	OS	HS-OR2	-		-	-	-
Fall 2007	EB	Seeded	OS	HS-OR3	-		-	-	-
Fall 2007	EB	Seeded	RR	HS-RR1	17		3	-	-
Fall 2007	EB	Seeded	RR	HS-RR2	19		1	-	-
Fall 2007	EB	Seeded	RR	HS-RR3	22		1	-	-
Fall 2007	EB	Seeded	CM	HS-CM1	-		-	28.8	-
Fall 2007	EB	Seeded	CM	HS-CM2	-		-	9.6	-
Fall 2007	EB	Seeded	CM	HS-CM3	-		-	22.4	-
Fall 2007	EB	Seeded	CB	HS-CB1	-		-	-	-
Fall 2007	EB	Seeded	CB	HS-CB2	-		-	-	-
Fall 2007	EB	Seeded	CB	HS-CB3	-		-	-	-
Fall 2008	LB	Unseeded	OS	CU-OR1	639		217	1445.2	2188.4
Fall 2008	LB	Unseeded	OS	CU-OR2	487		143	1178.1	1667.8
Fall 2008	LB	Unseeded	OS	CU-OR3	443		144	1024	1517.1
Fall 2008	LB	Unseeded	RR	CU-RR1	123		25	596.9	750.0
Fall 2008	LB	Unseeded	RR	CU-RR2	161		45	706.6	981.7
Fall 2008	LB	Unseeded	RR	CU-RR3	105		19	523.8	640.2
Fall 2008	LB	Unseeded	CM	CU-CM1	82		10	615.2	700.7

Living Shoreline (LSE) -- Continued

Sampling Period	Site	Cage Control	Substrate	Substrate #	Total Set	Total Live	Total Dead	Live Density	Total Density (#/m2)
Fall 2008	LB	Unseeded	CM	CU-CM2	59		8	435.8	504.1
Fall 2008	LB	Unseeded	CM	CU-CM3	122		22	854.5	1042.5
Fall 2008	LB	Unseeded	CB	CU-CB1	75		19	727.3	974.0
Fall 2008	LB	Unseeded	CB	CU-CB2	78		18	779.2	1013.0
Fall 2008	LB	Unseeded	CB	CU-CB3	60		7	668.3	779.2
Fall 2008	LB	Seeded	OS	CS-OR1	542		151	1339.0	1856.2
Fall 2008	LB	Seeded	OS	CS-OR2	358		164	1226.0	3007.8
Fall 2008	LB	Seeded	OS	CS-OR3	-		-	-	-
Fall 2008	LB	Seeded	RR	CS-RR1	48		6	651.2	744.2
Fall 2008	LB	Seeded	RR	CS-RR2	49		11	589.1	759.7
Fall 2008	LB	Seeded	RR	CS-RR3	97		25	1116.3	1503.9
Fall 2008	LB	Seeded	CM	CS-CM1	233		39	621.8	746.8
Fall 2008	LB	Seeded	CM	CS-CM2	353		78	881.4	1131.4
Fall 2008	LB	Seeded	CM	CS-CM3	48		12	115.4	153.8
Fall 2008	LB	Seeded	CB	CS-CB1	120		33	1129.9	1558.4
Fall 2008	LB	Seeded	CB	CS-CB2	133		32	1311.7	1727.3
Fall 2008	LB	Seeded	CB	CS-CB3	138		25	1467.5	1792.2
Fall 2008	EB	Unseeded	OS	HU-OR1	341		196	496.6	1167.8
Fall 2008	EB	Unseeded	OS	HU-OR2	313		130	626.7	1071.9
Fall 2008	EB	Unseeded	OS	HU-OR3	221		126	325.3	756.8
Fall 2008	EB	Unseeded	RR	HU-RR1	140		77	384.1	853.7

Living Shoreline (LSE) -- Continued

Sampling Period	Site	Cage Control	Substrate	Substrate #	Total Set	Total Live	Total Dead	Live Density	Total Density (#/m2)
Fall 2008	EB	Unseeded	RR	HU-RR2	142		72	426.8	865.9
Fall 2008	EB	Unseeded	RR	HU-RR3	93		64	176.8	567.1
Fall 2008	EB	Unseeded	CM	HU-CM1	29		10	162.4	247.8
Fall 2008	EB	Unseeded	CM	HU-CM2	28		8	170.9	239.3
Fall 2008	EB	Unseeded	CM	HU-CM3	22		7	128.2	188.0
Fall 2008	EB	Unseeded	CB	HU-CB1	-		-	-	-
Fall 2008	EB	Unseeded	CB	HU-CB2	-		-	-	-
Fall 2008	EB	Unseeded	CB	HU-CB3	-		-	-	-
Fall 2008	EB	Seeded	OS	HS-OR1	372		176	671.2	1274
Fall 2008	EB	Seeded	OS	HS-OR2	238		98	815.1	2170.5
Fall 2008	EB	Seeded	OS	HS-OR3	-		-	-	-
Fall 2008	EB	Seeded	RR	HS-RR1	26		9	263.6	403.1
Fall 2008	EB	Seeded	RR	HS-RR2	-		-	-	-
Fall 2008	EB	Seeded	RR	HS-RR3	52		21	480.6	806.2
Fall 2008	EB	Seeded	CM	HS-CM1	18		6	38.5	57.7
Fall 2008	EB	Seeded	CM	HS-CM2	12		3	28.8	38.5
Fall 2008	EB	Seeded	CM	HS-CM3	15		28.8	48.1	
Fall 2008	EB	Seeded	CB	HS-CB1	-		-	-	
Fall 2008	EB	Seeded	CB	HS-CB2	-		-	-	
Fall 2008	EB	Seeded	CB	HS-CB3	-		-	-	

Living Shoreline (LSE) -- Continued

Sampling Period	Site	Cage Control	Substrate	Substrate #	Ash Free Dry Mass (g)	Biomass (g/m^2)
Summer 2007	LB	Unseeded	OS	CU-OR1	8.74	29.94
Summer 2007	LB	Unseeded	OS	CU-OR2	8.82	30.20
Summer 2007	LB	Unseeded	OS	CU-OR3	7.3	25.00
Summer 2007	LB	Unseeded	RR	CU-RR1	2.35	14.31
Summer 2007	LB	Unseeded	RR	CU-RR2	1.77	10.76
Summer 2007	LB	Unseeded	RR	CU-RR3	2.45	14.90
Summer 2007	LB	Unseeded	CM	CU-CM1	0.70	6.00
Summer 2007	LB	Unseeded	CM	CU-CM2	1.98	16.90
Summer 2007	LB	Unseeded	CM	CU-CM3	0.76	6.50
Summer 2007	LB	Unseeded	CB	CU-CB1	-	-
Summer 2007	LB	Unseeded	CB	CU-CB2	-	-
Summer 2007	LB	Unseeded	CB	CU-CB3	-	-
Summer 2007	LB	Seeded	OS	CS-OR1		
Summer 2007	LB	Seeded	OS	CS-OR2	-	-
Summer 2007	LB	Seeded	OS	CS-OR3	-	-
Summer 2007	LB	Seeded	RR	CS-RR1	-	-
Summer 2007	LB	Seeded	RR	CS-RR2	-	-
Summer 2007	LB	Seeded	RR	CS-RR3	-	-
Summer 2007	LB	Seeded	CM	CS-CM1	-	-
Summer 2007	LB	Seeded	CM	CS-CM2	-	-

Living Shoreline (LSE) -- Continued

Sampling Period	Site	Cage Control	Substrate	Substrate #	Ash Free Dry Mass (g)	Biomass (g/m^2)
Summer 2007	LB	Seeded	CM	CS-CM3	-	-
Summer 2007	LB	Seeded	CB	CS-CB1	-	-
Summer 2007	LB	Seeded	CB	CS-CB2	-	-
Summer 2007	LB	Seeded	CB	CS-CB3	-	-
Summer 2007	EB	Unseeded	OS	HU-OR1	186.76	639.57
Summer 2007	EB	Unseeded	OS	HU-OR2	158.88	544.10
Summer 2007	EB	Unseeded	OS	HU-OR3	127.46	436.52
Summer 2007	EB	Unseeded	RR	HU-RR1	21.88	133.28
Summer 2007	EB	Unseeded	RR	HU-RR2	9.66	58.85
Summer 2007	EB	Unseeded	RR	HU-RR3	4.24	25.80
Summer 2007	EB	Unseeded	CM	HU-CM1	12.35	105.20
Summer 2007	EB	Unseeded	CM	HU-CM2	1.80	15.40
Summer 2007	EB	Unseeded	CM	HU-CM3	4.78	40.70
Summer 2007	EB	Unseeded	CB	HU-CB1	-	-
Summer 2007	EB	Unseeded	CB	HU-CB2	-	-
Summer 2007	EB	Unseeded	CB	HU-CB3	-	-
Summer 2007	EB	Seeded	OS	HS-OR1		
Summer 2007	EB	Seeded	OS	HS-OR2	-	-
Summer 2007	EB	Seeded	OS	HS-OR3	-	-
Summer 2007	EB	Seeded	RR	HS-RR1	-	-
Summer 2007	EB	Seeded	RR	HS-RR2	-	-

Living Shoreline (LSE) -- Continued

Sampling Period	Site	Cage Control	Substrate	Substrate #	Ash Free Dry Mass (g)	Biomass (g/m^2)
Summer 2007	EB	Seeded	RR	HS-RR3	-	-
Summer 2007	EB	Seeded	CM	HS-CM1	-	-
Summer 2007	EB	Seeded	CM	HS-CM2	-	-
Summer 2007	EB	Seeded	CM	HS-CM3	-	-
Summer 2007	EB	Seeded	CB	HS-CB1	-	-
Summer 2007	EB	Seeded	CB	HS-CB2	-	-
Summer 2007	EB	Seeded	CB	HS-CB3	-	-
Fall 2007	LB	Unseeded	OS	CU-OR1	90.14	308.71
Fall 2007	LB	Unseeded	OS	CU-OR2	108.82	372.67
Fall 2007	LB	Unseeded	OS	CU-OR3	136.16	466.32
Fall 2007	LB	Unseeded	RR	CU-RR1	18.94	115.37
Fall 2007	LB	Unseeded	RR	CU-RR2	46.88	285.50
Fall 2007	LB	Unseeded	RR	CU-RR3	32.22	196.91
Fall 2007	LB	Unseeded	CM	CU-CM1	21.79	185.7
Fall 2007	LB	Unseeded	CM	CU-CM2	20.42	174.1
Fall 2007	LB	Unseeded	CM	CU-CM3	18.17	154.9
Fall 2007	LB	Unseeded	CB	CU-CB1	-	-
Fall 2007	LB	Unseeded	CB	CU-CB2	-	-
Fall 2007	LB	Unseeded	CB	CU-CB3	-	-
Fall 2007	LB	Seeded	OS	CS-OR1	-	-
Fall 2007	LB	Seeded	OS	CS-OR2	-	-

Living Shoreline (LSE) -- Continued

Sampling Period	Site	Cage Control	Substrate	Substrate #	Ash Free Dry Mass (g)	Biomass (g/m^2)
Fall 2007	LB	Seeded	OS	CS-OR3	-	-
Fall 2007	LB	Seeded	RR	CS-RR1	-	-
Fall 2007	LB	Seeded	RR	CS-RR2	-	-
Fall 2007	LB	Seeded	RR	CS-RR3	-	-
Fall 2007	LB	Seeded	CM	CS-CM1	-	-
Fall 2007	LB	Seeded	CM	CS-CM2	-	-
Fall 2007	LB	Seeded	CM	CS-CM3	-	-
Fall 2007	LB	Seeded	CB	CS-CB1	-	-
Fall 2007	LB	Seeded	CB	CS-CB2	-	-
Fall 2007	LB	Seeded	CB	CS-CB3	-	-
Fall 2007	EB	Unseeded	OS	HU-OR1	198.147	678.6
Fall 2007	EB	Unseeded	OS	HU-OR2	125.003	428.1
Fall 2007	EB	Unseeded	OS	HU-OR3	136.338	466.9
Fall 2007	EB	Unseeded	RR	HU-RR1	20.154	122.8
Fall 2007	EB	Unseeded	RR	HU-RR2	17.797	108.4
Fall 2007	EB	Unseeded	RR	HU-RR3	26.547	161.7
Fall 2007	EB	Unseeded	CM	HU-CM1	5.87	50.1
Fall 2007	EB	Unseeded	CM	HU-CM2	11.02	93.9
Fall 2007	EB	Unseeded	CM	HU-CM3	28.03	239.0
Fall 2007	EB	Unseeded	CB	HU-CB1	-	-
Fall 2007	EB	Unseeded	CB	HU-CB2	-	-

Living Shoreline (LSE) -- Continued

Sampling Period	Site	Cage Control	Substrate	Substrate #	Ash Free Dry Mass (g)	Biomass (g/m^2)
Fall 2007	EB	Unseeded	CB	HU-CB3	-	-
Fall 2007	EB	Seeded	OS	HS-OR1	-	-
Fall 2007	EB	Seeded	OS	HS-OR2	-	-
Fall 2007	EB	Seeded	OS	HS-OR3	-	-
Fall 2007	EB	Seeded	RR	HS-RR1	-	-
Fall 2007	EB	Seeded	RR	HS-RR2	-	-
Fall 2007	EB	Seeded	RR	HS-RR3	-	-
Fall 2007	EB	Seeded	CM	HS-CM1	-	-
Fall 2007	EB	Seeded	CM	HS-CM2	-	-
Fall 2007	EB	Seeded	CM	HS-CM3	-	-
Fall 2007	EB	Seeded	CB	HS-CB1	-	-
Fall 2007	EB	Seeded	CB	HS-CB2	-	-
Fall 2007	EB	Seeded	CB	HS-CB3	-	-
Fall 2008	LB	Unseeded	OS	CU-OR1	237.23	812.45
Fall 2008	LB	Unseeded	OS	CU-OR2	158.12	541.52
Fall 2008	LB	Unseeded	OS	CU-OR3	144.25	494.0
Fall 2008	LB	Unseeded	RR	CU-RR1	79.12	481.82
Fall 2008	LB	Unseeded	RR	CU-RR2	77.7	473.08
Fall 2008	LB	Unseeded	RR	CU-RR3	46.7	284.56
Fall 2008	LB	Unseeded	CM	CU-CM1	52.84	450.5
Fall 2008	LB	Unseeded	CM	CU-CM2	40.77	347.6

Living Shoreline (LSE) -- Continued

Sampling Period	Site	Cage Control	Substrate	Substrate #	Ash Free Dry Mass (g)	Biomass (g/m^2)
Fall 2008	LB	Unseeded	CM	CU-CM3	62.19	530.2
Fall 2008	LB	Unseeded	CB	CU-CB1	39.45	512.3
Fall 2008	LB	Unseeded	CB	CU-CB2	46.18	599.7
Fall 2008	LB	Unseeded	CB	CU-CB3	42.99	558.3
Fall 2008	LB	Seeded	OS	CS-OR1	402.051	1376.9
Fall 2008	LB	Seeded	OS	CS-OR2	163.968	2542.1
Fall 2008	LB	Seeded	OS	CS-OR3	-	-
Fall 2008	LB	Seeded	RR	CS-RR1	45.686	708.31
Fall 2008	LB	Seeded	RR	CS-RR2	37.053	574.47
Fall 2008	LB	Seeded	RR	CS-RR3	84.566	1311.10
Fall 2008	LB	Seeded	CM	CS-CM1	182.147	583.80
Fall 2008	LB	Seeded	CM	CS-CM2	256.333	821.58
Fall 2008	LB	Seeded	CM	CS-CM3	54.200	173.72
Fall 2008	LB	Seeded	CB	CS-CB1	82.580	1072.47
Fall 2008	LB	Seeded	CB	CS-CB2	87.255	1133.18
Fall 2008	LB	Seeded	CB	CS-CB3	96.045	1247.34
Fall 2008	EB	Unseeded	OS	HU-OR1	177.6	608.4
Fall 2008	EB	Unseeded	OS	HU-OR2	189.8	649.9
Fall 2008	EB	Unseeded	OS	HU-OR3	117.5	402.6
Fall 2008	EB	Unseeded	RR	HU-RR1	34.1	116.0
Fall 2008	EB	Unseeded	RR	HU-RR2	29.6	101.5

Living Shoreline (LSE) -- Continued

Sampling Period	Site	Cage Control	Substrate	Substrate #	Ash Free Dry Mass (g)	Biomass (g/m^2)
Fall 2008	EB	Unseeded	RR	HU-RR3	13.3	45.5
Fall 2008	EB	Unseeded	CM	HU-CM1	18.4	157.1
Fall 2008	EB	Unseeded	CM	HU-CM2	13.1	112.3
Fall 2008	EB	Unseeded	CM	HU-CM3	11.5	98.2
Fall 2008	EB	Unseeded	CB	HU-CB1	-	-
Fall 2008	EB	Unseeded	CB	HU-CB2	-	-
Fall 2008	EB	Unseeded	CB	HU-CB3	-	-
Fall 2008	EB	Seeded	OS	HS-OR1	247.737	848.41
Fall 2008	EB	Seeded	OS	HS-OR2	146.021	2263.89
Fall 2008	EB	Seeded	OS	HS-OR3	-	-
Fall 2008	EB	Seeded	RR	HS-RR1	19.194	297.58
Fall 2008	EB	Seeded	RR	HS-RR2	-	-
Fall 2008	EB	Seeded	RR	HS-RR3	24.560	380.78
Fall 2008	EB	Seeded	CM	HS-CM1	9.341	29.94
Fall 2008	EB	Seeded	CM	HS-CM2	3.902	12.51
Fall 2008	EB	Seeded	CM	HS-CM3	8.713	27.93
Fall 2008	EB	Seeded	CB	HS-CB1	-	-
Fall 2008	EB	Seeded	CB	HS-CB2	-	-
Fall 2008	EB	Seeded	CB	HS-CB3	-	-

Alternative Substrate (ASE)
Locations: Long Creek

Sampling Period	Site	Cage Control	Substrate	Substrate #	Temp	Salinity	DO	Depth
Fall 2005	Marsh	Caged	CVS	CVS1	11.01	17.92	12	1
Fall 2005	Marsh	Uncaged	CVS	CVS2	11.01	17.82	12	1
Fall 2005	Marsh	Caged	CVS	CVS3	11.01	17.92	12	1
Fall 2005	Marsh	Uncaged	CVS	CVS4	11.01	17.82	12	1
Fall 2005	Marsh	Caged	CVS	CVS5	11.01	17.92	12	1
Fall 2005	Marsh	Uncaged	CVS	CVS6	11.01	17.82	12	1
Fall 2005	Marsh	Caged	GL	GL1	11.01	17.92	12	1
Fall 2005	Marsh	Uncaged	GL	GL2	11.01	17.82	12	1
Fall 2005	Marsh	Caged	GL	GL3	11.01	17.92	12	1
Fall 2005	Marsh	Uncaged	GL	GL4	11.01	17.82	12	1
Fall 2005	Marsh	Caged	GL	GL5	11.01	17.92	12	1
Fall 2005	Marsh	Uncaged	GL	GL6	11.01	17.82	12	1
Fall 2005	Marsh	Caged	GS	GS1	11.01	17.92	12	1
Fall 2005	Marsh	Uncaged	GS	GS2	11.01	17.82	12	1
Fall 2005	Marsh	Caged	GS	GS3	11.01	17.92	12	1
Fall 2005	Marsh	Uncaged	GS	GS4	11.01	17.82	12	1
Fall 2005	Marsh	Caged	GS	GS5	11.01	17.92	12	1
Fall 2005	Marsh	Uncaged	GS	GS6	11.01	17.82	12	1
Fall 2005	Marsh	Caged	LML	LML1	11.01	17.92	12	1
Fall 2005	Marsh	Uncaged	LML	LML2	11.01	17.82	12	1
Fall 2005	Marsh	Caged	LML	LML3	11.01	17.92	12	1
Fall 2005	Marsh	Uncaged	LML	LML4	11.01	17.82	12	1

Alternative Substrate (ASE) -- Continued

Sampling Period	Site	Cage Control	Substrate	Substrate #	Temp	Salinity	DO	Depth
Fall 2005	Marsh	Caged	LML	LML5	11.01	17.92	12	1
Fall 2005	Marsh	Uncaged	LML	LML6	11.01	17.82	12	1
Fall 2005	Marsh	Caged	LMS	LMS1	11.01	17.92	12	1
Fall 2005	Marsh	Uncaged	LMS	LMS2	11.01	17.82	12	1
Fall 2005	Marsh	Caged	LMS	LMS3	11.01	17.92	12	1
Fall 2005	Marsh	Uncaged	LMS	LMS4	11.01	17.82	12	1
Fall 2005	Marsh	Caged	LMS	LMS5	11.01	17.92	12	1
Fall 2005	Marsh	Uncaged	LMS	LMS6	11.01	17.82	12	1
Fall 2005	Marsh	Caged	OSU	OSU1	11.01	17.92	12	1
Fall 2005	Marsh	Uncaged	OSU	OSU2	11.01	17.82	12	1
Fall 2005	Marsh	Caged	OSU	OSU3	11.01	17.92	12	1
Fall 2005	Marsh	Uncaged	OSU	OSU4	11.01	17.82	12	1
Fall 2005	Marsh	Caged	OSU	OSU5	11.01	17.92	12	1
Fall 2005	Marsh	Uncaged	OSU	OSU6	11.01	17.82	12	1
Fall 2005	Oyster Reef	Uncaged	CVS	CVS1	11.01	17.92	12	1
Fall 2005	Oyster Reef	Caged	CVS	CVS2	11.01	17.82	12	1
Fall 2005	Oyster Reef	Uncaged	CVS	CVS3	11.01	17.92	12	1
Fall 2005	Oyster Reef	Caged	CVS	CVS4	11.01	17.82	12	1
Fall 2005	Oyster Reef	Uncaged	CVS	CVS5	11.01	17.92	12	1
Fall 2005	Oyster Reef	Caged	CVS	CVS6	11.01	17.82	12	1
Fall 2005	Oyster Reef	Uncaged	GL	GL1	11.01	17.92	12	1
Fall 2005	Oyster Reef	Caged	GL	GL2	11.01	17.82	12	1
Fall 2005	Oyster Reef	Uncaged	GL	GL3	11.01	17.92	12	1
Fall 2005	Oyster Reef	Caged	GL	GL4	11.01	17.82	12	1

Alternative Substrate (ASE) -- Continued

Sampling Period	Site	Cage Control	Substrate	Substrate #	Temp	Salinity	DO	Depth
Fall 2005	Oyster Reef	Uncaged	GL	GL5	11.01	17.92	12	1
Fall 2005	Oyster Reef	Caged	GL	GL6	11.01	17.82	12	1
Fall 2005	Oyster Reef	Uncaged	GS	GS1	11.01	17.92	12	1
Fall 2005	Oyster Reef	Caged	GS	GS2	11.01	17.82	12	1
Fall 2005	Oyster Reef	Uncaged	GS	GS3	11.01	17.92	12	1
Fall 2005	Oyster Reef	Caged	GS	GS4	11.01	17.82	12	1
Fall 2005	Oyster Reef	Uncaged	GS	GS5	11.01	17.92	12	1
Fall 2005	Oyster Reef	Caged	GS	GS6	11.01	17.82	12	1
Fall 2005	Oyster Reef	Uncaged	LML	LML1	11.01	17.92	12	1
Fall 2005	Oyster Reef	Caged	LML	LML2	11.01	17.82	12	1
Fall 2005	Oyster Reef	Uncaged	LML	LML3	11.01	17.92	12	1
Fall 2005	Oyster Reef	Caged	LML	LML4	11.01	17.82	12	1
Fall 2005	Oyster Reef	Uncaged	LML	LML5	11.01	17.92	12	1
Fall 2005	Oyster Reef	Caged	LML	LML6	11.01	17.82	12	1
Fall 2005	Oyster Reef	Uncaged	LMS	LMS1	11.01	17.92	12	1
Fall 2005	Oyster Reef	Caged	LMS	LMS2	11.01	17.82	12	1
Fall 2005	Oyster Reef	Uncaged	LMS	LMS3	11.01	17.92	12	1
Fall 2005	Oyster Reef	Caged	LMS	LMS4	11.01	17.82	12	1
Fall 2005	Oyster Reef	Uncaged	LMS	LMS5	11.01	17.92	12	1
Fall 2005	Oyster Reef	Caged	LMS	LMS6	11.01	17.82	12	1
Fall 2005	Oyster Reef	Uncaged	OSU	OSU1	11.01	17.92	12	1
Fall 2005	Oyster Reef	Caged	OSU	OSU2	11.01	17.82	12	1
Fall 2005	Oyster Reef	Uncaged	OSU	OSU3	11.01	17.92	12	1
Fall 2005	Oyster Reef	Caged	OSU	OSU4	11.01	17.82	12	1

Alternative Substrate (ASE) -- Continued

Sampling Period	Site	Cage Control	Substrate	Substrate #	Temp	Salinity	DO	Depth
Fall 2005	Oyster Reef	Uncaged	OSU	OSU5	11.01	17.92	12	1
Fall 2005	Oyster Reef	Caged	OSU	OSU6	11.01	17.82	12	1
Fall 2005	Riprap	Uncaged	CVS	CVS1	11.01	17.92	12	1
Fall 2005	Riprap	Caged	CVS	CVS2	11.01	17.82	12	1
Fall 2005	Riprap	Uncaged	CVS	CVS3	11.01	17.92	12	1
Fall 2005	Riprap	Caged	CVS	CVS4	11.01	17.82	12	1
Fall 2005	Riprap	Uncaged	CVS	CVS5	11.01	17.92	12	1
Fall 2005	Riprap	Caged	CVS	CVS6	11.01	17.82	12	1
Fall 2005	Riprap	Uncaged	GL	GL1	11.01	17.92	12	1
Fall 2005	Riprap	Caged	GL	GL2	11.01	17.82	12	1
Fall 2005	Riprap	Uncaged	GL	GL3	11.01	17.92	12	1
Fall 2005	Riprap	Caged	GL	GL4	11.01	17.82	12	1
Fall 2005	Riprap	Uncaged	GL	GL5	11.01	17.92	12	1
Fall 2005	Riprap	Caged	GL	GL6	11.01	17.82	12	1
Fall 2005	Riprap	Uncaged	GS	GS1	11.01	17.92	12	1
Fall 2005	Riprap	Caged	GS	GS2	11.01	17.82	12	1
Fall 2005	Riprap	Uncaged	GS	GS3	11.01	17.92	12	1
Fall 2005	Riprap	Caged	GS	GS4	11.01	17.82	12	1
Fall 2005	Riprap	Uncaged	GS	GS5	11.01	17.92	12	1
Fall 2005	Riprap	Caged	GS	GS6	11.01	17.82	12	1
Fall 2005	Riprap	Uncaged	LML	LML1	11.01	17.92	12	1
Fall 2005	Riprap	Caged	LML	LML2	11.01	17.82	12	1
Fall 2005	Riprap	Uncaged	LML	LML3	11.01	17.92	12	1
Fall 2005	Riprap	Caged	LML	LML4	11.01	17.82	12	1

Alternative Substrate (ASE) -- Continued

Sampling Period	Site	Cage Control	Substrate	Substrate #	Temp	Salinity	DO	Depth
Fall 2005	Riprap	Uncaged	LML	LML5	11.01	17.92	12	1
Fall 2005	Riprap	Caged	LML	LML6	11.01	17.82	12	1
Fall 2005	Riprap	Uncaged	LMS	LMS1	11.01	17.92	12	1
Fall 2005	Riprap	Caged	LMS	LMS2	11.01	17.82	12	1
Fall 2005	Riprap	Uncaged	LMS	LMS3	11.01	17.92	12	1
Fall 2005	Riprap	Caged	LMS	LMS4	11.01	17.82	12	1
Fall 2005	Riprap	Uncaged	LMS	LMS5	11.01	17.92	12	1
Fall 2005	Riprap	Caged	LMS	LMS6	11.01	17.82	12	1
Fall 2005	Riprap	Uncaged	OSU	OSU1	11.01	17.92	12	1
Fall 2005	Riprap	Caged	OSU	OSU2	11.01	17.82	12	1
Fall 2005	Riprap	Uncaged	OSU	OSU3	11.01	17.92	12	1
Fall 2005	Riprap	Caged	OSU	OSU4	11.01	17.82	12	1
Fall 2005	Riprap	Uncaged	OSU	OSU5	11.01	17.92	12	1
Fall 2005	Riprap	Caged	OSU	OSU6	11.01	17.82	12	1
Fall 2006	Marsh	Caged	CVS	CVS1	23.81	22.61	7.8	1
Fall 2006	Marsh	Uncaged	CVS	CVS2	23.81	22.61	7.8	1
Fall 2006	Marsh	Caged	CVS	CVS3	23.81	22.61	7.8	1
Fall 2006	Marsh	Uncaged	CVS	CVS4	23.81	22.61	7.8	1
Fall 2006	Marsh	Caged	CVS	CVS5	23.81	22.61	7.8	1
Fall 2006	Marsh	Uncaged	CVS	CVS6	23.81	22.61	7.8	1
Fall 2006	Marsh	Caged	GL	GL1	23.81	22.61	7.8	1
Fall 2006	Marsh	Uncaged	GL	GL2	23.81	22.61	7.8	1
Fall 2006	Marsh	Caged	GL	GL3	23.81	22.61	7.8	1
Fall 2006	Marsh	Uncaged	GL	GL4	23.81	22.61	7.8	1

Alternative Substrate (ASE) -- Continued

Sampling Period	Site	Cage Control	Substrate	Substrate #	Temp	Salinity	DO	Depth
Fall 2006	Marsh	Caged	GL	GL5	23.81	22.61	7.8	1
Fall 2006	Marsh	Uncaged	GL	GL6	23.81	22.61	7.8	1
Fall 2006	Marsh	Caged	GS	GS1	23.81	22.61	7.8	1
Fall 2006	Marsh	Uncaged	GS	GS2	23.81	22.61	7.8	1
Fall 2006	Marsh	Caged	GS	GS3	23.81	22.61	7.8	1
Fall 2006	Marsh	Uncaged	GS	GS4	23.81	22.61	7.8	1
Fall 2006	Marsh	Caged	GS	GS5	23.81	22.61	7.8	1
Fall 2006	Marsh	Uncaged	GS	GS6	23.81	22.61	7.8	1
Fall 2006	Marsh	Caged	LML	LML1	23.81	22.61	7.8	1
Fall 2006	Marsh	Uncaged	LML	LML2	23.81	22.61	7.8	1
Fall 2006	Marsh	Caged	LML	LML3	23.81	22.61	7.8	1
Fall 2006	Marsh	Uncaged	LML	LML4	23.81	22.61	7.8	1
Fall 2006	Marsh	Caged	LML	LML5	23.81	22.61	7.8	1
Fall 2006	Marsh	Uncaged	LML	LML6	23.81	22.61	7.8	1
Fall 2006	Marsh	Caged	LMS	LMS1	23.81	22.61	7.8	1
Fall 2006	Marsh	Uncaged	LMS	LMS2	23.81	22.61	7.8	1
Fall 2006	Marsh	Caged	LMS	LMS3	23.81	22.61	7.8	1
Fall 2006	Marsh	Uncaged	LMS	LMS4	23.81	22.61	7.8	1
Fall 2006	Marsh	Caged	LMS	LMS5	23.81	22.61	7.8	1
Fall 2006	Marsh	Uncaged	LMS	LMS6	23.81	22.61	7.8	1
Fall 2006	Marsh	Caged	OSU	OSU1	23.81	22.61	7.8	1
Fall 2006	Marsh	Uncaged	OSU	OSU2	23.81	22.61	7.8	1
Fall 2006	Marsh	Caged	OSU	OSU3	23.81	22.61	7.8	1
Fall 2006	Marsh	Uncaged	OSU	OSU4	23.81	22.61	7.8	1

Alternative Substrate (ASE) -- Continued

Sampling Period	Site	Cage Control	Substrate	Substrate #	Temp	Salinity	DO	Depth
Fall 2006	Marsh	Caged	OSU	OSU5	23.81	22.61	7.8	1
Fall 2006	Marsh	Uncaged	OSU	OSU6	23.81	22.61	7.8	1
Fall 2006	Oyster Reef	Uncaged	CVS	CVS1	23.81	22.61	7.8	1
Fall 2006	Oyster Reef	Caged	CVS	CVS2	23.81	22.61	7.8	1
Fall 2006	Oyster Reef	Uncaged	CVS	CVS3	23.81	22.61	7.8	1
Fall 2006	Oyster Reef	Caged	CVS	CVS4	23.81	22.61	7.8	1
Fall 2006	Oyster Reef	Uncaged	CVS	CVS5	23.81	22.61	7.8	1
Fall 2006	Oyster Reef	Caged	CVS	CVS6	23.81	22.61	7.8	1
Fall 2006	Oyster Reef	Uncaged	GL	GL1	23.81	22.61	7.8	1
Fall 2006	Oyster Reef	Caged	GL	GL2	23.81	22.61	7.8	1
Fall 2006	Oyster Reef	Uncaged	GL	GL3	23.81	22.61	7.8	1
Fall 2006	Oyster Reef	Caged	GL	GL4	23.81	22.61	7.8	1
Fall 2006	Oyster Reef	Uncaged	GL	GL5	23.81	22.61	7.8	1
Fall 2006	Oyster Reef	Caged	GL	GL6	23.81	22.61	7.8	1
Fall 2006	Oyster Reef	Uncaged	GS	GS1	23.81	22.61	7.8	1
Fall 2006	Oyster Reef	Caged	GS	GS2	23.81	22.61	7.8	1
Fall 2006	Oyster Reef	Uncaged	GS	GS3	23.81	22.61	7.8	1
Fall 2006	Oyster Reef	Caged	GS	GS4	23.81	22.61	7.8	1
Fall 2006	Oyster Reef	Uncaged	GS	GS5	23.81	22.61	7.8	1
Fall 2006	Oyster Reef	Caged	GS	GS6	23.81	22.61	7.8	1
Fall 2006	Oyster Reef	Uncaged	LML	LML1	23.81	22.61	7.8	1
Fall 2006	Oyster Reef	Caged	LML	LML2	23.81	22.61	7.8	1
Fall 2006	Oyster Reef	Uncaged	LML	LML3	23.81	22.61	7.8	1
Fall 2006	Oyster Reef	Caged	LML	LML4	23.81	22.61	7.8	1

Alternative Substrate (ASE) -- Continued

Sampling Period	Site	Cage Control	Substrate	Substrate #	Temp	Salinity	DO	Depth
Fall 2006	Riprap	Uncaged	GL	GL5	23.81	22.61	7.8	1
Fall 2006	Riprap	Caged	GL	GL6	23.81	22.61	7.8	1
Fall 2006	Riprap	Uncaged	GS	GS1	23.81	22.61	7.8	1
Fall 2006	Riprap	Caged	GS	GS2	23.81	22.61	7.8	1
Fall 2006	Riprap	Uncaged	GS	GS3	23.81	22.61	7.8	1
Fall 2006	Riprap	Caged	GS	GS4	23.81	22.61	7.8	1
Fall 2006	Riprap	Uncaged	GS	GS5	23.81	22.61	7.8	1
Fall 2006	Riprap	Caged	GS	GS6	23.81	22.61	7.8	1
Fall 2006	Riprap	Uncaged	LML	LML1	23.81	22.61	7.8	1
Fall 2006	Riprap	Caged	LML	LML2	23.81	22.61	7.8	1
Fall 2006	Riprap	Uncaged	LML	LML3	23.81	22.61	7.8	1
Fall 2006	Riprap	Caged	LML	LML4	23.81	22.61	7.8	1
Fall 2006	Riprap	Uncaged	LML	LML5	23.81	22.61	7.8	1
Fall 2006	Riprap	Caged	LML	LML6	23.81	22.61	7.8	1
Fall 2006	Riprap	Uncaged	LMS	LMS1	23.81	22.61	7.8	1
Fall 2006	Riprap	Caged	LMS	LMS2	23.81	22.61	7.8	1
Fall 2006	Riprap	Uncaged	LMS	LMS3	23.81	22.61	7.8	1
Fall 2006	Riprap	Caged	LMS	LMS4	23.81	22.61	7.8	1
Fall 2006	Riprap	Uncaged	LMS	LMS5	23.81	22.61	7.8	1
Fall 2006	Riprap	Caged	LMS	LMS6	23.81	22.61	7.8	1
Fall 2006	Riprap	Uncaged	OSU	OSU1	23.81	22.61	7.8	1
Fall 2006	Riprap	Caged	OSU	OSU2	23.81	22.61	7.8	1
Fall 2006	Riprap	Uncaged	OSU	OSU3	23.81	22.61	7.8	1
Fall 2006	Riprap	Caged	OSU	OSU4	23.81	22.61	7.8	1

Alternative Substrate (ASE) -- Continued

Sampling Period	Site	Cage Control	Substrate	Substrate #	Temp	Salinity	DO	Depth
Fall 2006	Riprap	Uncaged	OSU	OSU5	23.81	22.61	7.8	1
Fall 2006	Riprap	Caged	OSU	OSU6	23.81	22.61	7.8	1
Fall 2007	Marsh	Caged	CVS	CVS1	27.94	21.45	7	1
Fall 2007	Marsh	Uncaged	CVS	CVS2	27.94	21.45	7	1
Fall 2007	Marsh	Caged	CVS	CVS3	27.94	21.45	7	1
Fall 2007	Marsh	Uncaged	CVS	CVS4	27.94	21.45	7	1
Fall 2007	Marsh	Caged	CVS	CVS5	27.94	21.45	7	1
Fall 2007	Marsh	Uncaged	CVS	CVS6	27.94	21.45	7	1
Fall 2007	Marsh	Caged	GL	GL1	27.94	21.45	7	1
Fall 2007	Marsh	Uncaged	GL	GL2	27.94	21.45	7	1
Fall 2007	Marsh	Caged	GL	GL3	27.94	21.45	7	1
Fall 2007	Marsh	Uncaged	GL	GL4	27.94	21.45	7	1
Fall 2007	Marsh	Caged	GL	GL5	27.94	21.45	7	1
Fall 2007	Marsh	Uncaged	GL	GL6	27.94	21.45	7	1
Fall 2007	Marsh	Caged	GS	GS1	27.94	21.45	7	1
Fall 2007	Marsh	Uncaged	GS	GS2	27.94	21.45	7	1
Fall 2007	Marsh	Caged	GS	GS3	27.94	21.45	7	1
Fall 2007	Marsh	Uncaged	GS	GS4	27.94	21.45	7	1
Fall 2007	Marsh	Caged	GS	GS5	27.94	21.45	7	1
Fall 2007	Marsh	Uncaged	GS	GS6	27.94	21.45	7	1
Fall 2007	Marsh	Caged	LML	LML1	27.94	21.45	7	1
Fall 2007	Marsh	Uncaged	LML	LML2	27.94	21.45	7	1
Fall 2007	Marsh	Caged	LML	LML3	27.94	21.45	7	1
Fall 2007	Marsh	Uncaged	LML	LML4	27.94	21.45	7	1

Alternative Substrate (ASE) -- Continued

Sampling Period	Site	Cage Control	Substrate	Substrate #	Temp	Salinity	DO	Depth
Fall 2007	Marsh	Caged	LML	LML5	27.94	21.45	7	1
Fall 2007	Marsh	Uncaged	LML	LML6	27.94	21.45	7	1
Fall 2007	Marsh	Caged	LMS	LMS1	27.94	21.45	7	1
Fall 2007	Marsh	Uncaged	LMS	LMS2	27.94	21.45	7	1
Fall 2007	Marsh	Caged	LMS	LMS3	27.94	21.45	7	1
Fall 2007	Marsh	Uncaged	LMS	LMS4	27.94	21.45	7	1
Fall 2007	Marsh	Caged	LMS	LMS5	27.94	21.45	7	1
Fall 2007	Marsh	Uncaged	LMS	LMS6	27.94	21.45	7	1
Fall 2007	Marsh	Caged	OSU	OSU1	27.94	21.45	7	1
Fall 2007	Marsh	Uncaged	OSU	OSU2	27.94	21.45	7	1
Fall 2007	Marsh	Caged	OSU	OSU3	27.94	21.45	7	1
Fall 2007	Marsh	Uncaged	OSU	OSU4	27.94	21.45	7	1
Fall 2007	Marsh	Caged	OSU	OSU5	27.94	21.45	7	1
Fall 2007	Marsh	Uncaged	OSU	OSU6	27.94	21.45	7	1
Fall 2007	Oyster Reef	Uncaged	CVS	CVS1	27.94	21.45	7	1
Fall 2007	Oyster Reef	Caged	CVS	CVS2	27.94	21.45	7	1
Fall 2007	Oyster Reef	Uncaged	CVS	CVS3	27.94	21.45	7	1
Fall 2007	Oyster Reef	Caged	CVS	CVS4	27.94	21.45	7	1
Fall 2007	Oyster Reef	Uncaged	CVS	CVS5	27.94	21.45	7	1
Fall 2007	Oyster Reef	Caged	CVS	CVS6	27.94	21.45	7	1
Fall 2007	Oyster Reef	Uncaged	GL	GL1	27.94	21.45	7	1
Fall 2007	Oyster Reef	Caged	GL	GL2	27.94	21.45	7	1
Fall 2007	Oyster Reef	Uncaged	GL	GL3	27.94	21.45	7	1
Fall 2007	Oyster Reef	Caged	GL	GL4	27.94	21.45	7	1

Alternative Substrate (ASE) -- Continued

Sampling Period	Site	Cage Control	Substrate	Substrate #	Temp	Salinity	DO	Depth
Fall 2006	Oyster Reef	Uncaged	LML	LML5	23.81	22.61	7.8	1
Fall 2006	Oyster Reef	Caged	LML	LML6	23.81	22.61	7.8	1
Fall 2006	Oyster Reef	Uncaged	LMS	LMS1	23.81	22.61	7.8	1
Fall 2006	Oyster Reef	Caged	LMS	LMS2	23.81	22.61	7.8	1
Fall 2006	Oyster Reef	Uncaged	LMS	LMS3	23.81	22.61	7.8	1
Fall 2006	Oyster Reef	Caged	LMS	LMS4	23.81	22.61	7.8	1
Fall 2006	Oyster Reef	Uncaged	LMS	LMS5	23.81	22.61	7.8	1
Fall 2006	Oyster Reef	Caged	LMS	LMS6	23.81	22.61	7.8	1
Fall 2006	Oyster Reef	Uncaged	OSU	OSU1	23.81	22.61	7.8	1
Fall 2006	Oyster Reef	Caged	OSU	OSU2	23.81	22.61	7.8	1
Fall 2006	Oyster Reef	Uncaged	OSU	OSU3	23.81	22.61	7.8	1
Fall 2006	Oyster Reef	Caged	OSU	OSU4	23.81	22.61	7.8	1
Fall 2006	Oyster Reef	Uncaged	OSU	OSU5	23.81	22.61	7.8	1
Fall 2006	Oyster Reef	Caged	OSU	OSU6	23.81	22.61	7.8	1
Fall 2006	Riprap	Uncaged	CVS	CVS1	23.81	22.61	7.8	1
Fall 2006	Riprap	Caged	CVS	CVS2	23.81	22.61	7.8	1
Fall 2006	Riprap	Uncaged	CVS	CVS3	23.81	22.61	7.8	1
Fall 2006	Riprap	Caged	CVS	CVS4	23.81	22.61	7.8	1
Fall 2006	Riprap	Uncaged	CVS	CVS5	23.81	22.61	7.8	1
Fall 2006	Riprap	Caged	CVS	CVS6	23.81	22.61	7.8	1
Fall 2006	Riprap	Uncaged	GL	GL1	23.81	22.61	7.8	1
Fall 2006	Riprap	Caged	GL	GL2	23.81	22.61	7.8	1
Fall 2006	Riprap	Uncaged	GL	GL3	23.81	22.61	7.8	1
Fall 2006	Riprap	Caged	GL	GL4	23.81	22.61	7.8	1

Alternative Substrate (ASE) -- Continued

Sampling Period	Site	Cage Control	Substrate	Substrate #	Temp	Salinity	DO	Depth
Fall 2007	Riprap	Uncaged	LML	LML5	27.94	21.45	7	1
Fall 2007	Riprap	Caged	LML	LML6	27.94	21.45	7	1
Fall 2007	Riprap	Uncaged	LMS	LMS1	27.94	21.45	7	1
Fall 2007	Riprap	Caged	LMS	LMS2	27.94	21.45	7	1
Fall 2007	Riprap	Uncaged	LMS	LMS3	27.94	21.45	7	1
Fall 2007	Riprap	Caged	LMS	LMS4	27.94	21.45	7	1
Fall 2007	Riprap	Uncaged	LMS	LMS5	27.94	21.45	7	1
Fall 2007	Riprap	Caged	LMS	LMS6	27.94	21.45	7	1
Fall 2007	Riprap	Uncaged	OSU	OSU1	27.94	21.45	7	1
Fall 2007	Riprap	Caged	OSU	OSU2	27.94	21.45	7	1
Fall 2007	Riprap	Uncaged	OSU	OSU3	27.94	21.45	7	1
Fall 2007	Riprap	Caged	OSU	OSU4	27.94	21.45	7	1
Fall 2007	Riprap	Uncaged	OSU	OSU5	27.94	21.45	7	1
Fall 2007	Riprap	Caged	OSU	OSU6	27.94	21.45	7	1
Spring 2006	Marsh	Caged	CVS	CVS1	20.81	18.8	6.5	1
Spring 2006	Marsh	Uncaged	CVS	CVS2	20.81	18.8	6.5	1
Spring 2006	Marsh	Caged	CVS	CVS3	20.81	18.8	6.5	1
Spring 2006	Marsh	Uncaged	CVS	CVS4	20.81	18.8	6.5	1
Spring 2006	Marsh	Caged	CVS	CVS5	20.81	18.8	6.5	1
Spring 2006	Marsh	Uncaged	CVS	CVS6	20.81	18.8	6.5	1
Spring 2006	Marsh	Caged	GL	GL1	20.81	18.8	6.5	1
Spring 2006	Marsh	Uncaged	GL	GL2	20.81	18.8	6.5	1
Spring 2006	Marsh	Caged	GL	GL3	20.81	18.8	6.5	1
Spring 2006	Marsh	Uncaged	GL	GL4	20.81	18.8	6.5	1

Alternative Substrate (ASE) -- Continued

Sampling Period	Site	Cage Control	Substrate	Substrate #	Temp	Salinity	DO	Depth
Spring 2006	Marsh	Caged	GL	GL5	20.81	18.8	6.5	1
Spring 2006	Marsh	Uncaged	GL	GL6	20.81	18.8	6.5	1
Spring 2006	Marsh	Caged	GS	GS1	20.81	18.8	6.5	1
Spring 2006	Marsh	Uncaged	GS	GS2	20.81	18.8	6.5	1
Spring 2006	Marsh	Caged	GS	GS3	20.81	18.8	6.5	1
Spring 2006	Marsh	Uncaged	GS	GS4	20.81	18.8	6.5	1
Spring 2006	Marsh	Caged	GS	GS5	20.81	18.8	6.5	1
Spring 2006	Marsh	Uncaged	GS	GS6	20.81	18.8	6.5	1
Spring 2006	Marsh	Caged	LML	LML1	20.81	18.8	6.5	1
Spring 2006	Marsh	Uncaged	LML	LML2	20.81	18.8	6.5	1
Spring 2006	Marsh	Caged	LML	LML3	20.81	18.8	6.5	1
Spring 2006	Marsh	Uncaged	LML	LML4	20.81	18.8	6.5	1
Spring 2006	Marsh	Caged	LML	LML5	20.81	18.8	6.5	1
Spring 2006	Marsh	Uncaged	LML	LML6	20.81	18.8	6.5	1
Spring 2006	Marsh	Caged	LMS	LMS1	20.81	18.8	6.5	1
Spring 2006	Marsh	Uncaged	LMS	LMS2	20.81	18.8	6.5	1
Spring 2006	Marsh	Caged	LMS	LMS3	20.81	18.8	6.5	1
Spring 2006	Marsh	Uncaged	LMS	LMS4	20.81	18.8	6.5	1
Spring 2006	Marsh	Caged	LMS	LMS5	20.81	18.8	6.5	1
Spring 2006	Marsh	Uncaged	LMS	LMS6	20.81	18.8	6.5	1
Spring 2006	Marsh	Caged	OSU	OSU1	20.81	18.8	6.5	1
Spring 2006	Marsh	Uncaged	OSU	OSU2	20.81	18.8	6.5	1
Spring 2006	Marsh	Caged	OSU	OSU3	20.81	18.8	6.5	1
Spring 2006	Marsh	Uncaged	OSU	OSU4	20.81	18.8	6.5	1

Alternative Substrate (ASE) -- Continued

Sampling Period	Site	Cage Control	Substrate	Substrate #	Temp	Salinity	DO	Depth
Spring 2006	Marsh	Caged	OSU	OSU5	20.81	18.8	6.5	1
Spring 2006	Marsh	Uncaged	OSU	OSU6	20.81	18.8	6.5	1
Spring 2006	Oyster Reef	Uncaged	CVS	CVS1	20.81	18.8	6.5	1
Spring 2006	Oyster Reef	Caged	CVS	CVS2	20.81	18.8	6..5	1
Spring 2006	Oyster Reef	Uncaged	CVS	CVS3	20.81	18.8	6.5	1
Spring 2006	Oyster Reef	Caged	CVS	CVS4	20.81	18.8	6.5	1
Spring 2006	Oyster Reef	Uncaged	CVS	CVS5	20.81	18.8	6.5	1
Spring 2006	Oyster Reef	Caged	CVS	CVS6	20.81	18.8	6.5	1
Spring 2006	Oyster Reef	Uncaged	GL	GL1	20.81	18.8	6.5	1
Spring 2006	Oyster Reef	Caged	GL	GL2	20.81	18.8	6.5	1
Spring 2006	Oyster Reef	Uncaged	GL	GL3	20.81	18.8	6.5	1
Spring 2006	Oyster Reef	Caged	GL	GL4	20.81	18.8	6.5	1
Spring 2006	Oyster Reef	Uncaged	GL	GL5	20.81	18.8	6.5	1
Spring 2006	Oyster Reef	Caged	GL	GL6	20.81	18.8	6.5	1
Spring 2006	Oyster Reef	Uncaged	GS	GS1	20.81	18.8	6.5	1
Spring 2006	Oyster Reef	Caged	GS	GS2	20.81	18.8	6.5	1
Spring 2006	Oyster Reef	Uncaged	GS	GS3	20.81	18.8	6.5	1
Spring 2006	Oyster Reef	Caged	GS	GS4	20.81	18.8	6.5	1
Spring 2006	Oyster Reef	Uncaged	GS	GS5	20.81	18.8	6.5	1
Spring 2006	Oyster Reef	Caged	GS	GS6	20.81	18.8	6.5	1
Spring 2006	Oyster Reef	Uncaged	LML	LML1	20.81	18.8	6.5	1
Spring 2006	Oyster Reef	Caged	LML	LML2	20.81	18.8	6.5	1
Spring 2006	Oyster Reef	Uncaged	LML	LML3	20.81	18.8	6.5	1
Spring 2006	Oyster Reef	Caged	LML	LML4	20.81	18.8	6.5	1

Alternative Substrate (ASE) -- Continued

Sampling Period	Site	Cage Control	Substrate	Substrate #	Temp	Salinity	DO	Depth
Spring 2006	Oyster Reef	Uncaged	LML	LML5	20.81	18.8	6.5	1
Spring 2006	Oyster Reef	Caged	LML	LML6	20.81	18.8	6.5	1
Spring 2006	Oyster Reef	Uncaged	LMS	LMS1	20.81	18.8	6.5	1
Spring 2006	Oyster Reef	Caged	LMS	LMS2	20.81	18.8	6.5	1
Spring 2006	Oyster Reef	Uncaged	LMS	LMS3	20.81	18.8	6.5	1
Spring 2006	Oyster Reef	Caged	LMS	LMS4	20.81	18.8	6.5	1
Spring 2006	Oyster Reef	Uncaged	LMS	LMS5	20.81	18.8	6.5	1
Spring 2006	Oyster Reef	Caged	LMS	LMS6	20.81	18.8	6.5	1
Spring 2006	Oyster Reef	Uncaged	OSU	OSU1	20.81	18.8	6.5	1
Spring 2006	Oyster Reef	Caged	OSU	OSU2	20.81	18.8	6.5	1
Spring 2006	Oyster Reef	Uncaged	OSU	OSU3	20.81	18.8	6.5	1
Spring 2006	Oyster Reef	Caged	OSU	OSU4	20.81	18.8	6.5	1
Spring 2006	Oyster Reef	Uncaged	OSU	OSU5	20.81	18.8	6.5	1
Spring 2006	Oyster Reef	Caged	OSU	OSU6	20.81	18.8	6.5	1
Spring 2006	Riprap	Uncaged	CVS	CVS1	20.81	18.8	6.5	1
Spring 2006	Riprap	Caged	CVS	CVS2	20.81	18.8	6.5	1
Spring 2006	Riprap	Uncaged	CVS	CVS3	20.81	18.8	6.5	1
Spring 2006	Riprap	Caged	CVS	CVS4	20.81	18.8	6.5	1
Spring 2006	Riprap	Uncaged	CVS	CVS5	20.81	18.8	6.5	1
Spring 2006	Riprap	Caged	CVS	CVS6	20.81	18.8	6.5	1
Spring 2006	Riprap	Uncaged	GL	GL1	20.81	18.8	6.5	1
Spring 2006	Riprap	Caged	GL	GL2	20.81	18.8	6.5	1
Spring 2006	Riprap	Uncaged	GL	GL3	20.81	18.8	6.5	1
Spring 2006	Riprap	Caged	GL	GL4	20.81	18.8	6.5	1

Alternative Substrate (ASE) -- Continued

Sampling Period	Site	Cage Control	Substrate	Substrate #	Temp	Salinity	DO	Depth
Spring 2006	Riprap	Uncaged	GL	GL5	20.81	18.8	6.5	1
Spring 2006	Riprap	Caged	GL	GL6	20.81	18.8	6.5	1
Spring 2006	Riprap	Uncaged	GS	GS1	20.81	18.8	6.5	1
Spring 2006	Riprap	Caged	GS	GS2	20.81	18.8	6.5	1
Spring 2006	Riprap	Uncaged	GS	GS3	20.81	18.8	6.5	1
Spring 2006	Riprap	Caged	GS	GS4	20.81	18.8	6.5	1
Spring 2006	Riprap	Uncaged	GS	GS5	20.81	18.8	6.5	1
Spring 2006	Riprap	Caged	GS	GS6	20.81	18.8	6.5	1
Spring 2006	Riprap	Uncaged	LML	LML1	20.81	18.8	6.5	1
Spring 2006	Riprap	Caged	LML	LML2	20.81	18.8	6.5	1
Spring 2006	Riprap	Uncaged	LML	LML3	20.81	18.8	6.5	1
Spring 2006	Riprap	Caged	LML	LML4	20.81	18.8	6.5	1
Spring 2006	Riprap	Uncaged	LML	LML5	20.81	18.8	6.5	1
Spring 2006	Riprap	Caged	LML	LML6	20.81	18.8	6.5	1
Spring 2006	Riprap	Uncaged	LMS	LMS1	20.81	18.8	6.5	1
Spring 2006	Riprap	Caged	LMS	LMS2	20.81	18.8	6.5	1
Spring 2006	Riprap	Uncaged	LMS	LMS3	20.81	18.8	6.5	1
Spring 2006	Riprap	Caged	LMS	LMS4	20.81	18.8	6.5	1
Spring 2006	Riprap	Uncaged	LMS	LMS5	20.81	18.8	6.5	1
Spring 2006	Riprap	Caged	LMS	LMS6	20.81	18.8	6.5	1
Spring 2006	Riprap	Uncaged	OSU	OSU1	20.81	18.8	6.5	1
Spring 2006	Riprap	Caged	OSU	OSU2	20.81	18.8	6.5	1
Spring 2006	Riprap	Uncaged	OSU	OSU3	20.81	18.8	6.5	1
Spring 2006	Riprap	Caged	OSU	OSU4	20.81	18.8	6.5	1

Alternative Substrate (ASE) -- Continued

Sampling Period	Site	Cage Control	Substrate	Substrate #	Temp	Salinity	DO	Depth
Spring 2006	Riprap	Uncaged	OSU	OSU5	20.81	18.8	6.5	1
Spring 2006	Riprap	Caged	OSU	OSU6	20.81	18.8	6.5	1
Spring 2007	Marsh	Caged	CVS	CVS1	13.69	21.01	7.12	1
Spring 2007	Marsh	Uncaged	CVS	CVS2	13.69	21.01	7.12	1
Spring 2007	Marsh	Caged	CVS	CVS3	13.69	21.01	7.12	1
Spring 2007	Marsh	Uncaged	CVS	CVS4	13.69	21.01	7.12	1
Spring 2007	Marsh	Caged	CVS	CVS5	13.69	21.01	7.12	1
Spring 2007	Marsh	Uncaged	CVS	CVS6	13.69	21.01	7.12	1
Spring 2007	Marsh	Caged	GL	GL1	13.69	21.01	7.12	1
Spring 2007	Marsh	Uncaged	GL	GL2	13.69	21.01	7.12	1
Spring 2007	Marsh	Caged	GL	GL3	13.69	21.01	7.12	1
Spring 2007	Marsh	Uncaged	GL	GL4	13.69	21.01	7.12	1
Spring 2007	Marsh	Caged	GL	GL5	13.69	21.01	7.12	1
Spring 2007	Marsh	Uncaged	GL	GL6	13.69	21.01	7.12	1
Spring 2007	Marsh	Caged	GS	GS1	13.69	21.01	7.12	1
Spring 2007	Marsh	Uncaged	GS	GS2	13.69	21.01	7.12	1
Spring 2007	Marsh	Caged	GS	GS3	13.69	21.01	7.12	1
Spring 2007	Marsh	Uncaged	GS	GS4	13.69	21.01	7.12	1
Spring 2007	Marsh	Caged	GS	GS5	13.69	21.01	7.12	1
Spring 2007	Marsh	Uncaged	GS	GS6	13.69	21.01	7.12	1
Spring 2007	Marsh	Caged	LML	LML1	13.69	21.01	7.12	1
Spring 2007	Marsh	Uncaged	LML	LML2	13.69	21.01	7.12	1
Spring 2007	Marsh	Caged	LML	LML3	13.69	21.01	7.12	1
Spring 2007	Marsh	Uncaged	LML	LML4	13.69	21.01	7.12	1

Alternative Substrate (ASE) -- Continued

Sampling Period	Site	Cage Control	Substrate	Substrate #	Temp	Salinity	DO	Depth
Spring 2007	Marsh	Caged	LML	LML5	13.69	21.01	7.12	1
Spring 2007	Marsh	Uncaged	LML	LML6	13.69	21.01	7.12	1
Spring 2007	Marsh	Caged	LMS	LMS1	13.69	21.01	7.12	1
Spring 2007	Marsh	Uncaged	LMS	LMS2	13.69	21.01	7.12	1
Spring 2007	Marsh	Caged	LMS	LMS3	13.69	21.01	7.12	1
Spring 2007	Marsh	Uncaged	LMS	LMS4	13.69	21.01	7.12	1
Spring 2007	Marsh	Caged	LMS	LMS5	13.69	21.01	7.12	1
Spring 2007	Marsh	Uncaged	LMS	LMS6	13.69	21.01	7.12	1
Spring 2007	Marsh	Caged	OSU	OSU1	13.69	21.01	7.12	1
Spring 2007	Marsh	Uncaged	OSU	OSU2	13.69	21.01	7.12	1
Spring 2007	Marsh	Caged	OSU	OSU3	13.69	21.01	7.12	1
Spring 2007	Marsh	Uncaged	OSU	OSU4	13.69	21.01	7.12	1
Spring 2007	Marsh	Caged	OSU	OSU5	13.69	21.01	7.12	1
Spring 2007	Marsh	Uncaged	OSU	OSU6	13.69	21.01	7.12	1
Spring 2007	Oyster Reef	Uncaged	CVS	CVS1	13.69	21.01	7.12	1
Spring 2007	Oyster Reef	Caged	CVS	CVS2	13.69	21.01	7.12	1
Spring 2007	Oyster Reef	Uncaged	CVS	CVS3	13.69	21.01	7.12	1
Spring 2007	Oyster Reef	Caged	CVS	CVS4	13.69	21.01	7.12	1
Spring 2007	Oyster Reef	Uncaged	CVS	CVS5	13.69	21.01	7.12	1
Spring 2007	Oyster Reef	Caged	CVS	CVS6	13.69	21.01	7.12	1
Spring 2007	Oyster Reef	Uncaged	GL	GL1	13.69	21.01	7.12	1
Spring 2007	Oyster Reef	Caged	GL	GL2	13.69	21.01	7.12	1
Spring 2007	Oyster Reef	Uncaged	GL	GL3	13.69	21.01	7.12	1
Spring 2007	Oyster Reef	Caged	GL	GL4	13.69	21.01	7.12	1

Alternative Substrate (ASE) -- Continued

Sampling Period	Site	Cage Control	Substrate	Substrate #	Temp	Salinity	DO	Depth
Spring 2007	Oyster Reef	Uncaged	GL	GL5	13.69	21.01	7.12	1
Spring 2007	Oyster Reef	Caged	GL	GL6	13.69	21.01	7.12	1
Spring 2007	Oyster Reef	Uncaged	GS	GS1	13.69	21.01	7.12	1
Spring 2007	Oyster Reef	Caged	GS	GS2	13.69	21.01	7.12	1
Spring 2007	Oyster Reef	Uncaged	GS	GS3	13.69	21.01	7.12	1
Spring 2007	Oyster Reef	Caged	GS	GS4	13.69	21.01	7.12	1
Spring 2007	Oyster Reef	Uncaged	GS	GS5	13.69	21.01	7.12	1
Spring 2007	Oyster Reef	Caged	GS	GS6	13.69	21.01	7.12	1
Spring 2007	Oyster Reef	Uncaged	LML	LML1	13.69	21.01	7.12	1
Spring 2007	Oyster Reef	Caged	LML	LML2	13.69	21.01	7.12	1
Spring 2007	Oyster Reef	Uncaged	LML	LML3	13.69	21.01	7.12	1
Spring 2007	Oyster Reef	Caged	LML	LML4	13.69	21.01	7.12	1
Spring 2007	Oyster Reef	Uncaged	LML	LML5	13.69	21.01	7.12	1
Spring 2007	Oyster Reef	Caged	LML	LML6	13.69	21.01	7.12	1
Spring 2007	Oyster Reef	Uncaged	LMS	LMS1	13.69	21.01	7.12	1
Spring 2007	Oyster Reef	Caged	LMS	LMS2	13.69	21.01	7.12	1
Spring 2007	Oyster Reef	Uncaged	LMS	LMS3	13.69	21.01	7.12	1
Spring 2007	Oyster Reef	Caged	LMS	LMS4	13.69	21.01	7.12	1
Spring 2007	Oyster Reef	Uncaged	LMS	LMS5	13.69	21.01	7.12	1
Spring 2007	Oyster Reef	Caged	LMS	LMS6	13.69	21.01	7.12	1
Spring 2007	Oyster Reef	Uncaged	OSU	OSU1	13.69	21.01	7.12	1
Spring 2007	Oyster Reef	Caged	OSU	OSU2	13.69	21.01	7.12	1
Spring 2007	Oyster Reef	Uncaged	OSU	OSU3	13.69	21.01	7.12	1
Spring 2007	Oyster Reef	Caged	OSU	OSU4	13.69	21.01	7.12	1

Alternative Substrate (ASE) -- Continued

Sampling Period	Site	Cage Control	Substrate	Substrate #	Temp	Salinity	DO	Depth
Spring 2007	Oyster Reef	Uncaged	OSU	OSU5	13.69	21.01	7.12	1
Spring 2007	Oyster Reef	Caged	OSU	OSU6	13.69	21.01	7.12	1
Spring 2007	Riprap	Uncaged	CVS	CVS1	13.69	21.01	7.12	1
Spring 2007	Riprap	Caged	CVS	CVS2	13.69	21.01	7.12	1
Spring 2007	Riprap	Uncaged	CVS	CVS3	13.69	21.01	7.12	1
Spring 2007	Riprap	Caged	CVS	CVS4	13.69	21.01	7.12	1
Spring 2007	Riprap	Uncaged	CVS	CVS5	13.69	21.01	7.12	1
Spring 2007	Riprap	Caged	CVS	CVS6	13.69	21.01	7.12	1
Spring 2007	Riprap	Uncaged	GL	GL1	13.69	21.01	7.12	1
Spring 2007	Riprap	Caged	GL	GL2	13.69	21.01	7.12	1
Spring 2007	Riprap	Uncaged	GL	GL3	13.69	21.01	7.12	1
Spring 2007	Riprap	Caged	GL	GL4	13.69	21.01	7.12	1
Spring 2007	Riprap	Uncaged	GL	GL5	13.69	21.01	7.12	1
Spring 2007	Riprap	Caged	GL	GL6	13.69	21.01	7.12	1
Spring 2007	Riprap	Uncaged	GS	GS1	13.69	21.01	7.12	1
Spring 2007	Riprap	Caged	GS	GS2	13.69	21.01	7.12	1
Spring 2007	Riprap	Uncaged	GS	GS3	13.69	21.01	7.12	1
Spring 2007	Riprap	Caged	GS	GS4	13.69	21.01	7.12	1
Spring 2007	Riprap	Uncaged	GS	GS5	13.69	21.01	7.12	1
Spring 2007	Riprap	Caged	GS	GS6	13.69	21.01	7.12	1
Spring 2007	Riprap	Uncaged	LML	LML1	13.69	21.01	7.12	1
Spring 2007	Riprap	Caged	LML	LML2	13.69	21.01	7.12	1
Spring 2007	Riprap	Uncaged	LML	LML3	13.69	21.01	7.12	1
Spring 2007	Riprap	Caged	LML	LML4	13.69	21.01	7.12	1

Alternative Substrate (ASE) -- Continued

Sampling Period	Site	Cage Control	Substrate	Substrate #	Temp	Salinity	DO	Depth
Spring 2007	Riprap	Uncaged	LML	LML5	13.69	21.01	7.12	1
Spring 2007	Riprap	Caged	LML	LML6	13.69	21.01	7.12	1
Spring 2007	Riprap	Uncaged	LMS	LMS1	13.69	21.01	7.12	1
Spring 2007	Riprap	Caged	LMS	LMS2	13.69	21.01	7.12	1
Spring 2007	Riprap	Uncaged	LMS	LMS3	13.69	21.01	7.12	1
Spring 2007	Riprap	Caged	LMS	LMS4	13.69	21.01	7.12	1
Spring 2007	Riprap	Uncaged	LMS	LMS5	13.69	21.01	7.12	1
Spring 2007	Riprap	Caged	LMS	LMS6	13.69	21.01	7.12	1
Spring 2007	Riprap	Uncaged	OSU	OSU1	13.69	21.01	7.12	1
Spring 2007	Riprap	Caged	OSU	OSU2	13.69	21.01	7.12	1
Spring 2007	Riprap	Uncaged	OSU	OSU3	13.69	21.01	7.12	1
Spring 2007	Riprap	Caged	OSU	OSU4	13.69	21.01	7.12	1
Spring 2007	Riprap	Uncaged	OSU	OSU5	13.69	21.01	7.12	1
Spring 2007	Riprap	Caged	OSU	OSU6	13.69	21.01	7.12	1
Spring 2008	Marsh	Caged	CVS	CVS1	12.86	18.89	6.5	1
Spring 2008	Marsh	Uncaged	CVS	CVS2	12.86	18.89	6.5	1
Spring 2008	Marsh	Caged	CVS	CVS3	12.86	18.89	6.5	1
Spring 2008	Marsh	Uncaged	CVS	CVS4	12.86	18.89	6.5	1
Spring 2008	Marsh	Caged	GL	GL1	12.86	18.89	6.5	1
Spring 2008	Marsh	Uncaged	GL	GL2	12.86	18.89	6.5	1
Spring 2008	Marsh	Caged	GL	GL3	12.86	18.89	6.5	1
Spring 2008	Marsh	Uncaged	GL	GL4	12.86	18.89	6.5	1
Spring 2008	Marsh	Caged	GS	GS1	12.86	18.89	6.5	1
Spring 2008	Marsh	Uncaged	GS	GS2	12.86	18.89	6.5	1

Alternative Substrate (ASE) -- Continued

Sampling Period	Site	Cage Control	Substrate	Substrate #	Temp	Salinity	DO	Depth
Spring 2008	Marsh	Caged	GS	GS3	12.86	18.89	6.5	1
Spring 2008	Marsh	Uncaged	GS	GS4	12.86	18.89	6.5	1
Spring 2008	Marsh	Caged	LML	LML1	12.86	18.89	6.5	1
Spring 2008	Marsh	Uncaged	LML	LML2	12.86	18.89	6.5	1
Spring 2008	Marsh	Caged	LML	LML3	12.86	18.89	6.5	1
Spring 2008	Marsh	Uncaged	LML	LML4	12.86	18.89	6.5	1
Spring 2008	Marsh	Caged	LMS	LMS1	12.86	18.89	6.5	1
Spring 2008	Marsh	Uncaged	LMS	LMS2	12.86	18.89	6.5	1
Spring 2008	Marsh	Caged	LMS	LMS3	12.86	18.89	6.5	1
Spring 2008	Marsh	Uncaged	LMS	LMS4	12.86	18.89	6.5	1
Spring 2008	Marsh	Caged	OSU	OSU1	12.86	18.89	6.5	1
Spring 2008	Marsh	Uncaged	OSU	OSU2	12.86	18.89	6.5	1
Spring 2008	Marsh	Caged	OSU	OSU3	12.86	18.89	6.5	1
Spring 2008	Marsh	Uncaged	OSU	OSU4	12.86	18.89	6.5	1
Spring 2008	Oyster Reef	Uncaged	CS	CVS1	12.86	18.89	6.5	1
Spring 2008	Oyster Reef	Caged	CVS	CVS2	12.86	18.89	6.5	1
Spring 2008	Oyster Reef	Uncaged	CVS	CVS3	12.86	18.89	6.5	1
Spring 2008	Oyster Reef	Caged	CVS	CVS4	12.86	18.89	6.5	1
Spring 2008	Oyster Reef	Uncaged	GL	GL1	12.86	18.89	6.5	1
Spring 2008	Oyster Reef	Caged	GL	GL2	12.86	18.89	6.5	1
Spring 2008	Oyster Reef	Uncaged	GL	GL3	12.86	18.89	6.5	1
Spring 2008	Oyster Reef	Caged	GL	GL4	12.86	18.89	6.5	1
Spring 2008	Oyster Reef	Uncaged	GS	GS1	12.86	18.89	6.5	1
Spring 2008	Oyster Reef	Caged	GS	GS2	12.86	18.89	6.5	1

Alternative Substrate (ASE) -- Continued

Sampling Period	Site	Cage Control	Substrate	Substrate #	Temp	Salinity	DO	Depth
Spring 2008	Oyster Reef	Uncaged	GS	GS3	12.86	18.89	6.5	1
Spring 2008	Oyster Reef	Caged	GS	GS4	12.86	18.89	6.5	1
Spring 2008	Oyster Reef	Uncaged	LML	LML1	12.86	18.89	6.5	1
Spring 2008	Oyster Reef	Caged	LML	LML2	12.86	18.89	6.5	1
Spring 2008	Oyster Reef	Uncaged	LML	LML3	12.86	18.89	6.5	1
Spring 2008	Oyster Reef	Caged	LML	LML4	12.86	18.89	6.5	1
Spring 2008	Oyster Reef	Uncaged	LMS	LMS1	12.86	18.89	6.5	1
Spring 2008	Oyster Reef	Caged	LMS	LMS2	12.86	18.89	6.5	1
Spring 2008	Oyster Reef	Uncaged	LMS	LMS3	12.86	18.89	6.5	1
Spring 2008	Oyster Reef	Caged	LMS	LMS4	12.86	18.89	6.5	1
Spring 2008	Oyster Reef	Uncaged	OSU	OSU1	12.86	18.89	6.5	1
Spring 2008	Oyster Reef	Caged	OSU	OSU2	12.86	18.89	6.5	1
Spring 2008	Oyster Reef	Uncaged	OSU	OSU3	12.86	18.89	6.5	1
Spring 2008	Oyster Reef	Caged	OSU	OSU4	12.86	18.89	6.5	1
Spring 2008	Riprap	Uncaged	CVS	CVS3	12.86	18.89	6.5	1
Spring 2008	Riprap	Caged	CVS	CVS4	12.86	18.89	6.5	1
Spring 2008	Riprap	Uncaged	CVS	CVS5	12.86	18.89	6.5	1
Spring 2008	Riprap	Caged	CVS	CVS6	12.86	18.89	6.5	1
Spring 2008	Riprap	Uncaged	GL	GL3	12.86	18.89	6.5	1
Spring 2008	Riprap	Caged	GL	GL4	12.86	18.89	6.5	1
Spring 2008	Riprap	Uncaged	GL	GL5	12.86	18.89	6.5	1
Spring 2008	Riprap	Caged	GL	GL6	12.86	18.89	6.5	1
Spring 2008	Riprap	Uncaged	GS	GS3	12.86	18.89	6.5	1
Spring 2008	Riprap	Caged	GS	GS4	12.86	18.89	6.5	1

Alternative Substrate (ASE) -- Continued

Sampling Period	Site	Cage Control	Substrate	Substrate #	Temp	Salinity	DO	Depth
Spring 2008	Riprap	Uncaged	GS	GS5	12.86	18.89	6.5	1
Spring 2008	Riprap	Caged	GS	GS6	12.86	18.89	6.5	1
Spring 2008	Riprap	Uncaged	LML	LML3	12.86	18.89	6.5	1
Spring 2008	Riprap	Caged	LML	LML4	12.86	18.89	6.5	1
Spring 2008	Riprap	Uncaged	LML	LML5	12.86	18.89	6.5	1
Spring 2008	Riprap	Caged	LML	LML6	12.86	18.89	6.5	1
Spring 2008	Riprap	Uncaged	LMS	LMS3	12.86	18.89	6.5	1
Spring 2008	Riprap	Caged	LMS	LMS4	12.86	18.89	6.5	1
Spring 2008	Riprap	Uncaged	LMS	LMS5	12.86	18.89	6.5	1
Spring 2008	Riprap	Caged	LMS	LMS6	12.86	18.89	6.5	1
Spring 2008	Riprap	Uncaged	OSU	OSU3	12.86	18.89	6.5	1
Spring 2008	Riprap	Caged	OSU	OSU4	12.86	18.89	6.5	1
Spring 2008	Riprap	Uncaged	OSU	OSU5	12.86	18.89	6.5	1
Spring 2008	Riprap	Caged	OSU	OSU6	12.86	18.89	6.5	1

Appendix II Factorial Model (SAS Source)

SAS File 2_aselse_5.sas – Initial Regression Analysis and Stepwise Selection

```
/*                                                              */
/*     Factorial MMC Analysis / Stephanie Long / MSEnvE        */
/*     sp2013    */
/*                                                              */
/* @@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@*/
/*     $Sc:  Jae Yoon <yoon@cee.odu.edu>                        */
/*           Kaufman 130 / 683-4724                             */
/*           Civil and Environmental Engineering                */
/*                                                              */
/*     $Ver: 2.07                                               */
/*     $Id:  03212013                                           */
/* @@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@*/


OPTIONS LINESIZE=98 NODATE;
TITLE1
'*****************************************************************';
TITLE2 'Oyster Restoration & Biomass Analysis';
TITLE3 'Factorial MMC Analysis / Sp2013';
TITLE4
'*****************************************************************';

/* define two data tables for ASE & LSE aggregates & parse */
/* ASE Site Location: Long Creek */

/*    season $    Sampling_Season                */
/*    period $    Sampling_Period                */
/*    site $            Sampling_Site                  */
/*    ccontrol $  Cage_Control                   */
/*    substrate $ Substrate                */
/*    subs_no $   Substrate_No                   */
/*    temperature Temp              */
/*    salinity    Salinity                 */
/*    doxy        DO                */
/*    depth       Depth             */
/*    tss         TSS               */
/*    ktn         Kjiedahl_Nitrogen              */
/*    tp          Phosphorus               */
/*    chl_a       Chl_A             */
/*    e_coli            E_coli                   */
/*    f_entrococci      F_Enterococcus                 */
/*    in_lns            Interior_Live_No_Shell               */
/*    ex_lns            Exterior_Live_No_Shell               */
/*    t_set       Total_Set                */
/*    t_live            Total_Live               */
/*    t_dead            Total_Dead               */
/*    l_density   Live_Density                   */
/*    t_density   Total_Density            (#/m2)      */
/*    afdm        Ash_Free_Dry_Mass        (g)   */
/*    biomass           Biomass            (g/m2)      */

/* @@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@*/
/*                                                              */
/*                 Subgrouping and reclassify                   */
/*                                                              */
/* @@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@*/
```

```
/* LSE Site Locations: Linkhorn Bay - Chalmers, Eastern Branch -
Handeland */

/*      season $        Sampling_Season                 */
/*    period $    Sampling_Period               */
/*    site $            Sampling_Site                 */
/*    ccontrol $  Cage_Control                  */
/*    substrate $ Substrate               */
/*    subs_no $   Substrate_No                  */
/*    temperature Temp              */
/*    salinity    Salinity                */
/*    doxy        DO                */
/*    depth       Depth             */
/*    tss         TSS               */
/*    tn          Nitrogen                */
/*    ktn         Kjiedahl_Nitrogen             */
/*    tp          Phosphorus              */
/*    e_coli            E_coli                  */
/*    f_entrococci      F_Enterococcus                */
/*    in_lns            Interior_Live_No_Shell              */
/*    ex_lns            Exterior_Live_No_Shell              */
/*    t_set       Total_Set               */
/*    t_live            Total_Live              */
/*    t_dead            Total_Dead              */
/*    l_density   Live_Density                  */
/*    t_density   Total_Density     (#/m2)            */
/*    afdm        Ash_Free_Dry_Mass (g)         */
/*    biomass           Biomass     (g/m2)            */

/* @@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@*/


DATA o_ase_nmss;
INFILE 'sl_ase_updated_good_nmss.dat';
INPUT season $ period $ site $ ccontrol $ substrate $ subs_no $
temperature
        salinity doxy depth tss ktn tp chl_a e_coli
        f_entrococci in_lns ex_lns t_set t_live t_dead l_density
t_density
        afdm biomass @@;

DATA o_lse_nmss;
INFILE 'sl_lse_updated_good_nmss.dat';
INPUT season $ period $ site $ ccontrol $ substrate $ subs_no $
        temperature salinity doxy depth tss tn ktn tp e_coli
        f_entrococci in_lns ex_lns t_set t_live t_dead l_density
        t_density afdm biomass @@;

DATA o_composite_nmss;
INFILE 'st_lse_ase_composite_nmss.dat';
INPUT location $ season $ period $ site $ ccontrol $ substrate $ subs_no
$ temperature
        salinity doxy depth tss ktn tp e_coli f_entrococci in_lns ex_lns
t_set t_live
        t_dead l_density t_density
        afdm biomass @@;


/* @@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@*/
/*                                                             */
/*  Third Parameter Screening via Reg & GLM                    */
/*  with no missing biomass values and only WQ parameters      */
/*  +no afdm                                                   */
```

```
/* @@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@*/

PROC REG DATA=o_ase_nmss ALPHA= 0.05;
TITLE1
'******************************************************************';
TITLE2 '3_Oyster Restoration & Biomass Analysis';
TITLE3 'Factorial MMC Analysis / Sp2013';
TITLE4 'STEPWISE Screening - NMSS+WQ+no afdm /  ASE Site Location: Long
Creek ';
TITLE5
'******************************************************************';
MODEL biomass = temperature salinity doxy depth tss ktn tp chl_a
      e_coli f_entrococci / SELECTION=STEPWISE NOINT;

PROC GLM DATA=o_ase_nmss ALPHA = 0.05;
TITLE1
'******************************************************************';
TITLE2 '3_Oyster Restoration & Biomass Analysis';
TITLE3 'Factorial MMC Analysis / Sp2013';
TITLE4 'GLM Screening - NMSS+WQ+no afdm /  ASE Site Location: Long Creek
';
TITLE5
'******************************************************************';
MODEL biomass = temperature salinity doxy depth tss ktn tp chl_a
      e_coli f_entrococci / NOINT;


PROC REG DATA=o_lse_nmss ALPHA=0.05;
TITLE1
'******************************************************************';
TITLE2 '3_Oyster Restoration & Biomass Analysis';
TITLE3 'Factorial MMC Analysis / Sp2013';
TITLE4 'STEPWISE Screening - NMSS+WQ+no afdm / LSE Site Locations:
Linkhorn Bay - Chalmers, Eastern Branch - Handeland';
TITLE5
'******************************************************************';
MODEL biomass = temperature salinity doxy depth tss ktn tp
      e_coli f_entrococci / SELECTION=STEPWISE NOINT ;

PROC GLM DATA=o_lse_nmss ALPHA=0.05;
TITLE1
'******************************************************************';
TITLE2 '3_Oyster Restoration & Biomass Analysis';
TITLE3 'Factorial MMC Analysis / Sp2013';
TITLE4 'GLM Screening - NMSS+WQ+no afdm / LSE Site Locations: Linkhorn
Bay - Chalmers, Eastern Branch - Handeland';
TITLE5
'******************************************************************';
MODEL biomass = temperature salinity doxy depth tss ktn tp e_coli
      f_entrococci / NOINT ;


PROC REG DATA=o_composite_nmss ALPHA=0.05;
TITLE1
'******************************************************************';
TITLE2 '3_Oyster Restoration & Biomass Analysis';
TITLE3 'Factorial MMC Analysis / Sp2013';
TITLE4 'STEPWISE Screening - NMSS+WQ+no afdm / Composite -- ASE+LSE Site
Locations';
TITLE5
'******************************************************************';
MODEL biomass = temperature salinity doxy depth tss ktn tp e_coli
```

```
      f_entrococci / SELECTION=STEPWISE NOINT ;

PROC GLM DATA=o_composite_nmss ALPHA=0.05;
TITLE1
'*****************************************************************';
TITLE2 '3_Oyster Restoration & Biomass Analysis';
TITLE3 'Factorial MMC Analysis / Sp2013';
TITLE4 'GLM Screening - NMSS+WQ+no afdm / Composite -- ASE+LSE Site
Locations';
TITLE5
'*****************************************************************';
MODEL biomass = temperature salinity doxy depth tss ktn tp e_coli
      f_entrococci / NOINT ;




/* @@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@*/
/*                                                               */
/*  Fifth Parameter Screening via Reg & GLM                      */
/*  with no missing biomass values and only WQ parameters        */
/*  +no afdm  + no Depth                                         */
/* @@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@*/

PROC REG DATA=o_ase_nmss ALPHA= 0.05;
TITLE1
'*****************************************************************';
TITLE2 '5_Oyster Restoration & Biomass Analysis';
TITLE3 'Factorial MMC Analysis / Sp2013';
TITLE4 'STEPWISE Screening - NMSS+WQ+no afdm & Depth /  ASE Site
Location: Long Creek ';
TITLE5
'*****************************************************************';
MODEL biomass = temperature salinity doxy tss ktn tp chl_a
      e_coli f_entrococci / SELECTION=STEPWISE NOINT;

PROC GLM DATA=o_ase_nmss ALPHA = 0.05;
TITLE1
'*****************************************************************';
TITLE2 '5_Oyster Restoration & Biomass Analysis';
TITLE3 'Factorial MMC Analysis / Sp2013';
TITLE4 'GLM Screening - NMSS+WQ+no afdm & Depth /  ASE Site Location:
Long Creek ';
TITLE5
'*****************************************************************';
MODEL biomass = temperature salinity doxy tss ktn tp chl_a
      e_coli f_entrococci / NOINT;


PROC REG DATA=o_lse_nmss ALPHA=0.05;
TITLE1
'*****************************************************************';
TITLE2 '5_Oyster Restoration & Biomass Analysis';
TITLE3 'Factorial MMC Analysis / Sp2013';
TITLE4 'STEPWISE Screening - NMSS+WQ+no afdm & Depth / LSE Site
Locations: Linkhorn Bay - Chalmers, Eastern Branch - Handeland';
TITLE5
'*****************************************************************';
MODEL biomass = temperature salinity doxy tss ktn tp
      e_coli f_entrococci / SELECTION=STEPWISE NOINT ;

PROC GLM DATA=o_lse_nmss ALPHA=0.05;
```

```
TITLE1
'*******************************************************************';
TITLE2 '5_Oyster Restoration & Biomass Analysis';
TITLE3 'Factorial MMC Analysis / Sp2013';
TITLE4 'GLM Screening - NMSS+WQ+no afdm & Depth / LSE Site Locations:
Linkhorn Bay - Chalmers, Eastern Branch - Handeland';
TITLE5
'*******************************************************************';
MODEL biomass = temperature salinity doxy tss ktn tp e_coli
      f_entrococci / NOINT ;



PROC REG DATA=o_composite_nmss ALPHA=0.05;
TITLE1
'*******************************************************************';
TITLE2 '5_Oyster Restoration & Biomass Analysis';
TITLE3 'Factorial MMC Analysis / Sp2013';
TITLE4 'STEPWISE Screening - NMSS+WQ+no afdm & Depth / Composite --
ASE+LSE Site Locations';
TITLE5
'*******************************************************************';
MODEL biomass = temperature salinity doxy tss ktn tp e_coli
      f_entrococci / SELECTION=STEPWISE NOINT ;

PROC GLM DATA=o_composite_nmss ALPHA=0.05;
TITLE1
'*******************************************************************';
TITLE2 '5_Oyster Restoration & Biomass Analysis';
TITLE3 'Factorial MMC Analysis / Sp2013';
TITLE4 'GLM Screening - NMSS+WQ+no afdm & Depth / Composite -- ASE+LSE
Site Locations';
TITLE5
'*******************************************************************';
MODEL biomass = temperature salinity doxy tss ktn tp e_coli
      f_entrococci / NOINT ;



/* @@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@*/
/*                          END of src                             */
/* @@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@*/
```

Appendix II Factorial Model (SAS Source) – (Continued)

SAS File 2_aselse_21.sas – Models From Regression Analysis For All Sites

```
/* @@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@*/
/*                                                              */
/*     Factorial MMC Analysis / Stephanie Long / MSEnvE        */
/*     sp2013    */
/*     ASE 2008 Oyster-Reef CS --> CVS                          */
/* @@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@*/
/*     $Sc:  Jae Yoon <yoon@cee.odu.edu>                        */
/*           Kaufman 130 / 683-4724                             */
/*           Civil and Environmental Engineering                */
/*                                                              */
/*     $Ver: 2.07                                               */
/*     $Id:  03212013                                           */
/* @@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@*/


OPTIONS LINESIZE=98 NODATE;
TITLE1
'*****************************************************************';
TITLE2 'Oyster Restoration & Biomass Analysis';
TITLE3 'Factorial MMC Analysis / Sp2013';
TITLE4
'*****************************************************************';

/* define two data tables for ASE & LSE aggregates & parse */
/* ASE Site Location: Long Creek */

/*    season $    Sampling_Season                */
/*    period $    Sampling_Period                */
/*    site $            $ampling_Site                  */
/*    ccontrol $  Cage_Control                   */
/*    substrate $ Substrate                */
/*    subs_no $   Substrate_No                   */
/*    temperature Temp          */
/*    salinity    Salinity                 */
/*    doxy        DO            */
/*    depth       Depth         */
/*    tss         TSS           */
/*    ktn         Kjiedahl_Nitrogen              */
/*    tp          Phosphorus               */
/*    chl_a       Chl_A         */
/*    e_coli            E_coli                   */
/*    f_entrococci      F_Enterococcus                 */
/*    in_lns            Interior_Live_No_Shell               */
/*    ex_lns            Exterior_Live_No_Shell               */
/*    t_set       Total_Set                */
/*    t_live            Total_Live               */
/*    t_dead            Total_Dead               */
/*    l_density   Live_Density                   */
/*    t_density   Total_Density            (#/m2)      */
/*    afdm        Ash_Free_Dry_Mass        (g)  */
/*    biomass           Biomass            (g/m2)      */


/* @@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@*/
/*                                                              */
/*                 Subgrouping and reclassify                   */
```

```
/*                                                              */
/* @@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@*/

/* LSE Site Locations: Linkhorn Bay - Chalmers, Eastern Branch -
Handeland */

/*      season $        Sampling_Season                  */
/*    period $    Sampling_Period                */
/*    site $            Sampling_Site                  */
/*    ccontrol $  Cage_Control                   */
/*    substrate $ Substrate                */
/*    subs_no $   Substrate_No                   */
/*    temperature Temp               */
/*    salinity    Salinity                 */
/*    doxy        DO                 */
/*    depth       Depth              */
/*    tss         TSS                */
/*    tn          Nitrogen                 */
/*    ktn         Kjiedahl_Nitrogen              */
/*    tp          Phosphorus               */
/*    e_coli            E_coli                   */
/*    f_entrococci      F_Enterococcus                 */
/*    in_lns            Interior_Live_No_Shell               */
/*    ex_lns            Exterior_Live_No_Shell               */
/*    t_set       Total_Set                */
/*    t_live            Total_Live               */
/*    t_dead            Total_Dead               */
/*    l_density   Live_Density                   */
/*    t_density   Total_Density      (#/m2)            */
/*    afdm        Ash_Free_Dry_Mass  (g)         */
/*    biomass           Biomass      (g/m2)            */

/* @@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@*/


DATA o_ase_nmss;
INFILE 'sl_ase_updated_good_nmss.dat';
INPUT season $ period $ site $ ccontrol $ substrate $ subs_no $
temperature
        salinity doxy depth tss ktn tp chl_a e_coli
        f_entrococci in_lns ex_lns t_set t_live t_dead l_density
t_density
        afdm biomass @@;

DATA o_lse_nmss;
INFILE 'sl_lse_updated_good_nmss.dat';
INPUT season $ period $ site $ ccontrol $ substrate $ subs_no $
        temperature salinity doxy depth tss tn ktn tp e_coli
        f_entrococci in_lns ex_lns t_set t_live t_dead l_density
        t_density afdm biomass @@;

DATA o_composite_nmss;
INFILE 'st_lse_ase_composite_nmss.dat';
INPUT location $ season $ period $ site $ ccontrol $ substrate $ subs_no
$ temperature
        salinity doxy depth tss ktn tp e_coli f_entrococci in_lns ex_lns
t_set t_live
        t_dead l_density t_density
        afdm biomass @@;


/* @@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@*/
/*                                                              */
```

```
/*  Seventh GLM with Factorial & MMC                              */
/*  with no missing biomass values and only WQ parameters         */
/*  +no afdm  + no Depth                                          */
/*  with factored terms                                           */
/* @@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@*/

PROC GLM DATA=o_ase_nmss ALPHA = 0.05;
TITLE1
'*****************************************************************';
TITLE2 '7_Oyster Restoration & Biomass Analysis';
TITLE3 'Factorial MMC Analysis / Sp2013';
TITLE4 'GLM Screening - NMSS+WQ+no afdm & Depth /  ASE Site Location:
Long Creek ';
TITLE5
'*****************************************************************';

CLASS season  period  site  ccontrol  substrate subs_no temperature
      salinity doxy tss ktn tp chl_a e_coli f_entrococci;

MODEL biomass = season  period  subs_no  site  ccontrol  substrate  ktn
e_coli temperature
| tp | chl_a / NOINT;


MEANS season  period  subs_no  site  ccontrol  substrate  ktn  e_coli
temperature | tp |
chl_a / DUNCAN;



PROC GLM DATA=o_lse_nmss ALPHA=0.05;
TITLE1
'*****************************************************************';
TITLE2 '6_Oyster Restoration & Biomass Analysis';
TITLE3 'Factorial MMC Analysis / Sp2013';
TITLE4 'GLM Screening - NMSS+WQ+no afdm & Depth / LSE Site Locations:
Linkhorn Bay - Chalmers, Eastern Branch - Handeland';
TITLE5
'*****************************************************************';
CLASS  season  period  site  ccontrol  substrate  subs_no  temperature
salinity  doxy
      tss  ktn  tp  e_coli;

MODEL biomass = season period site ccontrol substrate subs_no e_coli |
doxy | tp / NOINT;


MEANS season period site ccontrol substrate subs_no  e_coli |  doxy | tp
      / DUNCAN;


PROC GLM DATA=o_composite_nmss ALPHA=0.05;
TITLE1
'*****************************************************************';
TITLE2 '6_Oyster Restoration & Biomass Analysis';
TITLE3 'Factorial MMC Analysis / Sp2013';
TITLE4 'GLM Screening - NMSS+WQ+no afdm & Depth / Composite -- ASE+LSE
Site Locations';
TITLE5
'*****************************************************************';
CLASS  season  period  site  ccontrol  substrate  subs_no  temperature
salinity  doxy
```

```
tss  ktn  tp  e_coli   f_entrococci;

MODEL biomass = temperature salinity tss  | e_coli | doxy | tp
       / NOINT ;

MEANS  temperature  salinity tss | e_coli | doxy | tp / DUNCAN;


/* @@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@*/
/*                      END of src                             */
/* @@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@*/
```

Appendix III Output from Factorial Model (SAS Listing)

SAS List File 2_aselse_5.lst – Initial Regression Analysis and Stepwise Selection

```
****************************************************************                1
                         3_Oyster Restoration & Biomass Analysis
                             Factorial MMC Analysis / Sp2013
              STEPWISE Screening - NMSS+WQ+no afdm /  ASE Site Location: Long Creek
                ****************************************************************

                                  The REG Procedure
                                    Model: MODEL1
                              Dependent Variable: biomass

                        Number of Observations Read         540
                        Number of Observations Used         540

                              Stepwise Selection: Step 1


               Variable tp Entered: R-Square = 0.4094 and C(p) = 134.7656

NOTE: No intercept in model. R-Square is redefined.

                                Analysis of Variance

                                          Sum of           Mean
          Source                   DF        Squares         Square    F Value    Pr > F

          Model                     1        3789479        3789479     373.66    <.0001
          Error                   539        5466309          10142
          Uncorrected Total       540        9255788

                           Parameter      Standard
               Variable     Estimate         Error   Type II SS  F Value   Pr > F

               tp         1328.71427      68.73763      3789479   373.66   <.0001

                          Bounds on condition number: 1, 1
--------------------------------------------------------------------------------
---------

                              Stepwise Selection: Step 2


             Variable e_coli Entered: R-Square = 0.4547 and C(p) = 85.1671

NOTE: No intercept in model. R-Square is redefined.

                                Analysis of Variance

                                          Sum of           Mean
          Source                   DF        Squares         Square    F Value    Pr > F

          Model                     2        4208724        2104362     224.32    <.0001
          Error                   538        5047064     9381.15963
          Uncorrected Total       540        9255788
```

```
                  ****************************************************************
2
                          3_Oyster Restoration & Biomass Analysis
                              Factorial MMC Analysis / Sp2013
               STEPWISE Screening - NMSS+WQ+no afdm /  ASE Site Location: Long Creek
                  ****************************************************************

                                     The REG Procedure
                                       Model: MODEL1
                                Dependent Variable: biomass

                                 Stepwise Selection: Step 2

                             Parameter     Standard
                Variable      Estimate        Error   Type II SS  F Value  Pr > F

                tp          1725.87939     88.88327      3537019   377.03  <.0001
                e_coli        -4.86476      0.72771       419245    44.69  <.0001

                          Bounds on condition number: 1.8076, 7.2304
------------------------------------------------------------------------------------------
---------

                                 Stepwise Selection: Step 3

                 Variable chl_a Entered: R-Square = 0.4773 and C(p) = 61.4139

NOTE: No intercept in model. R-Square is redefined.

                                    Analysis of Variance

                                                Sum of           Mean
           Source                    DF        Squares         Square    F Value    Pr > F

           Model                      3        4417972        1472657     163.47    <.0001
           Error                    537        4837816     9008.96856
           Uncorrected Total        540        9255788

                             Parameter     Standard
                Variable      Estimate        Error   Type II SS  F Value  Pr > F

                tp           750.55572    220.32307       104549    11.61  0.0007
                chl_a          8.93313      1.85358       209248    23.23  <.0001
                e_coli        -8.22977      0.99803       612583    68.00  <.0001

                          Bounds on condition number: 17.988, 99.281
------------------------------------------------------------------------------------------
---------

                                 Stepwise Selection: Step 4

              Variable temperature Entered: R-Square = 0.5241 and C(p) = 10.1619

NOTE: No intercept in model. R-Square is redefined.
```

```
                  *****************************************************************
3
                              3_Oyster Restoration & Biomass Analysis
                                  Factorial MMC Analysis / Sp2013
                  STEPWISE Screening - NMSS+WQ+no afdm /  ASE Site Location: Long Creek
                  *****************************************************************

                                       The REG Procedure
                                         Model: MODEL1
                                  Dependent Variable: biomass

                                   Stepwise Selection: Step 4

                                      Analysis of Variance

                                                 Sum of           Mean
         Source                     DF          Squares         Square    F Value    Pr > F

         Model                       4          4850651        1212663     147.55    <.0001
         Error                     536          4405137     8218.53842
         Uncorrected Total         540          9255788

                        Parameter       Standard
              Variable   Estimate          Error    Type II SS  F Value  Pr > F

              temperature   7.52587        1.03722      432680    52.65  <.0001
              tp        -3624.92587      638.69415      264732    32.21  <.0001
              chl_a        28.96556        3.27975      641027    78.00  <.0001
              e_coli      -17.24537        1.56607      996597   121.26  <.0001

                             Bounds on condition number: 106.54, 831.12
-----------------------------------------------------------------------------------------
---------

                                   Stepwise Selection: Step 5

                     Variable ktn Entered: R-Square = 0.5313 and C(p) = 3.9255

NOTE: No intercept in model. R-Square is redefined.

                                      Analysis of Variance

                                                 Sum of           Mean
         Source                     DF          Squares         Square    F Value    Pr > F

         Model                       5          4917573         983515     121.29    <.0001
         Error                     535          4338215     8108.81337
         Uncorrected Total         540          9255788

                        Parameter       Standard
              Variable   Estimate          Error    Type II SS  F Value  Pr > F

              temperature   7.52962        1.03027      433110    53.41  <.0001
              ktn          62.53958       21.76963       66921     8.25  0.0042
              tp        -4671.79175      731.62603      330633    40.77  <.0001
              chl_a        31.32852        3.36002      704943    86.94  <.0001
              e_coli      -20.54787        1.93426      915087   112.85  <.0001
```

```
                    ****************************************************************
4
                               3_Oyster Restoration & Biomass Analysis
                                   Factorial MMC Analysis / Sp2013
                    STEPWISE Screening - NMSS+WQ+no afdm /  ASE Site Location: Long Creek
                    ****************************************************************

                                         The REG Procedure
                                           Model: MODEL1
                                    Dependent Variable: biomass

                                      Stepwise Selection: Step 5

                              Bounds on condition number: 141.69, 1429.7
-----------------------------------------------------------------------------------------
---------


                  All variables left in the model are significant at the 0.1500 level.

             No other variable met the 0.1500 significance level for entry into the model.


NOTE: No intercept in model. R-Square is redefined.

                                   Summary of Stepwise Selection

        Variable        Variable        Number    Partial     Model
 Step   Entered         Removed         Vars In   R-Square    R-Square      C(p)     F Value
Pr > F

   1    tp                                 1       0.4094      0.4094    134.766     373.66
<.0001
   2    e_coli                             2       0.0453      0.4547    85.1671      44.69
<.0001
   3    chl_a                              3       0.0226      0.4773    61.4139      23.23
<.0001
   4    temperature                        4       0.0467      0.5241    10.1619      52.65
<.0001
   5    ktn                                5       0.0072      0.5313     3.9255       8.25
0.0042
```

```
                   *****************************************************************
5
                          3_Oyster Restoration & Biomass Analysis
                              Factorial MMC Analysis / Sp2013
                GLM Screening - NMSS+WQ+no afdm /  ASE Site Location: Long Creek
                   *****************************************************************

                                     The GLM Procedure

                          Number of Observations Read         540
                          Number of Observations Used         540

                   *****************************************************************
6
                          3_Oyster Restoration & Biomass Analysis
                              Factorial MMC Analysis / Sp2013
                GLM Screening - NMSS+WQ+no afdm /  ASE Site Location: Long Creek
                   *****************************************************************

                                     The GLM Procedure

Dependent Variable: biomass

                                                   Sum of
       Source                      DF             Squares     Mean Square    F Value    Pr >
F

       Model                        7         4925092.902      703584.700      86.59
<.0001

       Error                      533         4330695.003        8125.131

       Uncorrected Total          540         9255787.904


                      R-Square     Coeff Var      Root MSE    biomass Mean

                      0.532110      113.6542      90.13951        79.31029

NOTE: No intercept term is used: R-square is not corrected for the mean.

       Source                      DF         Type I SS     Mean Square    F Value    Pr >
F

       temperature                  1       3180347.603     3180347.603     391.42
<.0001
       salinity                     1        263978.175      263978.175      32.49
<.0001
       doxy                         1        239223.703      239223.703      29.44
<.0001
       depth                        1          9335.984        9335.984       1.15
0.2842
       tss                          1        905019.532      905019.532     111.39
<.0001
       ktn                          1        326453.539      326453.539      40.18
<.0001
       tp                           1           734.366         734.366       0.09
0.7638
       chl_a                        0             0.000             .           .         .
       e_coli                       0             0.000             .           .         .
       f_entrococci                 0             0.000             .           .         .

       Source                      DF       Type III SS     Mean Square    F Value    Pr >
F

       temperature                  0        0.00000000             .           .         .
       salinity                     1        0.00024543      0.00024543       0.00
0.9999
       doxy                         0        0.00000000             .           .         .
       depth                        0        0.00000000             .           .         .
       tss                          0        0.00000000             .           .         .
       ktn                          0        0.00000000             .           .         .
       tp                           0        0.00000000             .           .         .
       chl_a                        0        0.00000000             .           .         .
       e_coli                       0        0.00000000             .           .         .
       f_entrococci                 0        0.00000000             .           .         .

                                                  Standard
```

```
                Parameter            Estimate              Error    t Value    Pr > |t|

                temperature          2.118303 B         70.66535       0.03      0.9761
                salinity             0.052221          300.46504       0.00      0.9999

                   ****************************************************************
7
                              3_Oyster Restoration & Biomass Analysis
                                  Factorial MMC Analysis / Sp2013
                 GLM Screening - NMSS+WQ+no afdm /  ASE Site Location: Long Creek
                   ****************************************************************

                                        The GLM Procedure

Dependent Variable: biomass

                                                        Standard
                Parameter            Estimate              Error    t Value    Pr > |t|

                doxy              -10.993018 B         214.22484      -0.05      0.9591
                depth             258.818712 B        8466.15690       0.03      0.9756
                tss               -15.170725 B         106.97165      -0.14      0.8873
                ktn              -391.435567 B        1688.58634      -0.23      0.8168
                tp               9783.566655 B       32542.88360       0.30      0.7638
                chl_a               0.000000 B                 .          .           .
                e_coli              0.000000 B                 .          .           .
                f_entrococci        0.000000 B                 .          .           .

NOTE: The X'X matrix has been found to be singular, and a generalized inverse was used to
solve
      the normal equations.  Terms whose estimates are followed by the letter 'B' are not
      uniquely estimable.
```

```
                ****************************************************************
8
                           3_Oyster Restoration & Biomass Analysis
                               Factorial MMC Analysis / Sp2013
STEPWISE Screening - NMSS+WQ+no afdm / LSE Site Locations: Linkhorn Bay - Chalmers,
Eastern Branch
                ****************************************************************

                                    The REG Procedure
                                      Model: MODEL1
                                Dependent Variable: biomass

                           Number of Observations Read          75
                           Number of Observations Used          75

                                 Stepwise Selection: Step 1


                  Variable doxy Entered: R-Square = 0.4614 and C(p) = 21.1967

NOTE: No intercept in model. R-Square is redefined.

                                    Analysis of Variance

                                             Sum of           Mean
          Source                    DF      Squares         Square    F Value    Pr > F

          Model                      1     13343200       13343200      63.40    <.0001
          Error                     74     15573529         210453
          Uncorrected Total         75     28916729

                               Parameter      Standard
               Variable         Estimate         Error    Type II SS  F Value  Pr > F

               doxy             47.69116       5.98943      13343200    63.40  <.0001

                              Bounds on condition number: 1, 1
------------------------------------------------------------------------------------------
---------

                                 Stepwise Selection: Step 2


                   Variable tp Entered: R-Square = 0.4837 and C(p) = 19.3027

NOTE: No intercept in model. R-Square is redefined.

                                    Analysis of Variance

                                             Sum of           Mean
          Source                    DF      Squares         Square    F Value    Pr > F

          Model                      2     13986994        6993497      34.20    <.0001
          Error                     73     14929734         204517
          Uncorrected Total         75     28916729
```

```
                    ****************************************************************
9
                                  3_Oyster Restoration & Biomass Analysis
                                      Factorial MMC Analysis / Sp2013
STEPWISE Screening - NMSS+WQ+no afdm / LSE Site Locations: Linkhorn Bay - Chalmers,
Eastern Branch
                    ****************************************************************

                                           The REG Procedure
                                             Model: MODEL1
                                      Dependent Variable: biomass

                                       Stepwise Selection: Step 2

                                 Parameter      Standard
               Variable           Estimate         Error    Type II SS  F Value  Pr > F

               doxy               67.79876      12.77897       5756799    28.15  <.0001
               tp              -2645.19870    1490.90267        643794     3.15  0.0802

                                 Bounds on condition number: 4.6843, 18.737
--------------------------------------------------------------------------------------------
---------


               All variables left in the model are significant at the 0.1500 level.

          No other variable met the 0.1500 significance level for entry into the model.


NOTE: No intercept in model. R-Square is redefined.

                                     Summary of Stepwise Selection

        Variable       Variable        Number    Partial     Model
 Step   Entered        Removed         Vars In   R-Square    R-Square      C(p)      F Value
Pr > F

   1    doxy                                1     0.4614      0.4614    21.1967        63.40
<.0001
   2    tp                                  2     0.0223      0.4837    19.3027         3.15
0.0802
```

```
                    **************************************************************
10
                              3_Oyster Restoration & Biomass Analysis
                                 Factorial MMC Analysis / Sp2013
GLM Screening - NMSS+WQ+no afdm / LSE Site Locations: Linkhorn Bay - Chalmers, Eastern
Branch - Ha
                    **************************************************************

                                       The GLM Procedure

                              Number of Observations Read          75
                              Number of Observations Used          75


                   **************************************************************
11
                              3_Oyster Restoration & Biomass Analysis
                                 Factorial MMC Analysis / Sp2013
GLM Screening - NMSS+WQ+no afdm / LSE Site Locations: Linkhorn Bay - Chalmers, Eastern
Branch - Ha
                    **************************************************************

                                       The GLM Procedure

Dependent Variable: biomass

                                                      Sum of
       Source                      DF             Squares       Mean Square     F Value     Pr >
F

       Model                        6         17508961.47        2918160.24       17.65
<.0001

       Error                       69         11407767.13         165329.96

       Uncorrected Total           75         28916728.59


                        R-Square      Coeff Var      Root MSE     biomass Mean

                        0.605496       99.83121      406.6079         407.2953

NOTE: No intercept term is used: R-square is not corrected for the mean.

       Source                      DF         Type I SS       Mean Square     F Value     Pr >
F

       temperature                  1       9692570.906       9692570.906       58.63
<.0001
       salinity                     1       3708459.670       3708459.670       22.43
<.0001
       doxy                         1         85454.409         85454.409        0.52
0.4746
       depth                        1       1880697.848       1880697.848       11.38
0.0012
       tss                          1        747171.453        747171.453        4.52
0.0371
       ktn                          1       1394607.179       1394607.179        8.44
0.0049
       tp                           0             0.000                 .           .        .
       e_coli                       0             0.000                 .           .        .
       f_entrococci                 0             0.000                 .           .        .

       Source                      DF       Type III SS       Mean Square     F Value     Pr >
F

       temperature                  0                 0                 .           .        .
       salinity                     0                 0                 .           .        .
       doxy                         0                 0                 .           .        .
       depth                        0                 0                 .           .        .
       tss                          0                 0                 .           .        .
       ktn                          0                 0                 .           .        .
       tp                           0                 0                 .           .        .
       e_coli                       0                 0                 .           .        .
       f_entrococci                 0                 0                 .           .        .


                                                     Standard
           Parameter            Estimate               Error     t Value     Pr > |t|
```

```
              temperature        177.268110 B       41.566199       4.26      <.0001
              salinity           -45.697190 B       77.395987      -0.59      0.5568
              doxy               622.706388 B      150.927698       4.13      0.0001
              depth            -5717.272498 B     2771.331125      -2.06      0.0429

                 ****************************************************************
12
                             3_Oyster Restoration & Biomass Analysis
                                 Factorial MMC Analysis / Sp2013
GLM Screening - NMSS+WQ+no afdm / LSE Site Locations: Linkhorn Bay - Chalmers, Eastern
Branch - Ha
                 ****************************************************************

                                        The GLM Procedure

Dependent Variable: biomass

                                                     Standard
              Parameter            Estimate             Error    t Value    Pr > |t|

              tss                  7.008734 B       16.431807       0.43      0.6710
              ktn              -1686.085880 B      580.536488      -2.90      0.0049
              tp                   0.000000 B        .               .         .
              e_coli               0.000000 B        .               .         .
              f_entrococci         0.000000 B        .               .         .

NOTE: The X'X matrix has been found to be singular, and a generalized inverse was used to
solve
      the normal equations.  Terms whose estimates are followed by the letter 'B' are not
      uniquely estimable.
```

```
                 ****************************************************************
13

                           3_Oyster Restoration & Biomass Analysis
                              Factorial MMC Analysis / Sp2013
            STEPWISE Screening - NMSS+WQ+no afdm / Composite -- ASE+LSE Site Locations
                 ****************************************************************

                                     The REG Procedure
                                      Model: MODEL1
                                Dependent Variable: biomass

                         Number of Observations Read         615
                         Number of Observations Used         615

                                Stepwise Selection: Step 1


                 Variable salinity Entered: R-Square = 0.2450 and C(p) = 150.1708

NOTE: No intercept in model. R-Square is redefined.

                                   Analysis of Variance

                                            Sum of           Mean
          Source                  DF       Squares         Square    F Value    Pr > F

          Model                    1       9352024        9352024     199.24    <.0001
          Error                  614      28820493          46939
          Uncorrected Total      615      38172516


                              Parameter     Standard
               Variable        Estimate        Error   Type II SS  F Value  Pr > F

               salinity         5.94252      0.42100      9352024   199.24  <.0001

                              Bounds on condition number: 1, 1
------------------------------------------------------------------------------------------
---------

                                Stepwise Selection: Step 2


                    Variable ktn Entered: R-Square = 0.2832 and C(p) = 113.5316

NOTE: No intercept in model. R-Square is redefined.

                                   Analysis of Variance

                                            Sum of           Mean
          Source                  DF       Squares         Square    F Value    Pr > F

          Model                    2      10811201        5405600     121.11    <.0001
          Error                  613      27361316          44635
          Uncorrected Total      615      38172516
```

```
                   *****************************************************************
14
                          3_Oyster Restoration & Biomass Analysis
                              Factorial MMC Analysis / Sp2013
             STEPWISE Screening - NMSS+WQ+no afdm / Composite -- ASE+LSE Site Locations
                   *****************************************************************

                                     The REG Procedure
                                       Model: MODEL1
                                Dependent Variable: biomass

                                 Stepwise Selection: Step 2

                            Parameter     Standard
               Variable      Estimate        Error   Type II SS  F Value  Pr > F

               salinity      13.43659      1.37349      4271744    95.70  <.0001
               ktn         -160.47998     28.06759      1459177    32.69  <.0001

                          Bounds on condition number: 11.193, 44.771
------------------------------------------------------------------------------------------
---------

                                 Stepwise Selection: Step 3

               Variable temperature Entered: R-Square = 0.2994 and C(p) = 99.1541

NOTE: No intercept in model. R-Square is redefined.

                                    Analysis of Variance

                                               Sum of           Mean
          Source                     DF       Squares         Square    F Value    Pr > F

          Model                       3      11429681        3809894      87.19    <.0001
          Error                     612      26742835          43697
          Uncorrected Total         615      38172516

                            Parameter     Standard
               Variable      Estimate        Error   Type II SS  F Value  Pr > F

               temperature   -5.82359      1.54795       618481    14.15  0.0002
               salinity      17.80850      1.78809      4334424    99.19  <.0001
               ktn         -136.96416     28.46597      1011622    23.15  <.0001

                           Bounds on condition number: 19.377, 135
------------------------------------------------------------------------------------------
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                                 Stepwise Selection: Step 4

                  Variable depth Entered: R-Square = 0.3189 and C(p) = 81.4692

NOTE: No intercept in model. R-Square is redefined.
```

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                  ****************************************************************
15
                        3_Oyster Restoration & Biomass Analysis
                            Factorial MMC Analysis / Sp2013
               STEPWISE Screening - NMSS+WQ+no afdm / Composite -- ASE+LSE Site Locations
                  ****************************************************************

                                  The REG Procedure
                                    Model: MODEL1
                              Dependent Variable: biomass

                               Stepwise Selection: Step 4

                                  Analysis of Variance

                                           Sum of           Mean
          Source                  DF      Squares         Square    F Value    Pr > F

          Model                    4     12173065        3043266      71.52    <.0001
          Error                  611     25999452          42552
          Uncorrected Total      615     38172516


                       Parameter     Standard
               Variable     Estimate        Error    Type II SS  F Value   Pr > F

               temperature  -7.76352      1.59648     1006263    23.65   <.0001
               salinity     40.50577      5.70984     2141454    50.33   <.0001
               depth      -503.93035    120.56619      743384    17.47   <.0001
               ktn         -65.69260     32.86094      170058     4.00   0.0460

                        Bounds on condition number: 210.09, 1776.9
-----------------------------------------------------------------------------------------
---------

                               Stepwise Selection: Step 5

                 Variable tp Entered: R-Square = 0.3568 and C(p) = 45.1940

NOTE: No intercept in model. R-Square is redefined.

                                  Analysis of Variance

                                           Sum of           Mean
          Source                  DF      Squares         Square    F Value    Pr > F

          Model                    5     13618495        2723699      67.67    <.0001
          Error                  610     24554022          40252
          Uncorrected Total      615     38172516


                       Parameter     Standard
               Variable     Estimate        Error    Type II SS  F Value   Pr > F

               temperature -10.20725      1.60540     1627209    40.43   <.0001
               salinity     49.40713      5.74863     2973329    73.87   <.0001
               depth      -780.75282    126.03410     1544699    38.38   <.0001
               ktn         -89.56045     32.20783      311245     7.73   0.0056
               tp         2650.01087    442.22725     1445430    35.91   <.0001
```

```
                    *****************************************************************
16
                              3_Oyster Restoration & Biomass Analysis
                                  Factorial MMC Analysis / Sp2013
                STEPWISE Screening - NMSS+WQ+no afdm / Composite -- ASE+LSE Site Locations
                    *****************************************************************

                                        The REG Procedure
                                          Model: MODEL1
                                   Dependent Variable: biomass

                                    Stepwise Selection: Step 5

                           Bounds on condition number: 242.69, 2525.8
------------------------------------------------------------------------------------------
---------

                                    Stepwise Selection: Step 6

                  Variable doxy Entered: R-Square = 0.3759 and C(p) = 27.8638

NOTE: No intercept in model. R-Square is redefined.

                                      Analysis of Variance

                                              Sum of           Mean
          Source                    DF       Squares         Square    F Value    Pr > F

          Model                      6      14348486        2391414      61.13    <.0001
          Error                    609      23824031          39120
          Uncorrected Total        615      38172516

                           Parameter     Standard
               Variable     Estimate        Error    Type II SS  F Value  Pr > F

               temperature  -7.36382      1.71408        722007    18.46  <.0001
               salinity     45.81835      5.72775       2503274    63.99  <.0001
               doxy         28.14105      6.51449        729991    18.66  <.0001
               depth      -980.37041    132.56338       2139593    54.69  <.0001
               ktn        -121.92947     32.62369        546448    13.97  0.0002
               tp         3282.52378    459.89358       1992962    50.94  <.0001

                           Bounds on condition number: 276.26, 3525.5
------------------------------------------------------------------------------------------
---------

                                    Stepwise Selection: Step 7

                  Variable tss Entered: R-Square = 0.3991 and C(p) = 6.4475

NOTE: No intercept in model. R-Square is redefined.
```

```
                 ***************************************************************
17
                      3_Oyster Restoration & Biomass Analysis
                          Factorial MMC Analysis / Sp2013
           STEPWISE Screening - NMSS+WQ+no afdm / Composite -- ASE+LSE Site Locations
                 ***************************************************************

                                  The REG Procedure
                                   Model: MODEL1
                             Dependent Variable: biomass

                              Stepwise Selection: Step 7

                                Analysis of Variance

                                           Sum of           Mean
        Source                  DF        Squares         Square    F Value    Pr > F

        Model                    7       15232780        2176111      57.68    <.0001
        Error                  608       22939736          37730
        Uncorrected Total      615       38172516


                          Parameter       Standard
             Variable      Estimate          Error    Type II SS  F Value   Pr > F

             temperature   -19.59642       3.03614       1571790    41.66   <.0001
             salinity       99.87252      12.50227       2407680    63.81   <.0001
             doxy           75.30159      11.65444       1575107    41.75   <.0001
             depth       -2569.33862     353.09211       1997798    52.95   <.0001
             tss            14.56962       3.00948        884295    23.44   <.0001
             ktn            44.77973      47.03482         34199     0.91   0.3414
             tp           1336.90088     604.56489        184500     4.89   0.0274

                         Bounds on condition number: 2032.2, 24257
-----------------------------------------------------------------------------------------
---------

                              Stepwise Selection: Step 8

                 Variable ktn Removed: R-Square = 0.3982 and C(p) = 5.3531

NOTE: No intercept in model. R-Square is redefined.

                                Analysis of Variance

                                           Sum of           Mean
        Source                  DF        Squares         Square    F Value    Pr > F

        Model                    6       15198582        2533097      67.15    <.0001
        Error                  609       22973935          37724
        Uncorrected Total      615       38172516
```

```
                    ****************************************************************
18
                         3_Oyster Restoration & Biomass Analysis
                             Factorial MMC Analysis / Sp2013
           STEPWISE Screening - NMSS+WQ+no afdm / Composite -- ASE+LSE Site Locations
                    ****************************************************************

                                    The REG Procedure
                                      Model: MODEL1
                                Dependent Variable: biomass

                                 Stepwise Selection: Step 8

                            Parameter      Standard
               Variable      Estimate         Error     Type II SS   F Value   Pr > F

               temperature    -17.45860       2.04336      2753883     73.00   <.0001
               salinity        90.92134       8.24012      4592852    121.75   <.0001
               doxy            69.46458       9.91071      1853254     49.13   <.0001
               depth        -2313.91838     229.54329      3833407    101.62   <.0001
               tss             12.47194       2.04982      1396544     37.02   <.0001
               tp            1671.86210     491.60697       436298     11.57   0.0007

                          Bounds on condition number: 858.99, 9072.7
--------------------------------------------------------------------------------------------------
---------

               All variables left in the model are significant at the 0.1500 level.

          No other variable met the 0.1500 significance level for entry into the model.


NOTE: No intercept in model. R-Square is redefined.

                                 Summary of Stepwise Selection

        Variable        Variable        Number    Partial      Model
 Step   Entered         Removed         Vars In   R-Square     R-Square      C(p)       F Value
Pr > F

   1    salinity                           1       0.2450       0.2450     150.171      199.24
<.0001
   2    ktn                                2       0.0382       0.2832     113.532       32.69
<.0001
   3    temperature                        3       0.0162       0.2994     99.1541       14.15
0.0002
   4    depth                              4       0.0195       0.3189     81.4692       17.47
<.0001
   5    tp                                 5       0.0379       0.3568     45.1940       35.91
<.0001
   6    doxy                               6       0.0191       0.3759     27.8638       18.66
<.0001
   7    tss                                7       0.0232       0.3991      6.4475       23.44
<.0001
   8                    ktn                6       0.0009       0.3982      5.3531        0.91
0.3414


                    ****************************************************************
19
                         3_Oyster Restoration & Biomass Analysis
                             Factorial MMC Analysis / Sp2013
             GLM Screening - NMSS+WQ+no afdm / Composite -- ASE+LSE Site Locations
                    ****************************************************************

                                    The GLM Procedure

                          Number of Observations Read         615
                          Number of Observations Used         615
```

```
                    ******************************************************************
20
                              3_Oyster Restoration & Biomass Analysis
                                 Factorial MMC Analysis / Sp2013
                  GLM Screening - NMSS+WQ+no afdm / Composite -- ASE+LSE Site Locations
                    ******************************************************************

                                        The GLM Procedure

Dependent Variable: biomass

                                                      Sum of
       Source                          DF            Squares      Mean Square    F Value    Pr >
F

       Model                            8        15249680.14       1906210.02      50.48
<.0001

       Error                          607        22922836.36         37764.15

       Uncorrected Total              615        38172516.50


                            R-Square     Coeff Var      Root MSE    biomass Mean

                            0.399494      162.8803      194.3300        119.3085

NOTE: No intercept term is used: R-square is not corrected for the mean.

       Source                          DF          Type I SS      Mean Square    F Value    Pr >
F

       temperature                      1        7052706.579      7052706.579     186.76
<.0001
       salinity                         1        3365352.902      3365352.902      89.12
<.0001
       doxy                             1          22587.975        22587.975       0.60
0.4396
       depth                            1        1681142.133      1681142.133      44.52
<.0001
       tss                              1        2640494.343      2640494.343      69.92
<.0001
       ktn                              1         285995.912       285995.912       7.57
0.0061
       tp                               1         184500.443       184500.443       4.89
0.0275
       e_coli                           1          16899.848        16899.848       0.45
0.5038
       f_entrococci                     0              0.000                .          .        .

       Source                          DF        Type III SS      Mean Square    F Value    Pr >
F

       temperature                      1        1551059.015      1551059.015      41.07
<.0001
       salinity                         1        2338584.972      2338584.972      61.93
<.0001
       doxy                             1        1517573.012      1517573.012      40.19
<.0001
       depth                            0              0.000                .          .        .
       tss                              1         839813.470       839813.470      22.24
<.0001
       ktn                              1          32233.442        32233.442       0.85
0.3559
       tp                               1         181304.381       181304.381       4.80
0.0288
       e_coli                           1          16899.848        16899.848       0.45
0.5038
       f_entrococci                     0              0.000                .          .        .


                                                         Standard
             Parameter              Estimate               Error    t Value    Pr > |t|

             temperature          -19.492297           3.0415061      -6.41      <.0001
             salinity              98.983292          12.5783927       7.87      <.0001
             doxy                  74.402717          11.7369115       6.34      <.0001
             depth              -2540.156640 B       355.9359196      -7.14      <.0001
```

```
                  *****************************************************************
21
                            3_Oyster Restoration & Biomass Analysis
                               Factorial MMC Analysis / Sp2013
              GLM Screening - NMSS+WQ+no afdm / Composite -- ASE+LSE Site Locations
                  *****************************************************************

                                     The GLM Procedure

Dependent Variable: biomass

                                                       Standard
              Parameter              Estimate             Error    t Value    Pr > |t|

              tss                   14.313124         3.0351687       4.72      <.0001
              ktn                   43.509458        47.0944971       0.92      0.3559
              tp                  1325.772067       605.0685034       2.19      0.0288
              e_coli                 0.110563         0.1652760       0.67      0.5038
              f_entrococci           0.000000 B               .          .           .

NOTE: The X'X matrix has been found to be singular, and a generalized inverse was used to
solve
      the normal equations.  Terms whose estimates are followed by the letter 'B' are not
      uniquely estimable.
```

```
               *****************************************************************
22
                           5_Oyster Restoration & Biomass Analysis
                               Factorial MMC Analysis / Sp2013
          STEPWISE Screening - NMSS+WQ+no afdm & Depth /  ASE Site Location: Long Creek
               *****************************************************************

                                     The REG Procedure
                                       Model: MODEL1
                                 Dependent Variable: biomass

                           Number of Observations Read         540
                           Number of Observations Used         540

                                 Stepwise Selection: Step 1

                  Variable tp Entered: R-Square = 0.4094 and C(p) = 134.7656

NOTE: No intercept in model. R-Square is redefined.

                                    Analysis of Variance

                                              Sum of           Mean
          Source                   DF        Squares         Square    F Value    Pr > F

          Model                     1        3789479        3789479     373.66    <.0001
          Error                   539        5466309          10142
          Uncorrected Total       540        9255788

                               Parameter     Standard
               Variable         Estimate        Error    Type II SS  F Value  Pr > F

               tp             1328.71427     68.73763       3789479   373.66  <.0001

                               Bounds on condition number: 1, 1
-------------------------------------------------------------------------------------------
---------

                                 Stepwise Selection: Step 2

                 Variable e_coli Entered: R-Square = 0.4547 and C(p) = 85.1671

NOTE: No intercept in model. R-Square is redefined.

                                    Analysis of Variance

                                              Sum of           Mean
          Source                   DF        Squares         Square    F Value    Pr > F

          Model                     2        4208724        2104362     224.32    <.0001
          Error                   538        5047064     9381.15963
          Uncorrected Total       540        9255788
```

```
                 ***************************************************************
23
                          5_Oyster Restoration & Biomass Analysis
                              Factorial MMC Analysis / Sp2013
          STEPWISE Screening - NMSS+WQ+no afdm & Depth /  ASE Site Location: Long Creek
                 ***************************************************************

                                     The REG Procedure
                                       Model: MODEL1
                               Dependent Variable: biomass

                                Stepwise Selection: Step 2

                          Parameter     Standard
          Variable         Estimate        Error    Type II SS  F Value  Pr > F

          tp             1725.87939     88.88327       3537019   377.03  <.0001
          e_coli           -4.86476      0.72771        419245    44.69  <.0001

                         Bounds on condition number: 1.8076, 7.2304
-------------------------------------------------------------------------------------------
---------

                                Stepwise Selection: Step 3

                Variable chl_a Entered: R-Square = 0.4773 and C(p) = 61.4139

NOTE: No intercept in model. R-Square is redefined.

                                   Analysis of Variance

                                            Sum of           Mean
       Source                     DF       Squares         Square    F Value    Pr > F

       Model                       3       4417972        1472657     163.47    <.0001
       Error                     537       4837816     9008.96856
       Uncorrected Total         540       9255788

                          Parameter     Standard
          Variable         Estimate        Error    Type II SS  F Value  Pr > F

          tp              750.55572    220.32307        104549    11.61  0.0007
          chl_a             8.93313      1.85358        209248    23.23  <.0001
          e_coli           -8.22977      0.99803        612583    68.00  <.0001

                         Bounds on condition number: 17.988, 99.281
-------------------------------------------------------------------------------------------
---------

                                Stepwise Selection: Step 4

             Variable temperature Entered: R-Square = 0.5241 and C(p) = 10.1619

NOTE: No intercept in model. R-Square is redefined.
```

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                    ****************************************************************
24
                           5_Oyster Restoration & Biomass Analysis
                               Factorial MMC Analysis / Sp2013
          STEPWISE Screening - NMSS+WQ+no afdm & Depth /  ASE Site Location: Long Creek
                    ****************************************************************

                                      The REG Procedure
                                        Model: MODEL1
                                 Dependent Variable: biomass

                                 Stepwise Selection: Step 4

                                    Analysis of Variance

                                               Sum of           Mean
          Source                      DF      Squares         Square    F Value    Pr > F

          Model                        4      4850651        1212663     147.55    <.0001
          Error                      536      4405137     8218.53842
          Uncorrected Total          540      9255788


                               Parameter     Standard
               Variable         Estimate        Error    Type II SS  F Value  Pr > F

               temperature       7.52587      1.03722        432680    52.65  <.0001
               tp            -3624.92587    638.69415        264732    32.21  <.0001
               chl_a            28.96556      3.27975        641027    78.00  <.0001
               e_coli          -17.24537      1.56607        996597   121.26  <.0001

                         Bounds on condition number: 106.54, 831.12
-----------------------------------------------------------------------------------------
---------

                                 Stepwise Selection: Step 5

                  Variable ktn Entered: R-Square = 0.5313 and C(p) = 3.9255

NOTE: No intercept in model. R-Square is redefined.

                                    Analysis of Variance

                                               Sum of           Mean
          Source                      DF      Squares         Square    F Value    Pr > F

          Model                        5      4917573         983515     121.29    <.0001
          Error                      535      4338215     8108.81337
          Uncorrected Total          540      9255788


                               Parameter     Standard
               Variable         Estimate        Error    Type II SS  F Value  Pr > F

               temperature       7.52962      1.03027        433110    53.41  <.0001
               ktn              62.53958     21.76963         66921     8.25  0.0042
               tp            -4671.79175    731.62603        330633    40.77  <.0001
               chl_a            31.32852      3.36002        704943    86.94  <.0001
               e_coli          -20.54787      1.93426        915087   112.85  <.0001
```

```
                    ***************************************************************
25
                          5_Oyster Restoration & Biomass Analysis
                              Factorial MMC Analysis / Sp2013
           STEPWISE Screening - NMSS+WQ+no afdm & Depth /  ASE Site Location: Long Creek
                    ***************************************************************

                                      The REG Procedure
                                        Model: MODEL1
                                 Dependent Variable: biomass

                                 Stepwise Selection: Step 5

                           Bounds on condition number: 141.69, 1429.7
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---------


                All variables left in the model are significant at the 0.1500 level.

           No other variable met the 0.1500 significance level for entry into the model.


NOTE: No intercept in model. R-Square is redefined.

                                 Summary of Stepwise Selection

        Variable        Variable        Number    Partial     Model
 Step   Entered         Removed         Vars In   R-Square    R-Square      C(p)      F Value
Pr > F

   1    tp                                 1       0.4094      0.4094    134.766     373.66
<.0001
   2    e_coli                             2       0.0453      0.4547    85.1671      44.69
<.0001
   3    chl_a                              3       0.0226      0.4773    61.4139      23.23
<.0001
   4    temperature                        4       0.0467      0.5241    10.1619      52.65
<.0001
   5    ktn                                5       0.0072      0.5313     3.9255       8.25
0.0042
```

```
                 ****************************************************************
26
                         5_Oyster Restoration & Biomass Analysis
                            Factorial MMC Analysis / Sp2013
             GLM Screening - NMSS+WQ+no afdm & Depth /  ASE Site Location: Long Creek
                 ****************************************************************

                                   The GLM Procedure

                         Number of Observations Read         540
                         Number of Observations Used         540


                 ****************************************************************
27
                         5_Oyster Restoration & Biomass Analysis
                            Factorial MMC Analysis / Sp2013
             GLM Screening - NMSS+WQ+no afdm & Depth /  ASE Site Location: Long Creek
                 ****************************************************************

                                   The GLM Procedure

Dependent Variable: biomass

                                                   Sum of
       Source                      DF             Squares      Mean Square     F Value     Pr >
F

       Model                        7         4925092.902       703584.700       86.59
<.0001

       Error                      533         4330695.003         8125.131

       Uncorrected Total          540         9255787.904


                       R-Square     Coeff Var      Root MSE     biomass Mean

                       0.532110      113.6542      90.13951         79.31029

NOTE: No intercept term is used: R-square is not corrected for the mean.

       Source                      DF           Type I SS      Mean Square     F Value     Pr >
F

       temperature                  1         3180347.603      3180347.603      391.42
<.0001
       salinity                     1          263978.175       263978.175       32.49
<.0001
       doxy                         1          239223.703       239223.703       29.44
<.0001
       tss                          1          191066.504       191066.504       23.52
<.0001
       ktn                          1            3086.396         3086.396        0.38
0.5379
       tp                           1         1047382.927      1047382.927      128.91
<.0001
       chl_a                        1               7.594            7.594        0.00
0.9756
       e_coli                       0               0.000             .             .          .
       f_entrococci                 0               0.000             .             .          .

       Source                      DF         Type III SS      Mean Square     F Value     Pr >
F

       temperature                  0          0.00000000           .              .          .
       salinity                     1          0.00024543       0.00024543        0.00
0.9999
       doxy                         0          0.00000000           .              .          .
       tss                          0          0.00000000           .              .          .
       ktn                          0          0.00000000           .              .          .
       tp                           0          0.00000000           .              .          .
       chl_a                        0          0.00000000           .              .          .
       e_coli                       0          0.00000000           .              .          .
       f_entrococci                 0          0.00000000           .              .          .


                                                         Standard
              Parameter             Estimate                Error     t Value     Pr > |t|
```

```
              temperature          -1.19520 B          37.7371        -0.03         0.9747
              salinity              0.05222           300.4650         0.00         0.9999
              doxy                 19.85159 B         794.7539         0.02         0.9801
              tss                 -15.60137 B         121.0574        -0.13         0.8975

                 ****************************************************************
28
                           5_Oyster Restoration & Biomass Analysis
                               Factorial MMC Analysis / Sp2013
              GLM Screening - NMSS+WQ+no afdm & Depth /  ASE Site Location: Long Creek
                 ****************************************************************

                                      The GLM Procedure

Dependent Variable: biomass

                                                            Standard
              Parameter            Estimate                    Error    t Value    Pr > |t|

              ktn                -385.50464 B            1494.6222      -0.26      0.7966
              tp                13497.03937 B          154006.1368       0.09      0.9302
              chl_a               -14.66602 B             479.7367      -0.03      0.9756
              e_coli                0.00000 B                 .           .          .
              f_entrococci          0.00000 B                 .           .          .

NOTE: The X'X matrix has been found to be singular, and a generalized inverse was used to
solve
      the normal equations.  Terms whose estimates are followed by the letter 'B' are not
      uniquely estimable.
```

```
                    ****************************************************************
29
                              5_Oyster Restoration & Biomass Analysis
                                  Factorial MMC Analysis / Sp2013
STEPWISE Screening - NMSS+WQ+no afdm & Depth / LSE Site Locations: Linkhorn Bay -
Chalmers, Easter
                    ****************************************************************

                                       The REG Procedure
                                         Model: MODEL1
                                  Dependent Variable: biomass

                              Number of Observations Read          75
                              Number of Observations Used          75

                                   Stepwise Selection: Step 1


                    Variable doxy Entered: R-Square = 0.4614 and C(p) = 21.1967

NOTE: No intercept in model. R-Square is redefined.

                                      Analysis of Variance

                                              Sum of           Mean
          Source                    DF       Squares         Square    F Value    Pr > F

          Model                      1      13343200       13343200      63.40    <.0001
          Error                     74      15573529         210453
          Uncorrected Total         75      28916729


                              Parameter     Standard
               Variable        Estimate        Error   Type II SS  F Value  Pr > F

               doxy            47.69116      5.98943     13343200    63.40  <.0001

                                 Bounds on condition number: 1, 1
-----------------------------------------------------------------------------------------
---------

                                   Stepwise Selection: Step 2

                    Variable tp Entered: R-Square = 0.4837 and C(p) = 19.3027

NOTE: No intercept in model. R-Square is redefined.

                                      Analysis of Variance

                                              Sum of           Mean
          Source                    DF       Squares         Square    F Value    Pr > F

          Model                      2      13986994        6993497      34.20    <.0001
          Error                     73      14929734         204517
          Uncorrected Total         75      28916729
```

```
                     ***************************************************************
30
                              5_Oyster Restoration & Biomass Analysis
                                  Factorial MMC Analysis / Sp2013
STEPWISE Screening - NMSS+WQ+no afdm & Depth / LSE Site Locations: Linkhorn Bay -
Chalmers, Easter
                     ***************************************************************

                                        The REG Procedure
                                          Model: MODEL1
                                   Dependent Variable: biomass

                                    Stepwise Selection: Step 2

                               Parameter      Standard
               Variable         Estimate         Error    Type II SS  F Value  Pr > F

               doxy             67.79876      12.77897       5756799    28.15  <.0001
               tp            -2645.19870    1490.90267        643794     3.15  0.0802

                              Bounds on condition number: 4.6843, 18.737
-------------------------------------------------------------------------------------
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               All variables left in the model are significant at the 0.1500 level.

            No other variable met the 0.1500 significance level for entry into the model.


NOTE: No intercept in model. R-Square is redefined.

                                   Summary of Stepwise Selection

        Variable         Variable         Number     Partial      Model
 Step   Entered          Removed          Vars In    R-Square     R-Square      C(p)       F Value
Pr > F

   1    doxy                                 1        0.4614       0.4614     21.1967        63.40
<.0001
   2    tp                                   2        0.0223       0.4837     19.3027         3.15
0.0802
```

```
                           ****************************************************************
31
                                  5_Oyster Restoration & Biomass Analysis
                                      Factorial MMC Analysis / Sp2013
GLM Screening - NMSS+WQ+no afdm & Depth / LSE Site Locations: Linkhorn Bay - Chalmers,
Eastern Bra
                           ****************************************************************

                                            The GLM Procedure

                                  Number of Observations Read          75
                                  Number of Observations Used          75


                           ****************************************************************
32
                                  5_Oyster Restoration & Biomass Analysis
                                      Factorial MMC Analysis / Sp2013
GLM Screening - NMSS+WQ+no afdm & Depth / LSE Site Locations: Linkhorn Bay - Chalmers,
Eastern Bra
                           ****************************************************************

                                            The GLM Procedure

Dependent Variable: biomass

                                                         Sum of
       Source                        DF                 Squares     Mean Square    F Value    Pr >
F

       Model                          6             17508961.47      2918160.24      17.65
<.0001

       Error                         69             11407767.13       165329.96

       Uncorrected Total             75             28916728.59


                         R-Square     Coeff Var      Root MSE    biomass Mean

                         0.605496      99.83121      406.6079        407.2953

NOTE: No intercept term is used: R-square is not corrected for the mean.

       Source                        DF               Type I SS     Mean Square    F Value    Pr >
F

       temperature                    1             9692570.906     9692570.906      58.63
<.0001
       salinity                       1             3708459.670     3708459.670      22.43
<.0001
       doxy                           1               85454.409       85454.409       0.52
0.4746
       tss                            1              409874.881      409874.881       2.48
0.1199
       ktn                            1             2908958.388     2908958.388      17.59
<.0001
       tp                             1              703643.211      703643.211       4.26
0.0429
       e_coli                         0                   0.000               .          .       .
       f_entrococci                   0                   0.000               .          .       .

       Source                        DF             Type III SS     Mean Square    F Value    Pr >
F

       temperature                    0                       0               .          .       .
       salinity                       0                       0               .          .       .
       doxy                           0                       0               .          .       .
       tss                            0                       0               .          .       .
       ktn                            0                       0               .          .       .
       tp                             0                       0               .          .       .
       e_coli                         0                       0               .          .       .
       f_entrococci                   0                       0               .          .       .


                                                              Standard
             Parameter             Estimate                  Error    t Value    Pr > |t|

             temperature        161.755081 B             41.504401       3.90      0.0002
```

```
                salinity              -154.630214 B        49.598062         -3.12         0.0027
                doxy                   382.233860 B        98.031718          3.90         0.0002
                tss                    -17.069457 B         8.759652         -1.95         0.0554
                ktn                  -2188.287591 B       524.455601         -4.17         <.0001
                tp                   -3483.950527 B      1688.773893         -2.06         0.0429

                   ****************************************************************
33
                                       5_Oyster Restoration & Biomass Analysis
                                           Factorial MMC Analysis / Sp2013
GLM Screening - NMSS+WQ+no afdm & Depth / LSE Site Locations: Linkhorn Bay - Chalmers,
Eastern Bra
                   ****************************************************************

                                                The GLM Procedure

Dependent Variable: biomass

                                                             Standard
                Parameter                Estimate               Error     t Value     Pr > |t|

                e_coli                   0.000000 B                 .           .            .
                f_entrococci             0.000000 B                 .           .            .

NOTE: The X'X matrix has been found to be singular, and a generalized inverse was used to
solve
      the normal equations.  Terms whose estimates are followed by the letter 'B' are not
      uniquely estimable.
```

```
                 ****************************************************************
34
                             5_Oyster Restoration & Biomass Analysis
                                 Factorial MMC Analysis / Sp2013
        STEPWISE Screening - NMSS+WQ+no afdm & Depth / Composite -- ASE+LSE Site
Locations
                 ****************************************************************

                                        The REG Procedure
                                          Model: MODEL1
                                   Dependent Variable: biomass

                             Number of Observations Read         615
                             Number of Observations Used         615

                                    Stepwise Selection: Step 1


                 Variable salinity Entered: R-Square = 0.2450 and C(p) = 150.1708

NOTE: No intercept in model. R-Square is redefined.

                                       Analysis of Variance

                                                Sum of           Mean
          Source                   DF          Squares         Square    F Value    Pr > F

          Model                     1          9352024        9352024     199.24    <.0001
          Error                   614         28820493          46939
          Uncorrected Total       615         38172516


                               Parameter     Standard
               Variable         Estimate        Error    Type II SS  F Value  Pr > F

               salinity          5.94252      0.42100       9352024   199.24  <.0001

                                 Bounds on condition number: 1, 1
-----------------------------------------------------------------------------------------
---------

                                    Stepwise Selection: Step 2


                   Variable ktn Entered: R-Square = 0.2832 and C(p) = 113.5316

NOTE: No intercept in model. R-Square is redefined.

                                       Analysis of Variance

                                                Sum of           Mean
          Source                   DF          Squares         Square    F Value    Pr > F

          Model                     2         10811201        5405600     121.11    <.0001
          Error                   613         27361316          44635
          Uncorrected Total       615         38172516
```

```
                ****************************************************************
35
                          5_Oyster Restoration & Biomass Analysis
                              Factorial MMC Analysis / Sp2013
        STEPWISE Screening - NMSS+WQ+no afdm & Depth / Composite -- ASE+LSE Site
Locations
                ****************************************************************

                                     The REG Procedure
                                       Model: MODEL1
                                Dependent Variable: biomass

                                 Stepwise Selection: Step 2

                             Parameter     Standard
               Variable       Estimate        Error   Type II SS  F Value  Pr > F

               salinity       13.43659      1.37349      4271744    95.70  <.0001
               ktn          -160.47998     28.06759      1459177    32.69  <.0001

                         Bounds on condition number: 11.193, 44.771
------------------------------------------------------------------------------------------
---------

                                 Stepwise Selection: Step 3

               Variable temperature Entered: R-Square = 0.2994 and C(p) = 99.1541

NOTE: No intercept in model. R-Square is redefined.

                                    Analysis of Variance

                                                Sum of           Mean
          Source                    DF         Squares         Square    F Value    Pr > F

          Model                      3        11429681        3809894      87.19    <.0001
          Error                    612        26742835          43697
          Uncorrected Total        615        38172516

                             Parameter     Standard
               Variable       Estimate        Error   Type II SS  F Value  Pr > F

               temperature    -5.82359      1.54795       618481    14.15  0.0002
               salinity       17.80850      1.78809      4334424    99.19  <.0001
               ktn          -136.96416     28.46597      1011622    23.15  <.0001

                          Bounds on condition number: 19.377, 135
------------------------------------------------------------------------------------------
---------

                                 Stepwise Selection: Step 4

              Variable f_entrococci Entered: R-Square = 0.3189 and C(p) = 81.4692

NOTE: No intercept in model. R-Square is redefined.
```

```
                ****************************************************************
36
                        5_Oyster Restoration & Biomass Analysis
                            Factorial MMC Analysis / Sp2013
        STEPWISE Screening - NMSS+WQ+no afdm & Depth / Composite -- ASE+LSE Site
Locations
                ****************************************************************

                                  The REG Procedure
                                    Model: MODEL1
                             Dependent Variable: biomass

                              Stepwise Selection: Step 4

                                 Analysis of Variance

                                         Sum of           Mean
          Source                  DF        Squares         Square    F Value    Pr > F

          Model                    4       12173065        3043266      71.52    <.0001
          Error                  611       25999452          42552
          Uncorrected Total      615       38172516


                       Parameter     Standard
               Variable      Estimate        Error    Type II SS  F Value  Pr > F

               temperature   -7.76352      1.59648       1006263    23.65  <.0001
               salinity      40.50577      5.70984       2141454    50.33  <.0001
               ktn          -65.69260     32.86094        170058     4.00  0.0460
               f_entrococci -20.15721      4.82265        743384    17.47  <.0001

                        Bounds on condition number: 210.09, 1776.9
------------------------------------------------------------------------------------------
---------

                              Stepwise Selection: Step 5


                  Variable tp Entered: R-Square = 0.3568 and C(p) = 45.1940

NOTE: No intercept in model. R-Square is redefined.

                                 Analysis of Variance

                                         Sum of           Mean
          Source                  DF        Squares         Square    F Value    Pr > F

          Model                    5       13618495        2723699      67.67    <.0001
          Error                  610       24554022          40252
          Uncorrected Total      615       38172516


                       Parameter     Standard
               Variable      Estimate        Error    Type II SS  F Value  Pr > F

               temperature  -10.20725      1.60540       1627209    40.43  <.0001
               salinity      49.40713      5.74863       2973329    73.87  <.0001
               ktn          -89.56045     32.20783        311245     7.73  0.0056
               tp          2650.01087    442.22725       1445430    35.91  <.0001
               f_entrococci -31.23011      5.04136       1544699    38.38  <.0001
```

```
                 ****************************************************************
37
                            5_Oyster Restoration & Biomass Analysis
                                Factorial MMC Analysis / Sp2013
        STEPWISE Screening - NMSS+WQ+no afdm & Depth / Composite -- ASE+LSE Site
Locations
                 ****************************************************************

                                      The REG Procedure
                                        Model: MODEL1
                                Dependent Variable: biomass

                                 Stepwise Selection: Step 5

                        Bounds on condition number: 242.69, 2525.8
------------------------------------------------------------------------------------------
---------

                                 Stepwise Selection: Step 6

                 Variable doxy Entered: R-Square = 0.3759 and C(p) = 27.8638

NOTE: No intercept in model. R-Square is redefined.

                                  Analysis of Variance

                                          Sum of           Mean
          Source                 DF      Squares         Square    F Value    Pr > F

          Model                   6     14348486        2391414      61.13    <.0001
          Error                 609     23824031          39120
          Uncorrected Total     615     38172516

                          Parameter     Standard
              Variable     Estimate        Error   Type II SS  F Value  Pr > F

              temperature  -7.36382      1.71408       722007    18.46  <.0001
              salinity     45.81835      5.72775      2503274    63.99  <.0001
              doxy         28.14105      6.51449       729991    18.66  <.0001
              ktn        -121.92947     32.62369       546448    13.97  0.0002
              tp         3282.52378    459.89358      1992962    50.94  <.0001
              f_entrococci -39.21482     5.30254      2139593    54.69  <.0001

                        Bounds on condition number: 276.26, 3525.5
------------------------------------------------------------------------------------------
---------

                                 Stepwise Selection: Step 7

                 Variable tss Entered: R-Square = 0.3991 and C(p) = 6.4475

NOTE: No intercept in model. R-Square is redefined.
```

```
                    *****************************************************************
38
                              5_Oyster Restoration & Biomass Analysis
                                  Factorial MMC Analysis / Sp2013
        STEPWISE Screening - NMSS+WQ+no afdm & Depth / Composite -- ASE+LSE Site
Locations
                    *****************************************************************

                                        The REG Procedure
                                          Model: MODEL1
                                   Dependent Variable: biomass

                                   Stepwise Selection: Step 7

                                      Analysis of Variance

                                                Sum of           Mean
          Source                   DF          Squares         Square    F Value    Pr > F

          Model                     7         15232780        2176111      57.68    <.0001
          Error                   608         22939736          37730
          Uncorrected Total       615         38172516


                             Parameter      Standard
               Variable       Estimate         Error    Type II SS  F Value   Pr > F

               temperature   -19.59642       3.03614       1571790    41.66   <.0001
               salinity       99.87252      12.50227       2407680    63.81   <.0001
               doxy           75.30159      11.65444       1575107    41.75   <.0001
               tss            14.56962       3.00948        884295    23.44   <.0001
               ktn            44.77973      47.03482         34199     0.91   0.3414
               tp           1336.90088     604.56489        184500     4.89   0.0274
               f_entrococci -102.77354      14.12368       1997798    52.95   <.0001

                            Bounds on condition number: 2032.2, 24257
--------------------------------------------------------------------------------------------
---------

                                   Stepwise Selection: Step 8

                         Variable ktn Removed: R-Square = 0.3982 and C(p) = 5.3531

NOTE: No intercept in model. R-Square is redefined.

                                      Analysis of Variance

                                                Sum of           Mean
          Source                   DF          Squares         Square    F Value    Pr > F

          Model                     6         15198582        2533097      67.15    <.0001
          Error                   609         22973935          37724
          Uncorrected Total       615         38172516
```

```
                  ****************************************************************
39
                               5_Oyster Restoration & Biomass Analysis
                                   Factorial MMC Analysis / Sp2013
        STEPWISE Screening - NMSS+WQ+no afdm & Depth / Composite -- ASE+LSE Site
Locations
                  ****************************************************************

                                         The REG Procedure
                                           Model: MODEL1
                                    Dependent Variable: biomass

                                     Stepwise Selection: Step 8

                             Parameter     Standard
              Variable        Estimate        Error    Type II SS  F Value  Pr > F

              temperature    -17.45860      2.04336       2753883    73.00  <.0001
              salinity        90.92134      8.24012       4592852   121.75  <.0001
              doxy            69.46458      9.91071       1853254    49.13  <.0001
              tss             12.47194      2.04982       1396544    37.02  <.0001
              tp            1671.86210    491.60697        436298    11.57  0.0007
              f_entrococci   -92.55674      9.18173       3833407   101.62  <.0001

                          Bounds on condition number: 858.99, 9072.7
------------------------------------------------------------------------------------------
---------


              All variables left in the model are significant at the 0.1500 level.

          No other variable met the 0.1500 significance level for entry into the model.


NOTE: No intercept in model. R-Square is redefined.

                                   Summary of Stepwise Selection

        Variable        Variable        Number    Partial     Model
 Step   Entered         Removed         Vars In   R-Square   R-Square     C(p)      F Value
Pr > F

    1   salinity                           1       0.2450     0.2450    150.171     199.24
<.0001
    2   ktn                                2       0.0382     0.2832    113.532      32.69
<.0001
    3   temperature                        3       0.0162     0.2994    99.1541      14.15
0.0002
    4   f_entrococci                       4       0.0195     0.3189    81.4692      17.47
<.0001
    5   tp                                 5       0.0379     0.3568    45.1940      35.91
<.0001
    6   doxy                               6       0.0191     0.3759    27.8638      18.66
<.0001
    7   tss                                7       0.0232     0.3991     6.4475      23.44
<.0001
    8                   ktn                6       0.0009     0.3982     5.3531       0.91
0.3414
```

```
                    *****************************************************************
40
                           5_Oyster Restoration & Biomass Analysis
                               Factorial MMC Analysis / Sp2013
             GLM Screening - NMSS+WQ+no afdm & Depth / Composite -- ASE+LSE Site Locations
                    *****************************************************************

                                      The GLM Procedure

                           Number of Observations Read         615
                           Number of Observations Used         615


                    *****************************************************************
41
                           5_Oyster Restoration & Biomass Analysis
                               Factorial MMC Analysis / Sp2013
             GLM Screening - NMSS+WQ+no afdm & Depth / Composite -- ASE+LSE Site Locations
                    *****************************************************************

                                      The GLM Procedure

Dependent Variable: biomass

                                                   Sum of
       Source                      DF             Squares      Mean Square     F Value     Pr >
F

       Model                        8         15249680.14       1906210.02       50.48
<.0001

       Error                      607         22922836.36         37764.15

       Uncorrected Total          615         38172516.50


                        R-Square     Coeff Var      Root MSE     biomass Mean

                        0.399494      162.8803      194.3300         119.3085

NOTE: No intercept term is used: R-square is not corrected for the mean.

       Source                      DF         Type I SS      Mean Square     F Value     Pr >
F

       temperature                  1       7052706.579      7052706.579      186.76
<.0001
       salinity                     1       3365352.902      3365352.902       89.12
<.0001
       doxy                         1         22587.975        22587.975        0.60
0.4396
       tss                          1        166331.533       166331.533        4.40
0.0363
       ktn                          1        921995.951       921995.951       24.41
<.0001
       tp                           1       1706007.676      1706007.676       45.18
<.0001
       e_coli                       1         91353.260        91353.260        2.42
0.1204
       f_entrococci                 1       1923344.258      1923344.258       50.93
<.0001


       Source                      DF       Type III SS      Mean Square     F Value     Pr >
F

       temperature                  1       1551059.015      1551059.015       41.07
<.0001
       salinity                     1       2338584.972      2338584.972       61.93
<.0001
       doxy                         1       1517573.012      1517573.012       40.19
<.0001
       tss                          1        839813.470       839813.470       22.24
<.0001
       ktn                          1         32233.442        32233.442        0.85
0.3559
       tp                           1        181304.381       181304.381        4.80
0.0288
       e_coli                       1         16899.848        16899.848        0.45
0.5038
```

```
            f_entrococci                    1      1923344.258      1923344.258       50.93
<.0001

                                                          Standard
                    Parameter            Estimate            Error    t Value    Pr > |t|

                    temperature        -19.492297        3.0415061      -6.41      <.0001
                    salinity            98.983292       12.5783927       7.87      <.0001
                    doxy                74.402717       11.7369115       6.34      <.0001
                    tss                 14.313124        3.0351687       4.72      <.0001
                    ktn                 43.509458       47.0944971       0.92      0.3559
                    tp                1325.772067      605.0685034       2.19      0.0288

                      ****************************************************************
42
                                5_Oyster Restoration & Biomass Analysis
                                    Factorial MMC Analysis / Sp2013
                    GLM Screening - NMSS+WQ+no afdm & Depth / Composite -- ASE+LSE Site Locations
                      ****************************************************************

                                           The GLM Procedure

Dependent Variable: biomass

                                                          Standard
                    Parameter            Estimate            Error    t Value    Pr > |t|

                    e_coli               0.110563        0.1652760       0.67      0.5038
                    f_entrococci      -101.606266       14.2374368      -7.14      <.0001
```

Appendix III Output from Factorial Model (SAS Listing) – (Continued)

SAS List File 2_aselse_21.lst – Final Run Including Models for All Sites

```
*****************************************************************                  1
                                      7_Oyster Restoration & Biomass Analysis
                                          Factorial MMC Analysis / Sp2013
            GLM Screening - NMSS+WQ+no afdm & Depth /  ASE Site Location: Long Creek
                          *****************************************************************

                                               The GLM Procedure

                                            Class Level Information

Class           Levels  Values

season               2  Fall Spring

period               4  2005 2006 2007 2008

site                 3  Marsh Oyster_R Riprap

ccontrol             2  Caged Uncaged

substrate            6  CVS GL GS LML LMS OSU

subs_no             36  CVS1 CVS2 CVS3 CVS4 CVS5 CVS6 GL1 GL2 GL3 GL4 GL5 GL6 GS1 GS2 GS3
GS4 GS5
                        GS6 LML1 LML2 LML3 LML4 LML5 LML6 LMS1 LMS2 LMS3 LMS4 LMS5 LMS6
OSU1 OSU2
                        OSU3 OSU4 OSU5 OSU6

temperature          6  11.01 12.86 13.69 20.81 23.81 27.94

salinity             7  17.82 17.92 18.8 18.89 21.01 21.45 22.61

doxy                 5  6.5 7 7.12 7.8 12

tss                  6  7 11.053 16.093 30 31 32

ktn                  5  0.6 0.8 1.1 1.2 1.338

tp                   5  0.035 0.04 0.054 0.07 0.09

chl_a                6  2.866 7.267 7.87 8.58 15.47 15.51

e_coli               6  0 2.45 3.16 7.35 8.45 21.8
```

```
f_entrococci         1  25

                                   Number of Observations Read        540

                                   Number of Observations Used        540
                          ***************************************************************
2

                                   7_Oyster Restoration & Biomass Analysis

                                       Factorial MMC Analysis / Sp2013

                 GLM Screening - NMSS+WQ+no afdm & Depth /  ASE Site Location: Long Creek
                          ***************************************************************

                                            The GLM Procedure


Dependent Variable: biomass

                                                     Sum of
       Source                      DF              Squares      Mean Square     F Value     Pr >
F

       Model                       44          7178471.397       163147.077       38.95
<.0001

       Error                      496          2077316.508         4188.138

       Uncorrected Total          540          9255787.904


                              R-Square      Coeff Var      Root MSE     biomass Mean

                              0.645456       81.59827      64.71583         79.31029

Source                      DF       Type I SS     Mean Square     F Value     Pr >F

season                       2     3400729.737     1700364.868      406.00     <.0001

period                       3     1522092.627      507364.209      121.14     <.0001

subs_no                     35      829710.684       23706.020        5.66     <.0001

site                         2     1379125.915      689562.957      164.65     <.0001
ccontrol                     1       44541.897       44541.897       10.64     0.0012
       ccontrol                    1        44541.897        44541.897       10.64
0.0012

substrate                    0           0.000             .            .         .

ktn                          1        2270.538        2270.538        0.54     0.4619

e_coli                       0           0.000             .            .         .

temperature                  0           0.000             .            .         .

tp                           0           0.000             .            .         .

temperature*tp               0           0.000             .            .         .

chl_a                        0           0.000             .            .         .

temperature*chl_a            0           0.000             .            .         .

tp*chl_a                     0           0.000             .            .         .

temperature*tp*chl_a         0           0.000             .            .         .
```

```
Source                    DF     Type III SS     Mean Square    F Value     Pr >F

season                     0           0.000               .          .         .

period                     0           0.000               .          .         .
subs_no                   30      100530.973        3351.032       0.80    0.7676

site                       2     1379125.915      689562.957     164.65    <.0001

ccontrol                   1       44541.897       44541.897      10.64     .0012

substrate                  0           0.000               .          .         .

ktn                        0           0.000               .          .         .

e_coli                     0           0.000               .          .         .

temperature                0           0.000               .          .         .

tp                         0           0.000               .          .         .

temperature*tp             0           0.000               .          .         .

chl_a                      0           0.000               .          .         .

temperature*chl_a          0           0.000               .          .         .

tp*chl_a                   0           0.000               .          .         .
```

```
                    ****************************************************************
3
                              7_Oyster Restoration & Biomass Analysis
                                 Factorial MMC Analysis / Sp2013
                GLM Screening - NMSS+WQ+no afdm & Depth /  ASE Site Location: Long Creek
                    ****************************************************************

                                       The GLM Procedure

Dependent Variable: biomass
       Source                     DF     Type III SS     Mean Square    F Value    Pr >F

       temperature*tp*chl_a        0           0.000               .          .        .
```

```
                  ****************************************************************
4
                          7_Oyster Restoration & Biomass Analysis

                              Factorial MMC Analysis / Sp2013

            GLM Screening - NMSS+WQ+no afdm & Depth /  ASE Site Location: Long Creek

                  ****************************************************************

                                     The GLM Procedure


                          Duncan's Multiple Range Test for biomass

NOTE: This test controls the Type I comparisonwise error rate, not the experimentwise
error rate.


                          Alpha                               0.05

                          Error Degrees of Freedom             496

                          Error Mean Square               4188.138

                          Harmonic Mean of Cell Sizes        268.8

                            NOTE: Cell sizes are not equal.


                               Number of Means          2

                               Critical Range       10.97


                  Means with the same letter are not significantly different.


                 Duncan Grouping          Mean      N    season

                               A        82.243    252    Fall

                               A

                               A        76.744    288    Spring
```

```
                 ****************************************************************
5
                           7_Oyster Restoration & Biomass Analysis
                              Factorial MMC Analysis / Sp2013
            GLM Screening - NMSS+WQ+no afdm & Depth /  ASE Site Location: Long Creek
                 ****************************************************************

                                    The GLM Procedure


                           Duncan's Multiple Range Test for biomass

NOTE: This test controls the Type I comparisonwise error rate, not the experimentwise
error rate.


                           Alpha                             0.05
                           Error Degrees of Freedom           496
                           Error Mean Square             4188.138
                           Harmonic Mean of Cell Sizes   78.54545

                             NOTE: Cell sizes are not equal.


                     Number of Means          2           3           4
                     Critical Range       20.29       21.36       22.08


                  Means with the same letter are not significantly different.


                Duncan Grouping          Mean      N    period

                              A        171.27     72    2008


                              B        101.24    216    2007


                              C         38.99    216    2006


                              D          5.73     36    2005
```

```
                   *****************************************************************
6
                          7_Oyster Restoration & Biomass Analysis

                              Factorial MMC Analysis / Sp2013

              GLM Screening - NMSS+WQ+no afdm & Depth /  ASE Site Location: Long Creek

                   *****************************************************************

                                     The GLM Procedure


                          Duncan's Multiple Range Test for biomass

NOTE: This test controls the Type I comparisonwise error rate, not the experimentwise
error rate.


                               Alpha                             0.05

                               Error Degrees of Freedom           496

                               Error Mean Square             4188.138

                               Harmonic Mean of Cell Sizes 14.95549

                                NOTE: Cell sizes are not equal.

    Number of Means      2      3      4      5      6      7      8      9     10     11     12
13

    Critical Range  46.50  48.95  50.59  51.81  52.76  53.53  54.17  54.72  55.20  55.62  56.00
56.34

    Number of Means     14     15     16     17     18     19     20     21     22     23     24
25

    Critical Range  56.64  56.91  57.17  57.40  57.61  57.81  58.00  58.17  58.33  58.48  58.63
58.76

  Number of Means     26      27      28      29      30      31      32      33      34      35
36

  Critical Range  58.89   59.01   59.12   59.23   59.33   59.43   59.52   59.61   59.70   59.78
59.86


                   Means with the same letter are not significantly different.


                    Duncan Grouping                          Mean       N    subs_no

                                 A                         158.46      14    GL2
                                 A
                                 A                         157.39      14    GS1
                                 A
              B                  A                         155.24      15    GL4
              B                  A
              B                  A         C               148.92      15    GL3
```

	B			A		C				
	B	D		A		C		135.76	14	GL1
	B	D		A		C				
	B	D		A		C		135.36	15	GS3
	B	D		A		C				
E	B	D		A		C		126.19	16	GL6
E	B	D		A		C				
E	B	D		A		C	F	122.97	16	GL5
E	B	D		A		C	F			
E	B	D		A	G	C	F	121.15	15	GS4
E	B	D		A	G	C	F			
E	B	D	H	A	G	C	F	112.37	14	GS2
E	B	D	H		G	C	F			
E	B	D	H	I	G	C	F	100.52	14	OSU1
E		D	H	I	G	C	F			
E	J	D	H	I	G	C	F	94.75	14	OSU2
E	J	D	H	I	G		F			

```
                    ***************************************************************
   7
                            7_Oyster Restoration & Biomass Analysis
                               Factorial MMC Analysis / Sp2013
              GLM Screening - NMSS+WQ+no afdm & Depth /  ASE Site Location: Long Creek
                    ***************************************************************

                                      The GLM Procedure

                            Duncan's Multiple Range Test for biomass

                      Means with the same letter are not significantly different.


                         Duncan Grouping                    Mean       N    subs_no

          E       J       D   H   I   G       F             92.83     14    CVS2
          E       J       D   H   I   G       F
          E       J       D   H   I   G   K   F             89.01     14    CVS1
          E       J       D   H   I   G   K   F
          E       J   L   D   H   I   G   K   F             85.03     16    GS5
          E       J   L   D   H   I   G   K   F
          E   M   J   L   D   H   I   G   K   F             80.41     16    GS6
          E   M   J   L       H   I   G   K   F
          E   M   J   L   N   H   I   G   K   F             77.03     15    OSU3
          E   M   J   L   N   H   I   G   K   F
          E   M   J   L   N   H   I   G   K   F             72.72     15    CVS3
              M   J   L   N   H   I   G   K   F
              M   J   L   N   H   I   G   K   F             67.31     15    CVS4
              M   J   L   N   H   I   G   K
              M   J   L   N   H   I   G   K                 65.87     14    LML1
              M   J   L   N   H   I       K
              M   J   L   N   H   I       K                 64.73     15    LML3
              M   J   L   N   H   I       K
              M   J   L   N   H   I       K                 60.71     15    OSU4
              M   J   L   N       I       K
              M   J   L   N       I       K                 54.64     16    OSU5
              M   J   L   N       I       K
              M   J   L   N       I       K                 50.39     15    LMS4
              M   J   L   N       I       K
              M   J   L   N       I       K                 47.80     16    LMS6
              M   J   L   N       I       K
              M   J   L   N       I       K                 46.65     14    LML2
```

M	J	L	N	I	K			
M	J	L	N	I	K	46.46	16	OSU6
M	J	L	N	I	K			
M	J	L	N	I	K	46.39	16	CVS5
M	J	L	N	I	K			
M	J	L	N	I	K	43.11	14	LMS2
M	J	L	N		K			
M	J	L	N		K	39.22	15	LMS3
M	J	L	N		K			
M	J	L	N		K	38.99	16	LML6
M		L	N		K			
M		L	N		K	33.61	15	LML4
M		L	N		K			
M		L	N		K	33.29	16	CVS6
M		L	N					
M		L	N			27.61	16	LML5
M			N					
M			N			26.52	14	LMS1

```
                  ****************************************************************
8
                             7_Oyster Restoration & Biomass Analysis
                                 Factorial MMC Analysis / Sp2013
              GLM Screening - NMSS+WQ+no afdm & Depth /  ASE Site Location: Long Creek
                  ****************************************************************

                                        The GLM Procedure


                             Duncan's Multiple Range Test for biomass

                       Means with the same letter are not significantly different.


                     Duncan Grouping                       Mean        N     subs_no

                          N
                          N                               21.89       16     LMS5
```

```
                   ****************************************************************
9

                           7_Oyster Restoration & Biomass Analysis
                               Factorial MMC Analysis / Sp2013
             GLM Screening - NMSS+WQ+no afdm & Depth /  ASE Site Location: Long Creek
                   ****************************************************************

                                      The GLM Procedure

                           Duncan's Multiple Range Test for biomass

NOTE: This test controls the Type I comparisonwise error rate, not the experimentwise
error rate.

                              Alpha                           0.05
                              Error Degrees of Freedom         496
                              Error Mean Square           4188.138

                            Number of Means          2           3
                            Critical Range       13.40       14.11

                    Means with the same letter are not significantly different.

                 Duncan Grouping          Mean       N    site

                              A        147.618     180    Marsh

                              B         63.699     180    Riprap

                              C         26.614     180    Oyster_R
```

```
                 ****************************************************************
10

                             7_Oyster Restoration & Biomass Analysis

                                 Factorial MMC Analysis / Sp2013

            GLM Screening - NMSS+WQ+no afdm & Depth /  ASE Site Location: Long Creek

                 ****************************************************************

                                        The GLM Procedure


                             Duncan's Multiple Range Test for biomass

NOTE: This test controls the Type I comparisonwise error rate, not the experimentwise
error rate.


                                Alpha                           0.05
                                Error Degrees of Freedom         496
                                Error Mean Square           4188.138


                                    Number of Means          2
                                    Critical Range       10.94


                   Means with the same letter are not significantly different.


                 Duncan Grouping          Mean        N    ccontrol

                               A        88.363      270    Uncaged


                               B        70.258      270    Caged
```

```
                ****************************************************************
11
                          7_Oyster Restoration & Biomass Analysis

                              Factorial MMC Analysis / Sp2013

          GLM Screening - NMSS+WQ+no afdm & Depth /  ASE Site Location: Long Creek

                ****************************************************************

                                    The GLM Procedure


                          Duncan's Multiple Range Test for biomass

NOTE: This test controls the Type I comparisonwise error rate, not the experimentwise
error rate.


                           Alpha                            0.05

                           Error Degrees of Freedom          496

                           Error Mean Square            4188.138


              Number of Means          2           3           4          5          6

              Critical Range       18.95       19.96       20.62      21.12      21.51


                   Means with the same letter are not significantly different.



                 Duncan Grouping          Mean       N    substrate

                              A        140.756      90    GL


                              B        114.125      90    GS


                              C         71.305      90    OSU
                              C
                              C         65.790      90    CVS


                              D         45.732      90    LML
                              D
                              D         38.154      90    LMS
```

```
                    ******************************************************************
12
                          7_Oyster Restoration & Biomass Analysis

                              Factorial MMC Analysis / Sp2013

          GLM Screening - NMSS+WQ+no afdm & Depth /  ASE Site Location: Long Creek

                    ******************************************************************

                                     The GLM Procedure


                          Duncan's Multiple Range Test for biomass

NOTE: This test controls the Type I comparisonwise error rate, not the experimentwise
error rate.


                          Alpha                              0.05

                          Error Degrees of Freedom            496

                          Error Mean Square              4188.138

                          Harmonic Mean of Cell Sizes    102.8571

                            NOTE: Cell sizes are not equal.


                Number of Means          2          3          4          5

                Critical Range       17.73      18.67      19.29      19.75


                Means with the same letter are not significantly different.


                Duncan Grouping         Mean       N     ktn

                              A      171.268      72     1.2


                              B      128.411     108     0.8


                              C       74.066     108     0.6
                              C
                              C       61.580     108     1.338


                              D       13.736     144     1.1
```

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                *****************************************************************
13
                     7_Oyster Restoration & Biomass Analysis

                         Factorial MMC Analysis / Sp2013

    GLM Screening - NMSS+WQ+no afdm & Depth /  ASE Site Location: Long Creek

                *****************************************************************

                              The GLM Procedure


                     Duncan's Multiple Range Test for biomass

NOTE: This test controls the Type I comparisonwise error rate, not the experimentwise
error rate.


                     Alpha                                0.05

                     Error Degrees of Freedom              496

                     Error Mean Square                4188.138

                     Harmonic Mean of Cell Sizes  76.23529

                       NOTE: Cell sizes are not equal.


          Number of Means          2          3          4          5          6

          Critical Range       20.59      21.68      22.41      22.95      23.37


              Means with the same letter are not significantly different.


               Duncan Grouping          Mean       N    e_coli

                             A        171.27      72    3.16


                             B        128.41     108    2.45


                             C         74.07     108    0
                             C
                             C         61.58     108    8.45


                             D         16.41     108    7.35
                             D
                             D          5.73      36    21.8
```

```
             ****************************************************************
14
                     7_Oyster Restoration & Biomass Analysis
                       Factorial MMC Analysis / Sp2013
      GLM Screening - NMSS+WQ+no afdm & Depth /  ASE Site Location: Long Creek
             ****************************************************************

                               The GLM Procedure

                    Duncan's Multiple Range Test for biomass

NOTE: This test controls the Type I comparisonwise error rate, not the experimentwise
error rate.

                   Alpha                                0.05
                   Error Degrees of Freedom              496
                   Error Mean Square                4188.138
                   Harmonic Mean of Cell Sizes      76.23529

                     NOTE: Cell sizes are not equal.

      Number of Means          2          3          4          5          6
      Critical Range       20.59      21.68      22.41      22.95      23.37

          Means with the same letter are not significantly different.

        Duncan Grouping          Mean      N     temperature

                      A        171.27     72     12.86

                      B        128.41    108     27.94

                      C         74.07    108     13.69
                      C
                      C         61.58    108     23.81

                      D         16.41    108     20.81
                      D
                      D          5.73     36     11.01
```

```
                ****************************************************************
15
                          7_Oyster Restoration & Biomass Analysis
                              Factorial MMC Analysis / Sp2013
      GLM Screening - NMSS+WQ+no afdm & Depth /  ASE Site Location: Long Creek
                ****************************************************************

                                    The GLM Procedure

                          Duncan's Multiple Range Test for biomass

NOTE: This test controls the Type I comparisonwise error rate, not the experimentwise
error rate.

                             Alpha                            0.05
                             Error Degrees of Freedom          496
                             Error Mean Square            4188.138
                             Harmonic Mean of Cell Sizes  77.14286

                               NOTE: Cell sizes are not equal.

                 Number of Means          2          3          4          5
                 Critical Range       20.47      21.55      22.28      22.81

                 Means with the same letter are not significantly different.


                 Duncan Grouping          Mean      N    tp

                              A         171.27     72    0.09

                              B          74.07    108    0.035
                              B
                              B          72.41    216    0.07
                              B
                              B          61.58    108    0.054

                              C           5.73     36    0.04
```

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                    *****************************************************************
16
                           7_Oyster Restoration & Biomass Analysis
                               Factorial MMC Analysis / Sp2013
              GLM Screening - NMSS+WQ+no afdm & Depth /  ASE Site Location: Long Creek
                    *****************************************************************

                                     The GLM Procedure


                 Level of        Level of                 -----------biomass----------
                 temperature     tp             N              Mean          Std Dev

                 11.01           0.04          36          5.726667         7.658328
                 12.86           0.09          72        171.268486       145.420192
                 13.69           0.035        108         74.066167        84.025220
                 20.81           0.07         108         16.405796        26.952188
                 23.81           0.054        108         61.580472        74.032969
                 27.94           0.07         108        128.411120       114.694896
```

```
                *****************************************************************
17
                         7_Oyster Restoration & Biomass Analysis
                            Factorial MMC Analysis / Sp2013
           GLM Screening - NMSS+WQ+no afdm & Depth /  ASE Site Location: Long Creek
                *****************************************************************

                                  The GLM Procedure

                       Duncan's Multiple Range Test for biomass

NOTE: This test controls the Type I comparisonwise error rate, not the experimentwise
error rate.

                        Alpha                             0.05
                        Error Degrees of Freedom           496
                        Error Mean Square             4188.138
                        Harmonic Mean of Cell Sizes   76.23529

                         NOTE: Cell sizes are not equal.

       Number of Means           2          3          4          5          6
       Critical Range        20.59      21.68      22.41      22.95      23.37

            Means with the same letter are not significantly different.

            Duncan Grouping          Mean      N    chl_a

                          A        171.27     72    15.51

                          B        128.41    108    7.87

                          C         74.07    108    2.866
                          C
                          C         61.58    108    7.267

                          D         16.41    108    8.58
                          D
                          D          5.73     36    15.47
```

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                ****************************************************************
18

                         7_Oyster Restoration & Biomass Analysis

                             Factorial MMC Analysis / Sp2013

           GLM Screening - NMSS+WQ+no afdm & Depth /  ASE Site Location: Long Creek

                ****************************************************************

                                    The GLM Procedure


                 Level of        Level of                -----------biomass----------
                 temperature     chl_a            N             Mean          Std Dev

                 11.01           15.47           36         5.726667         7.658328
                 12.86           15.51           72       171.268486       145.420192
                 13.69           2.866          108        74.066167        84.025220
                 20.81           8.58           108        16.405796        26.952188
                 23.81           7.267          108        61.580472        74.032969
                 27.94           7.87           108       128.411120       114.694896


                  Level of      Level of                -----------biomass-----------
                  tp            chl_a            N             Mean          Std Dev

                  0.035         2.866          108        74.066167        84.025220
                  0.04          15.47           36         5.726667         7.658328
                  0.054         7.267          108        61.580472        74.032969
                  0.07          7.87           108       128.411120       114.694896
                  0.07          8.58           108        16.405796        26.952188
                  0.09          15.51           72       171.268486       145.420192


         Level of        Level of      Level of                -----------biomass-----------
         temperature     tp            chl_a            N             Mean          Std Dev

         11.01           0.04          15.47           36         5.726667         7.658328
         12.86           0.09          15.51           72       171.268486       145.420192
         13.69           0.035         2.866          108        74.066167        84.025220
         20.81           0.07          8.58           108        16.405796        26.952188
         23.81           0.054         7.267          108        61.580472        74.032969
         27.94           0.07          7.87           108       128.411120       114.694896
```

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                  *****************************************************************
19

                            6_Oyster Restoration & Biomass Analysis

                               Factorial MMC Analysis / Sp2013

GLM Screening - NMSS+WQ+no afdm & Depth / LSE Site Locations: Linkhorn Bay - Chalmers,
Eastern Bra

                  *****************************************************************

                                     The GLM Procedure

                                  Class Level Information


Class          Levels  Values

season              2  Fall Summer

period              2  2007 2008

site                2  EB LB

ccontrol            2  Seeded Unseeded

substrate           4  CB CM OS RR

subs_no            39  CS.CB1 CS.CB2 CS.CB3 CS.CM1 CS.CM2 CS.CM3 CS.OR1 CS.OR2 CS.RR1
CS.RR2

                       CS.RR3 CU.CB1 CU.CB2 CU.CB3 CU.CM1 CU.CM2 CU.CM3 CU.OR1 CU.OR2
                       CU.OR3

                       CU.RR1 CU.RR2 CU.RR3 HS.CM1 HS.CM2 HS.CM3 HS.OR1 HS.OR2 HS.RR1
HS.RR3

                       HU.CM1 HU.CM2 HU.CM3 HU.OR1 HU.OR2 HU.OR3 HU.RR1 HU.RR2 HU.RR3

temperature         6  7.9 11.7 15.9 16 25.7 26.5

salinity            4  19.1 20.7 22.4 24.8

doxy                6  5.5 7 8.3 9.2 9.6 11.4

tss                 5  4 6 13 18 40

ktn                 5  0.5 0.8 0.9 1 1.4

tp                  5  0.05 0.06 0.07 0.09 0.14

e_coli              6  0 2.45 2.83 7.42 40.91 407.93


                           Number of Observations Read          75
                           Number of Observations Used          75
```

```
                 ****************************************************************
20
                          6_Oyster Restoration & Biomass Analysis

                              Factorial MMC Analysis / Sp2013

GLM Screening - NMSS+WQ+no afdm & Depth / LSE Site Locations: Linkhorn Bay - Chalmers,
Eastern Bra

                 ****************************************************************

                                     The GLM Procedure


Dependent Variable: biomass

Sum of
       Source                      DF        Squares     Mean Square    F Value    Pr >F

       Model                       43    28703722.51       667528.43     100.28   <.0001

       Error                       32      213006.08         6656.44

       Uncorrected Total           75    28916728.59


                      R-Square     Coeff Var      Root MSE     biomass Mean

                      0.987071      20.03141      81.58701         407.2953

       Source                      DF      Type I SS     Mean Square    F Value    Pr >F

       season                       2    14401165.28      7200582.64    1081.75   <.0001
       period                       1     1541108.15      1541108.15     231.52   <.0001
       site                         1      377385.13       377385.13      56.69    .0001
       ccontrol                     1     1975525.92      1975525.92     296.78    .0001
       substrate                    3     3912853.80      1304284.60     195.94    .0001
       subs_no                     33     6056129.19       183519.07      27.57    .0001
       e_coli                       2      439555.04       219777.52      33.02    .0001
       doxy                         0           0.00               .          .        .
       doxy*e_coli                  0           0.00               .          .        .
       tp                           0           0.00               .          .        .
       tp*e_coli                    0           0.00               .          .        .
       doxy*tp                      0           0.00               .          .        .
       doxy*tp*e_coli               0           0.00               .          .        .

       Source                      DF    Type III SS     Mean Square    F Value    Pr >F

       season                       0          0.000               .          .        .
       period                       0          0.000               .          .        .
       site                         0          0.000               .          .        .
       ccontrol                     0          0.000               .          .        .
       substrate                    0          0.000               .          .        .
```

```
subs_no              33    5542256.882    167947.178     25.23   <.0001
e_coli                0          0.000             .         .        .
doxy                  0          0.000             .         .        .
doxy*e_coli           0          0.000             .         .        .
tp                    0          0.000             .         .        .
tp*e_coli             0          0.000             .         .        .
doxy*tp               0          0.000             .         .        .
doxy*tp*e_coli        0          0.000             .         .        .
```

```
                 ******************************************************************
21
                        6_Oyster Restoration & Biomass Analysis

                            Factorial MMC Analysis / Sp2013

GLM Screening - NMSS+WQ+no afdm & Depth / LSE Site Locations: Linkhorn Bay - Chalmers,
Eastern Bra
                 ******************************************************************

                                  The GLM Procedure


                       Duncan's Multiple Range Test for biomass

NOTE: This test controls the Type I comparisonwise error rate, not the experimentwise
error rate.

                         Alpha                              0.05

                         Error Degrees of Freedom             32

                         Error Mean Square               6656.44

                         Harmonic Mean of Cell Sizes       27.36

                           NOTE: Cell sizes are not equal.


                              Number of Means           2

                              Critical Range        44.93


                  Means with the same letter are not significantly different.


                  Duncan Grouping           Mean      N    season

                                A         498.13     57    Fall


                                B         119.66     18    Summer
```

```
                  ****************************************************************
22
                            6_Oyster Restoration & Biomass Analysis
                               Factorial MMC Analysis / Sp2013
GLM Screening - NMSS+WQ+no afdm & Depth / LSE Site Locations: Linkhorn Bay - Chalmers,
Eastern Bra
                  ****************************************************************

                                     The GLM Procedure


                            Duncan's Multiple Range Test for biomass

NOTE: This test controls the Type I comparisonwise error rate, not the experimentwise
error rate.


                             Alpha                            0.05
                             Error Degrees of Freedom           32
                             Error Mean Square             6656.44
                             Harmonic Mean of Cell Sizes     37.44

                               NOTE: Cell sizes are not equal.


                                  Number of Means          2
                                  Critical Range       38.41


                    Means with the same letter are not significantly different.


                   Duncan Grouping          Mean      N    period

                                A         609.83     39    2008


                                B         187.88     36    2007
```

```
                  ****************************************************************
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                           6_Oyster Restoration & Biomass Analysis

                               Factorial MMC Analysis / Sp2013

GLM Screening - NMSS+WQ+no afdm & Depth / LSE Site Locations: Linkhorn Bay - Chalmers,
Eastern Bra

                  ****************************************************************

                                      The GLM Procedure


                           Duncan's Multiple Range Test for biomass

NOTE: This test controls the Type I comparisonwise error rate, not the experimentwise
error rate.


                             Alpha                                0.05

                             Error Degrees of Freedom               32

                             Error Mean Square                 6656.44

                             Harmonic Mean of Cell Sizes  37.17333

                               NOTE: Cell sizes are not equal.


                                  Number of Means          2

                                  Critical Range       38.55


                    Means with the same letter are not significantly different.


                    Duncan Grouping          Mean       N     site

                                  A        488.92      41     LB


                                  B        308.87      34     EB
```

```
                ****************************************************************
24
                     6_Oyster Restoration & Biomass Analysis
                         Factorial MMC Analysis / Sp2013
GLM Screening - NMSS+WQ+no afdm & Depth / LSE Site Locations: Linkhorn Bay - Chalmers,
Eastern Bra
                ****************************************************************

                                The GLM Procedure

                     Duncan's Multiple Range Test for biomass

NOTE: This test controls the Type I comparisonwise error rate, not the experimentwise
error rate.

                       Alpha                            0.05
                       Error Degrees of Freedom           32
                       Error Mean Square             6656.44
                       Harmonic Mean of Cell Sizes     27.36

                         NOTE: Cell sizes are not equal.

                            Number of Means          2
                            Critical Range       44.93

             Means with the same letter are not significantly different.

            Duncan Grouping          Mean       N    ccontrol

                          A        855.89      18    Seeded

                          B        265.63      57    Unseeded
```

```
                 *****************************************************************
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                          6_Oyster Restoration & Biomass Analysis

                              Factorial MMC Analysis / Sp2013

GLM Screening - NMSS+WQ+no afdm & Depth / LSE Site Locations: Linkhorn Bay - Chalmers,
Eastern Bra

                 *****************************************************************

                                     The GLM Procedure


                          Duncan's Multiple Range Test for biomass

NOTE: This test controls the Type I comparisonwise error rate, not the experimentwise
error rate.


                            Alpha                          0.05

                            Error Degrees of Freedom         32

                            Error Mean Square           6656.44

                            Harmonic Mean of Cell Sizes 13.45596

                              NOTE: Cell sizes are not equal.


                        Number of Means          2          3          4

                        Critical Range       64.07      67.34      69.47


                    Means with the same letter are not significantly different.


                Duncan Grouping          Mean      N    substrate

                              A        853.88      6    CB


                              B        680.31     22    OS


                              C        261.88     23    RR


                              D        184.74     24    CM
```

```
                   *****************************************************************
26

                          6_Oyster Restoration & Biomass Analysis

                              Factorial MMC Analysis / Sp2013

GLM Screening - NMSS+WQ+no afdm & Depth / LSE Site Locations: Linkhorn Bay - Chalmers,
Eastern Bra
                   *****************************************************************

                                      The GLM Procedure


                          Duncan's Multiple Range Test for biomass

NOTE: This test controls the Type I comparisonwise error rate, not the experimentwise
error rate.


                            Alpha                              0.05

                            Error Degrees of Freedom             32

                            Error Mean Square               6656.44

                            Harmonic Mean of Cell Sizes 1.444444

                              NOTE: Cell sizes are not equal.

Number of Means      2     3     4     5     6     7     8     9    10    11    12    13
14

  Critical Range  195.6 205.5 212.0 216.7 220.2 222.9 225.2 227.0 228.5 229.8 230.9 231.8
232.6

Number of Means     15    16    17    18    19    20    21    22    23    24    25    26
27

  Critical Range  233.3 233.9 234.4 234.8 235.2 235.5 235.8 236.1 236.3 236.4 236.6 236.7
236.8

     Number of Means     28    29    30    31    32    33    34    35    36    37    38
39

     Critical Range  236.8 236.9 236.9 236.9 236.9 236.9 236.9 236.8 236.8 236.7 236.6
236.6


                  Means with the same letter are not significantly different.


                       Duncan Grouping                Mean      N    subs_no

                                  A                2542.10      1    CS.OR2


                                  B                2263.89      1    HS.OR2


                                  C                1376.90      1    CS.OR1
                                  C
                       D          C                1311.10      1    CS.RR3
```

D	C				
D	C	E	1247.34	1	CS.CB3
D		E			
D		E	1133.18	1	CS.CB2
		E			
		E	1072.47	1	CS.CB1
	F		848.41	1	HS.OR1
	F				
	F		821.58	1	CS.CM2
	F				
G	F		708.31	1	CS.RR1
G	F				
G	F	H	642.19	3	HU.OR1
G		H			
G	I	H	599.70	1	CU.CB2
G	I	H			

```
                 ****************************************************************
27
                             6_Oyster Restoration & Biomass Analysis

                                 Factorial MMC Analysis / Sp2013

GLM Screening - NMSS+WQ+no afdm & Depth / LSE Site Locations: Linkhorn Bay - Chalmers,
Eastern Bra

                 ****************************************************************

                                        The GLM Procedure


                             Duncan's Multiple Range Test for biomass

                   Means with the same letter are not significantly different.


                         Duncan Grouping                  Mean      N    subs_no

                      G         I         H             583.80      1    CS.CM1
                      G         I         H
                      G         I         H             574.47      1    CS.RR2
                      G         I         H
                      G         I         H             558.30      1    CU.CB3
                      G         I         H
                      G    J    I         H             540.70      3    HU.OR2
                      G    J    I         H
                 K    G    J    I         H             512.30      1    CU.CB1
                 K         J    I         H
                 K    L    J    I         H             435.34      3    HU.OR3
                 K    L    J    I
                 K    L    J    I         M             383.70      3    CU.OR1
                 K    L    J    I         M
                 K    L    J    I         M             380.78      1    HS.RR3
                 K    L    J              M
                 K    L    J    N         M             328.44      3    CU.OR3
                 K    L         N         M
                 K    L    O    N         M             314.80      3    CU.OR2
                 K    L    O    N         M
                 K    L    O    N         M    P        297.58      1    HS.RR1
                      L    O    N         M    P
                 Q    L    O    N         M    P        256.45      3    CU.RR2
                 Q    L    O    N         M    P
                 Q    L    O    N    R    M    P        230.53      3    CU.CM3
                 Q    L    O    N    R    M    P
                 Q    L    O    N    R    M    P        214.07      3    CU.CM1
```

Q	O	N	R	M	P			
Q	O	N	R	M	P	203.83	3	CU.RR1
Q	O	N	R	M	P			
Q	O	N	R	M	P	179.53	3	CU.CM2
Q	O	N	R	M	P			
Q	O	N	R	M	P	173.72	1	CS.CM3
Q	O	N	R	M	P			
Q	O	N	R	M	P	165.46	3	CU.RR3
Q	O	N	R		P			
Q	O	N	R		P	125.97	3	HU.CM3
Q	O	N	R		P			
Q	O	N	R		P	124.03	3	HU.RR1
Q	O	N	R		P			
Q	O	N	R		P	104.13	3	HU.CM1
Q	O		R		P			
Q	O		R		P	89.58	3	HU.RR2
Q			R		P			
Q			R		P	77.67	3	HU.RR3

```
                   ****************************************************************
28
                             6_Oyster Restoration & Biomass Analysis

                                 Factorial MMC Analysis / Sp2013

GLM Screening - NMSS+WQ+no afdm & Depth / LSE Site Locations: Linkhorn Bay - Chalmers,
Eastern Bra
                   ****************************************************************

                                        The GLM Procedure


                             Duncan's Multiple Range Test for biomass

                        Means with the same letter are not significantly different.


                        Duncan Grouping                Mean       N    subs_no

                   Q                   R          P
                   Q                   R          P       73.87       3    HU.CM2
                   Q                   R
                   Q                   R                  29.94       1    HS.CM1
                   Q                   R
                   Q                   R                  27.93       1    HS.CM3
                                       R
                                       R                  12.51       1    HS.CM2
```

```
                 ****************************************************************
29
                         6_Oyster Restoration & Biomass Analysis

                             Factorial MMC Analysis / Sp2013

GLM Screening - NMSS+WQ+no afdm & Depth / LSE Site Locations: Linkhorn Bay - Chalmers,
Eastern Bra

                 ****************************************************************

                                    The GLM Procedure


                         Duncan's Multiple Range Test for biomass

NOTE: This test controls the Type I comparisonwise error rate, not the experimentwise
error rate.


                          Alpha                              0.05

                          Error Degrees of Freedom             32

                          Error Mean Square               6656.44

                          Harmonic Mean of Cell Sizes 10.90071

                            NOTE: Cell sizes are not equal.


              Number of Means          2          3          4          5          6

              Critical Range       71.18      74.82      77.18      78.87      80.15


                 Means with the same letter are not significantly different.


                   Duncan Grouping          Mean      N     e_coli

                                 A        766.57     23     2.45


                                 B        384.53     16     40.91


                                 C        261.06      9     7.42
                                 C
                                 C        251.13      9     2.83
                                 C
                                 C        222.16      9     407.93


                                 D         17.17      9     0
```

```
                    *****************************************************************
30
                              6_Oyster Restoration & Biomass Analysis

                                  Factorial MMC Analysis / Sp2013

GLM Screening - NMSS+WQ+no afdm & Depth / LSE Site Locations: Linkhorn Bay - Chalmers,
Eastern Bra
                    *****************************************************************


                                        The GLM Procedure


                              Duncan's Multiple Range Test for biomass

NOTE: This test controls the Type I comparisonwise error rate, not the experimentwise
error rate.


                               Alpha                                0.05

                               Error Degrees of Freedom               32

                               Error Mean Square                 6656.44

                               Harmonic Mean of Cell Sizes 10.90071

                                 NOTE: Cell sizes are not equal.


                Number of Means          2          3          4          5          6

                Critical Range       71.18      74.82      77.18      78.87      80.15


                      Means with the same letter are not significantly different.


                      Duncan Grouping            Mean        N     doxy

                                    A          766.57       23     9.6


                                    B          384.53       16     8.3


                                    C          261.06        9     9.2
                                    C
                                    C          251.13        9     11.4
                                    C
                                    C          222.16        9     5.5


                                    D           17.17        9     7
```

```
                 ****************************************************************
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                          6_Oyster Restoration & Biomass Analysis

                              Factorial MMC Analysis / Sp2013

GLM Screening - NMSS+WQ+no afdm & Depth / LSE Site Locations: Linkhorn Bay - Chalmers,
Eastern Bra

                 ****************************************************************

                                     The GLM Procedure


                 Level of     Level of                ------------biomass-----------

                 doxy         e_coli         N               Mean           Std Dev

                 5.5          407.93         9         222.157778        246.553953
                 7            0              9          17.167778          9.268724
                 8.3          40.91         16         384.533750        562.250787
                 9.2          7.42           9         261.055556        215.011239
                 9.6          2.45          23         766.565217        509.126713
                 11.4         2.83           9         251.131111        115.336988
```

```
                    ****************************************************************
32
                           6_Oyster Restoration & Biomass Analysis

                               Factorial MMC Analysis / Sp2013

GLM Screening - NMSS+WQ+no afdm & Depth / LSE Site Locations: Linkhorn Bay - Chalmers,
Eastern Bra
                    ****************************************************************


                                     The GLM Procedure


                          Duncan's Multiple Range Test for biomass

NOTE: This test controls the Type I comparisonwise error rate, not the experimentwise
error rate.


                               Alpha                            0.05

                               Error Degrees of Freedom           32

                               Error Mean Square             6656.44

                               Harmonic Mean of Cell Sizes  11.70732

                                 NOTE: Cell sizes are not equal.


                   Number of Means          2          3          4          5

                   Critical Range       68.69      72.19      74.47      76.10


                    Means with the same letter are not significantly different.


                    Duncan Grouping           Mean      N    tp

                                  A         621.60     32    0.05


                                  B         384.53     16    0.06


                                  C         261.06      9    0.14
                                  C
                                  C         222.16      9    0.09


                                  D          17.17      9    0.07
```

```
                  ******************************************************************
33
                            6_Oyster Restoration & Biomass Analysis

                                Factorial MMC Analysis / Sp2013

GLM Screening - NMSS+WQ+no afdm & Depth / LSE Site Locations: Linkhorn Bay - Chalmers,
Eastern Bra

                  ******************************************************************

                                     The GLM Procedure


                   Level of      Level of            -----------biomass-----------

                   tp            e_coli        N            Mean         Std Dev

                   0.05          2.45         23      766.565217      509.126713

                   0.05          2.83          9      251.131111      115.336988

                   0.06          40.91        16      384.533750      562.250787

                   0.07          0             9       17.167778        9.268724

                   0.09          407.93        9      222.157778      246.553953

                   0.14          7.42          9      261.055556      215.011239


                   Level of      Level of            -----------biomass-----------

                   doxy          tp            N            Mean         Std Dev

                   5.5           0.09          9      222.157778      246.553953

                   7             0.07          9       17.167778        9.268724

                   8.3           0.06         16      384.533750      562.250787

                   9.2           0.14          9      261.055556      215.011239

                   9.6           0.05         23      766.565217      509.126713

                   11.4          0.05          9      251.131111      115.336988


           Level of      Level of      Level of            -----------biomass-----------

           doxy          tp            e_coli        N            Mean         Std Dev

           5.5           0.09          407.93        9      222.157778      246.553953

           7             0.07          0             9       17.167778        9.268724

           8.3           0.06          40.91        16      384.533750      562.250787

           9.2           0.14          7.42          9      261.055556      215.011239

           9.6           0.05          2.45         23      766.565217      509.126713

           11.4          0.05          2.83          9      251.131111      115.336988
```

```
                 ****************************************************************
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                         6_Oyster Restoration & Biomass Analysis
                            Factorial MMC Analysis / Sp2013
          GLM Screening - NMSS+WQ+no afdm & Depth / Composite -- ASE+LSE Site Locations
                 ****************************************************************

                                    The GLM Procedure

                                 Class Level Information

Class             Levels  Values

season                 3  Fall Spring Summer

period                 4  2005 2006 2007 2008

site                   5  EB LB Marsh Oyster_R Riprap

ccontrol               4  Caged Seeded Uncaged Unseeded

substrate             10  CB CM CVS GL GS LML LMS OS OSU RR

subs_no               75  CS.CB1 CS.CB2 CS.CB3 CS.CM1 CS.CM2 CS.CM3 CS.OR1 CS.OR2 CS.RR1
CS.RR2
                          CS.RR3 CU.CB1 CU.CB2 CU.CB3 CU.CM1 CU.CM2 CU.CM3 CU.OR1 CU.OR2
CU.OR3
                          CU.RR1 CU.RR2 CU.RR3 CVS1 CVS2 CVS3 CVS4 CVS5 CVS6 GL1 GL2 GL3
GL4 GL5 GL6
                          GS1 GS2 GS3 GS4 GS5 GS6 HS.CM1 HS.CM2 HS.CM3 HS.OR1 HS.OR2 HS.RR1
HS.RR3
                          HU.CM1 HU.CM2 HU.CM3 HU.OR1 HU.OR2 HU.OR3 HU.RR1 HU.RR2 HU.RR3
LML1 LML2
                          LML3 LML4 LML5 LML6 LMS1 LMS2 LMS3 LMS4 LMS5 LMS6 OSU1 OSU2 OSU3
OSU4 OSU5
                          OSU6

temperature           12  7.9 11.01 11.7 12.86 13.69 15.9 16 20.81 23.81 25.7 26.5 27.94

salinity              11  17.82 17.92 18.8 18.89 19.1 20.7 21.01 21.45 22.4 22.61 24.8

doxy                  10  5.5 6.5 7 7.12 7.8 8.3 9.2 9.6 11.4 12

tss                   11  4 6 7 11.053 13 16.093 18 30 31 32 40

ktn                    9  0.5 0.6 0.8 0.9 1 1.1 1.2 1.338 1.4

tp                     8  0.035 0.04 0.05 0.054 0.06 0.07 0.09 0.14

e_coli                10  0 2.45 2.83 3.16 7.35 7.42 8.45 21.8 40.91 407.93

f_entrococci           1  25
```

```
Number of Observations Read        615
Number of Observations Used        615
```

```
                *****************************************************************
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                         6_Oyster Restoration & Biomass Analysis

                             Factorial MMC Analysis / Sp2013

        GLM Screening - NMSS+WQ+no afdm & Depth / Composite -- ASE+LSE Site Locations

                *****************************************************************

                                   The GLM Procedure

Dependent Variable: biomass

                                             Sum of
Source                       DF            Squares     Mean Square    F Value    Pr > F

Model                        13        22434054.37      1725696.49      66.01    <.0001

Error                       602        15738462.13        26143.62

Uncorrected Total           615        38172516.50


                       R-Square     Coeff Var      Root MSE    biomass Mean

                       0.465011      135.5226      161.6899        119.3085


      Source                     DF       Type I SS     Mean Square    F Value    Pr >F

      temperature                12     22434054.37      1869504.53      71.51    <.0001
      salinity                    1            0.00            0.00       0.00    0.9999
      tss                         0            0.00               .          .         .
      e_coli                      0            0.00               .          .         .
      tss*e_coli                  0            0.00               .          .         .
      doxy                        0            0.00               .          .         .
      doxy*tss                    0            0.00               .          .         .
      doxy*e_coli                 0            0.00               .          .         .
      doxy*tss*e_coli             0            0.00               .          .         .
      tp                          0            0.00               .          .         .
      tss*tp                      0            0.00               .          .         .
      tp*e_coli                   0            0.00               .          .         .
      tss*tp*e_coli               0            0.00               .          .         .
      doxy*tp                     0            0.00               .          .         .
      doxy*tss*tp                 0            0.00               .          .         .
      doxy*tp*e_coli              0            0.00               .          .         .
      doxy*tss*tp*e_coli          0            0.00               .          .         .

      Source                     DF     Type III SS     Mean Square    F Value    Pr >F

      temperature                 0      0.00000000               .          .         .
      salinity                    1      0.00024544      0.00024544       0.00    0.9999

      tss                         0      0.00000000               .          .         .
```

```
e_coli                  0      0.00000000        .          .       .
tss*e_coli              0      0.00000000        .          .       .
doxy                    0      0.00000000        .          .       .
doxy*tss                0      0.00000000        .          .       .
doxy*e_coli             0      0.00000000        .          .       .
doxy*tss*e_coli         0      0.00000000        .          .       .
tp                      0      0.00000000        .          .       .
tss*tp                  0      0.00000000        .          .       .
tp*e_coli               0      0.00000000        .          .       .
```

```
                  ****************************************************************
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                           6_Oyster Restoration & Biomass Analysis

                               Factorial MMC Analysis / Sp2013

          GLM Screening - NMSS+WQ+no afdm & Depth / Composite -- ASE+LSE Site Locations

                  ****************************************************************

                                     The GLM Procedure

Dependent Variable: biomass

       Source                       DF     Type III SS     Mean Square    F Value    Pr >F

       tss*tp*e_coli                 0      0.00000000           .            .         .
       doxy*tp                       0      0.00000000           .            .         .
       doxy*tss*tp                   0      0.00000000           .            .         .
       doxy*tp*e_coli                0      0.00000000           .            .         .
       doxy*tss*tp*e_coli            0      0.00000000           .            .         .
```

```
                 ****************************************************************
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                        6_Oyster Restoration & Biomass Analysis

                            Factorial MMC Analysis / Sp2013

          GLM Screening - NMSS+WQ+no afdm & Depth / Composite -- ASE+LSE Site Locations

                 ****************************************************************

                                   The GLM Procedure


                        Duncan's Multiple Range Test for biomass

NOTE: This test controls the Type I comparisonwise error rate, not the experimentwise
rror rate.


                              Alpha                              0.05

                              Error Degrees of Freedom            602

                              Error Mean Square              26143.62

                              Harmonic Mean of Cell Sizes 19.07407

                                NOTE: Cell sizes are not equal.

Number of Means        2       3       4       5       6       7       8       9      10      11
12

   Critical Range   102.8   108.3   111.9   114.6   116.7   118.4   119.8   121.0   122.1   123.0
123.9


                   Means with the same letter are not significantly different.


                      Duncan Grouping          Mean       N    temperature

                              A              766.57      23    16


                              B              384.53      16    15.9


                              C              261.06       9    11.7
                              C
                              C              251.13       9    7.9
                              C
                         D    C              222.16       9    26.5
                         D    C
                         D    C    E         171.27      72    12.86
                         D         E
                         D    F    E         128.41     108    27.94
                              F    E
```

G	F	E	74.07	108	13.69
G	F	E			
G	F	E	61.58	108	23.81
G	F				
G	F		17.17	9	25.7
G	F				
G	F		16.41	108	20.81
G					
G			5.73	36	11.01

```
                ****************************************************************
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                       6_Oyster Restoration & Biomass Analysis

                          Factorial MMC Analysis / Sp2013

      GLM Screening - NMSS+WQ+no afdm & Depth / Composite -- ASE+LSE Site Locations

                ****************************************************************

                               The GLM Procedure


                       Duncan's Multiple Range Test for biomass

NOTE: This test controls the Type I comparisonwise error rate, not the experimentwise
rror rate.

                       Alpha                              0.05

                       Error Degrees of Freedom            602

                       Error Mean Square              26143.62

                       Harmonic Mean of Cell Sizes 26.03836

                        NOTE: Cell sizes are not equal.

 Number of Means       2       3       4       5       6       7       8       9      10
11

 Critical Range     88.0    92.7    95.8    98.1    99.9   101.3   102.5   103.6   104.5
105.3


                 Means with the same letter are not significantly different.


                 Duncan Grouping          Mean        N    salinity

                               A        624.39       32    22.4


                               B        384.53       16    24.8


                               C        251.13        9    19.1
                               C
                          D    C        171.27       72    18.89
                          D
                          D    E        128.41      108    21.45
                          D    E
                          D    E        119.66       18    20.7
                               E
                          F    E         74.07      108    21.01
                          F    E
```

F	E	61.58	108	22.61
F				
F		16.41	108	18.8
F				
F		5.73	18	17.92
F				
F		5.72	18	17.82

```
                   *****************************************************************
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                           6_Oyster Restoration & Biomass Analysis
                               Factorial MMC Analysis / Sp2013
          GLM Screening - NMSS+WQ+no afdm & Depth / Composite -- ASE+LSE Site Locations
                   *****************************************************************

                                     The GLM Procedure


                           Duncan's Multiple Range Test for biomass

NOTE: This test controls the Type I comparisonwise error rate, not the experimentwise
rror rate.


                               Alpha                                0.05
                               Error Degrees of Freedom              602
                               Error Mean Square                26143.62
                               Harmonic Mean of Cell Sizes      21.74828

                                 NOTE: Cell sizes are not equal.

 Number of Means        2       3       4       5       6       7       8       9      10
11

 Critical Range      96.3   101.4   104.8   107.3   109.3   110.9   112.2   113.4   114.3
115.2


                    Means with the same letter are not significantly different.


                      Duncan Grouping            Mean       N     tss

                                 A             624.39      32     6


                                 B             384.53      16     13


                                 C             251.13       9     4
                                 C
                            D    C             222.16       9     40
                            D    C
                            D    C    E        171.27      72     30
                            D         E
                            D    F    E        128.41     108     32
                                 F    E
                            G    F    E         74.07     108     16.093
                            G    F
```

G	F	61.58	108	11.053
G				
G		17.17	9	18
G				
G		16.41	108	31
G				
G		5.73	36	7

```
                *****************************************************************
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                          6_Oyster Restoration & Biomass Analysis

                             Factorial MMC Analysis / Sp2013

        GLM Screening - NMSS+WQ+no afdm & Depth / Composite -- ASE+LSE Site Locations

                *****************************************************************

                                   The GLM Procedure


                         Duncan's Multiple Range Test for biomass

NOTE: This test controls the Type I comparisonwise error rate, not the experimentwise
rror rate.


                          Alpha                             0.05

                          Error Degrees of Freedom           602

                          Error Mean Square             26143.62

                          Harmonic Mean of Cell Sizes 21.17751

                            NOTE: Cell sizes are not equal.


 Number of Means          2         3         4         5         6         7         8         9
10

 Critical Range        97.6     102.7     106.2     108.7     110.7     112.3     113.7     114.9
115.9


                    Means with the same letter are not significantly different.


                    Duncan Grouping          Mean       N    e_coli

                                  A        384.53      16    40.91

                                  B        261.06       9    7.42
                                  B
                                  B        251.13       9    2.83
                                  B
                                  B        240.45     131    2.45
                                  B
                                  B        222.16       9    407.93
                                  B
                                  B        171.27      72    3.16


                                  C         69.69     117    0
                                  C
```

C	61.58	108	8.45
C			
C	16.41	108	7.35
C			
C	5.73	36	21.8

```
                     ****************************************************************
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                              6_Oyster Restoration & Biomass Analysis

                                 Factorial MMC Analysis / Sp2013

               GLM Screening - NMSS+WQ+no afdm & Depth / Composite -- ASE+LSE Site Locations

                     ****************************************************************

                                       The GLM Procedure


                     Level of     Level of                ------------biomass-----------

                     tss          e_coli          N               Mean          Std Dev

                     4            2.83            9         251.131111       115.336988

                     6            2.45           23         766.565217       509.126713

                     6            7.42            9         261.055556       215.011239

                     7            21.8           36           5.726667         7.658328

                     11.053       8.45          108          61.580472        74.032969

                     13           40.91          16         384.533750       562.250787

                     16.093       0             108          74.066167        84.025220

                     18           0               9          17.167778         9.268724

                     30           3.16           72         171.268486       145.420192

                     31           7.35          108          16.405796        26.952188

                     32           2.45          108         128.411120       114.694896

                     40           407.93          9         222.157778       246.553953
```

```
                 ***************************************************************
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                          6_Oyster Restoration & Biomass Analysis

                             Factorial MMC Analysis / Sp2013

         GLM Screening - NMSS+WQ+no afdm & Depth / Composite -- ASE+LSE Site Locations
                 ***************************************************************


                                   The GLM Procedure


                          Duncan's Multiple Range Test for biomass

NOTE: This test controls the Type I comparisonwise error rate, not the experimentwise
rror rate.


                           Alpha                           0.05

                           Error Degrees of Freedom         602

                           Error Mean Square           26143.62

                           Harmonic Mean of Cell Sizes 20.01159

                             NOTE: Cell sizes are not equal.


 Number of Means        2         3         4         5         6         7         8         9
10

 Critical Range     100.4     105.7     109.2     111.9     113.9     115.6     117.0     118.2
119.2


                  Means with the same letter are not significantly different.


                     Duncan Grouping          Mean      N     doxy

                                   A        766.57     23     9.6


                                   B        384.53     16     8.3


                                   C        261.06      9     9.2
                                   C
                                   C        251.13      9     11.4
                                   C
                                   C        222.16      9     5.5


                                   D        119.85    117     7
                                   D
                              E    D         78.35    180     6.5
                              E    D
```

E	D	74.07	108	7.12
E	D			
E	D	61.58	108	7.8
E				
E		5.73	36	12

```
                  ****************************************************************
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                           6_Oyster Restoration & Biomass Analysis

                              Factorial MMC Analysis / Sp2013

        GLM Screening - NMSS+WQ+no afdm & Depth / Composite -- ASE+LSE Site Locations

                  ****************************************************************

                                     The GLM Procedure


                  Level of     Level of                 -----------biomass-----------

                  doxy         tss            N              Mean          Std Dev

                  5.5          40             9        222.157778       246.553953

                  6.5          30            72        171.268486       145.420192

                  6.5          31           108         16.405796        26.952188

                  7            18             9         17.167778         9.268724

                  7            32           108        128.411120       114.694896

                  7.12         16.093       108         74.066167        84.025220

                  7.8          11.053       108         61.580472        74.032969

                  8.3          13            16        384.533750       562.250787

                  9.2          6              9        261.055556       215.011239

                  9.6          6             23        766.565217       509.126713

                  11.4         4              9        251.131111       115.336988

                  12           7             36          5.726667         7.658328


                  Level of     Level of                 -----------biomass-----------

                  doxy         e_coli         N              Mean          Std Dev

                  5.5          407.93         9        222.157778       246.553953

                  6.5          3.16          72        171.268486       145.420192

                  6.5          7.35         108         16.405796        26.952188

                  7            0              9         17.167778         9.268724

                  7            2.45         108        128.411120       114.694896

                  7.12         0            108         74.066167        84.025220

                  7.8          8.45         108         61.580472        74.032969

                  8.3          40.91         16        384.533750       562.250787

                  9.2          7.42           9        261.055556       215.011239

                  9.6          2.45          23        766.565217       509.126713

                  11.4         2.83           9        251.131111       115.336988

                  12           21.8          36          5.726667         7.658328


            Level of     Level of     Level of               -----------biomass-----------
```

doxy	tss	e_coli	N	Mean	Std Dev
5.5	40	407.93	9	222.157778	246.553953
6.5	30	3.16	72	171.268486	145.420192
6.5	31	7.35	108	16.405796	26.952188
7	18	0	9	17.167778	9.268724
7	32	2.45	108	128.411120	114.694896
7.12	16.093	0	108	74.066167	84.025220
7.8	11.053	8.45	108	61.580472	74.032969
8.3	13	40.91	16	384.533750	562.250787
9.2	6	7.42	9	261.055556	215.011239
9.6	6	2.45	23	766.565217	509.126713
11.4	4	2.83	9	251.131111	115.336988
12	7	21.8	36	5.726667	7.658328

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                              6_Oyster Restoration & Biomass Analysis

                                 Factorial MMC Analysis / Sp2013

          GLM Screening - NMSS+WQ+no afdm & Depth / Composite -- ASE+LSE Site Locations

                    ****************************************************************

                                        The GLM Procedure


                              Duncan's Multiple Range Test for biomass

NOTE: This test controls the Type I comparisonwise error rate, not the experimentwise
error rate.

                              Alpha                              0.05

                              Error Degrees of Freedom            602

                              Error Mean Square              26143.62

                              Harmonic Mean of Cell Sizes    29.85659

                                NOTE: Cell sizes are not equal.


Number of Means           2          3          4          5          6          7
8

   Critical Range     82.19      86.53      89.43      91.58      93.25      94.62
95.77


                   Means with the same letter are not significantly different.


                   Duncan Grouping          Mean       N    tp

                                 A        621.60      32    0.05


                                 B        384.53      16    0.06


                                 C        261.06       9    0.14


                                 D        176.92      81    0.09


                                 E         74.07     108    0.035
                                 E
                                 E         70.20     225    0.07
                                 E
                                 E         61.58     108    0.054
                                 E
```

```
                          E          5.73     36    0.04
                 ****************************************************************
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                        6_Oyster Restoration & Biomass Analysis
                            Factorial MMC Analysis / Sp2013
         GLM Screening - NMSS+WQ+no afdm & Depth / Composite -- ASE+LSE Site Locations
                 ****************************************************************

                                  The GLM Procedure


                 Level of     Level of              -----------biomass-----------
                 tss          tp            N              Mean          Std Dev

                 4            0.05          9        251.131111       115.336988
                 6            0.05         23        766.565217       509.126713
                 6            0.14          9        261.055556       215.011239
                 7            0.04         36          5.726667         7.658328
                 11.053       0.054       108         61.580472        74.032969
                 13           0.06         16        384.533750       562.250787
                 16.093       0.035       108         74.066167        84.025220
                 18           0.07          9         17.167778         9.268724
                 30           0.09         72        171.268486       145.420192
                 31           0.07        108         16.405796        26.952188
                 32           0.07        108        128.411120       114.694896
                 40           0.09          9        222.157778       246.553953


                 Level of     Level of              -----------biomass-----------
                 tp           e_coli        N              Mean          Std Dev

                 0.035        0           108         74.066167        84.025220
                 0.04         21.8         36          5.726667         7.658328
                 0.05         2.45         23        766.565217       509.126713
                 0.05         2.83          9        251.131111       115.336988
                 0.054        8.45        108         61.580472        74.032969
                 0.06         40.91        16        384.533750       562.250787
                 0.07         0             9         17.167778         9.268724
                 0.07         2.45        108        128.411120       114.694896
                 0.07         7.35        108         16.405796        26.952188
                 0.09         3.16         72        171.268486       145.420192
                 0.09         407.93        9        222.157778       246.553953
                 0.14         7.42          9        261.055556       215.011239
```

```
Level of      Level of      Level of               -----------biomass-----------
tss           tp            e_coli          N             Mean           Std Dev

4             0.05          2.83            9       251.131111        115.336988

6             0.05          2.45           23       766.565217        509.126713

6             0.14          7.42            9       261.055556        215.011239

7             0.04          21.8           36         5.726667          7.658328

11.053        0.054         8.45          108        61.580472         74.032969

13            0.06          40.91          16       384.533750        562.250787

16.093        0.035         0             108        74.066167         84.025220

18            0.07          0               9        17.167778          9.268724

30            0.09          3.16           72       171.268486        145.420192
31            0.07          7.35          108        16.405796         26.952188

32            0.07          2.45          108       128.411120        114.694896

40            0.09          407.93          9       222.157778        246.553953
```

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                          6_Oyster Restoration & Biomass Analysis
                            Factorial MMC Analysis / Sp2013
         GLM Screening - NMSS+WQ+no afdm & Depth / Composite -- ASE+LSE Site Locations
                 ****************************************************************

                                   The GLM Procedure

                 Level of     Level of            -----------biomass-----------
                 doxy         tp            N             Mean          Std Dev

                 5.5          0.09          9       222.157778       246.553953
                 6.5          0.07        108        16.405796        26.952188
                 6.5          0.09         72       171.268486       145.420192
                 7            0.07        117       119.853940       114.133617
                 7.12         0.035       108        74.066167        84.025220
                 7.8          0.054       108        61.580472        74.032969
                 8.3          0.06         16       384.533750       562.250787
                 9.2          0.14          9       261.055556       215.011239
                 9.6          0.05         23       766.565217       509.126713
                 11.4         0.05          9       251.131111       115.336988
                 12           0.04         36         5.726667         7.658328

         Level of     Level of     Level of            -----------biomass-----------
         doxy         tss          tp            N             Mean          Std Dev

         5.5          40           0.09          9       222.157778       246.553953
         6.5          30           0.09         72       171.268486       145.420192
         6.5          31           0.07        108        16.405796        26.952188
         7            18           0.07          9        17.167778         9.268724
         7            32           0.07        108       128.411120       114.694896
         7.12         16.093       0.035       108        74.066167        84.025220
         7.8          11.053       0.054       108        61.580472        74.032969
         8.3          13           0.06         16       384.533750       562.250787
         9.2          6            0.14          9       261.055556       215.011239
         9.6          6            0.05         23       766.565217       509.126713
         11.4         4            0.05          9       251.131111       115.336988
         12           7            0.04         36         5.726667         7.658328

         Level of     Level of     Level of            -----------biomass-----------
         doxy         tp           e_coli        N             Mean          Std Dev
```

```
             5.5           0.09          407.93             9       222.157778        246.553953
             6.5           0.07          7.35             108        16.405796         26.952188
             6.5           0.09          3.16              72       171.268486        145.420192
             7             0.07          0                  9        17.167778          9.268724
             7             0.07          2.45             108       128.411120        114.694896
             7.12          0.035         0                108        74.066167         84.025220
             7.8           0.054         8.45             108        61.580472         74.032969
             8.3           0.06          40.91             16       384.533750        562.250787
             9.2           0.14          7.42               9       261.055556        215.011239
             9.6           0.05          2.45              23       766.565217        509.126713
             11.4          0.05          2.83               9       251.131111        115.336988
             12            0.04          21.8              36         5.726667          7.658328

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                           6_Oyster Restoration & Biomass Analysis

                               Factorial MMC Analysis / Sp2013

        GLM Screening - NMSS+WQ+no afdm & Depth / Composite -- ASE+LSE Site Locations

                     ****************************************************************

                                     The GLM Procedure

    Level of      Level of      Level of      Level of                ------------biomass------
    doxy          tss           tp            e_coli             N             Mean             Std
Dev

    5.5           40            0.09          407.93             9       222.157778
246.553953

    6.5           30            0.09          3.16              72       171.268486
145.420192

    6.5           31            0.07          7.35             108        16.405796
26.952188

    7             18            0.07          0                  9        17.167778
9.268724

    7             32            0.07          2.45             108       128.411120
114.694896

    7.12          16.093        0.035         0                108        74.066167
84.025220

    7.8           11.053        0.054         8.45             108        61.580472
74.032969

    8.3           13            0.06          40.91             16       384.533750
562.250787

    9.2           6             0.14          7.42               9       261.055556
215.011239

    9.6           6             0.05          2.45              23       766.565217
509.126713

    11.4          4             0.05          2.83               9       251.131111
115.336988

    12            7             0.04          21.8              36         5.726667
7.658328
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VITA

STEPHANIE ROBERTS LONG

Stephanie was born in Richmond, Virginia on September 5, 1951. She was raised in Richmond and graduated from Thomas Jefferson High School in 1969. Stephanie studied biology and math as an undergraduate at Westhampton College, University of Richmond and graduated with a B.S. in Biology and Math in May, 1973. Stephanie began a graduate program in Biological Oceanography at Old Dominion University in the 80's. Her job relocated her to Richmond and she moved back to the Tidewater area in 2004 and began taking some classes at VIMS in 2006. She transferred back to ODU in the fall of 2009 to the Environmental Engineering program.