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Coupled Physical and Biological Modeling of Atlantic Surfclam Larval Transport and Sub-Population Connectivity in the Middle Atlantic Bight and Georges Bank

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ABSTRACTS OF TECHNICAL PAPERS

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successful survival in its habitats. To explore its molecular mechanism of euryhaline adaptation in this non-model species, *de novo* transcriptome and transcriptional response to an acute salinity variation were analyzed. The RNA from various tissues and early developmental stages were pooled and normalized after reverse transcription. Through a full 454 GS-FLX titanium sequencing, approximately 1.6 million reads were generated with an average length of 387 bp, which resulted in assembly of 35,207 contigs, with 1,271bp of N50. Using Blast searches of NCBI non-redundant protein database, around 16,000 transcripts with conserved protein domains were identified and approximately 10,000 transcripts were assigned with Gene Ontology terms. Digital gene expression (DGE) analysis showed a significant up- or down-regulation of salinity-responsive transcripts involved in osmotic effector proteins, osmotic stress specific transcription factors, osmo-sensory signal molecules, osmo-regulatory hormone and their receptors, suggesting a high complexity and universality of osmo-regulation in oysters. These results provided global insight into the fundament of physiological adaptability to acute salinity fluctuation at genomic level.

BIOACOUSTIC EVALUATION OF RESTORED OYSTER REEFS – SPATIAL, TEMPORAL AND SPECIES SPECIFIC VARIATION IN BIOLOGICAL SOUND PRODUCTION.

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Passive acoustics uses naturally occurring sounds produced by marine organisms to study their behavior, biology and location. The aim of this research was to use passive acoustic technology to measure the progress (reef use and colonization) of a large restoration oyster reef project, where more than 24 acres of oyster reefs were restored. Three sites along the Saint Lucie Estuary, Florida were acoustically monitored. Oyster toadfish, naked goby, mud crabs, and snapping shrimps inhabit oyster reefs, and they are known to produce sounds. This study focused on the sound production of snapping shrimp because they are one of the most abundant decapod crustacean species in oyster reefs, and they are well known for their sound production. Total power and number of snapping shrimp snaps were calculated for each field recording. Results indicated that total power and number of snaps can be useful in detecting differences between natural and restored reefs, seasons, river regions, and day periods. In addition, number of snaps can be useful for estimating number of species present in an oyster reef. As snapping shrimp are common in various ecosystems, this methodology could be extrapolated to monitor number of snapping shrimp and number of species in other ecosystems.

COUPLED PHYSICAL AND BIOLOGICAL MODELING OF ATLANTIC SURFCLAM LARVAL TRANSPORT AND SUB-POPULATION CONNECTIVITY IN THE MIDDLE ATLANTIC BIGHT AND GEORGES BANK.

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The Atlantic Surfclam (*Spisula solidissima*) is one of the most commercially important shellfish species along the Northeast U.S. coast. In the past, systematic variations in the surfclam sub-populations in this region, thought to be associated with progressive environmental change, have been reported. The larval dispersal stage of the surfclam plays a key role in total recruitment rate and sub-population connectivity. With this in mind, we couple a physical circulation model, based upon the Regional Ocean Modeling System, and a surfclam individual-based larval model to simulate surfclam larval transport and sub-population connectivity throughout the Middle Atlantic Bight (MAB) and Georges Bank (GBK) regions. Preliminary results for the period 2006–2009 show the connection direction among the surfclam sub-populations inside the MAB and GBK to be downstream, from the northeast to the southwest. Typically, only two adjacent regions are closely connected. As expected from its retentive circulation, the GBK surfclam population is relatively isolated. The coupled simulations also confirm large inter-annual variation in surfclam sub-population connectivity patterns.

CLONING AND EXPRESSION OF VITELLOGENIN GENE IN NOBLE SCALLOP *CHLAMYS NOBILIS* (BIVALVE: PECTINIDAE) WITH BROWN AND ORANGE SHELL COLORS.

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In this study, the full-length cDNA encoding vitellogenin (Vg) in noble scallop *Chlamys nobilis* was cloned and expressed at different tissues and different gonadal development stages using male and female individuals with orange and brown shell. The complete Vg cDNA consists of 7760 nucleotides with an open reading frame encoding 2289 amino acid residues. According to the phylogenetic analysis of Vg gene, *Ch. nobilis* was clustered together firstly with its sister species *Ch. farreri* and another scallop *M. yessoensis*, next with other molluscs such as oyster and abalone, and then other invertebrates, finally with vertebrates. In common with molluscs Vgs, the Vg gene was expressed only in the ovary. Both orange and brown shell color scallops show the same trend that the amount of Vg mRNA expression significantly increased at