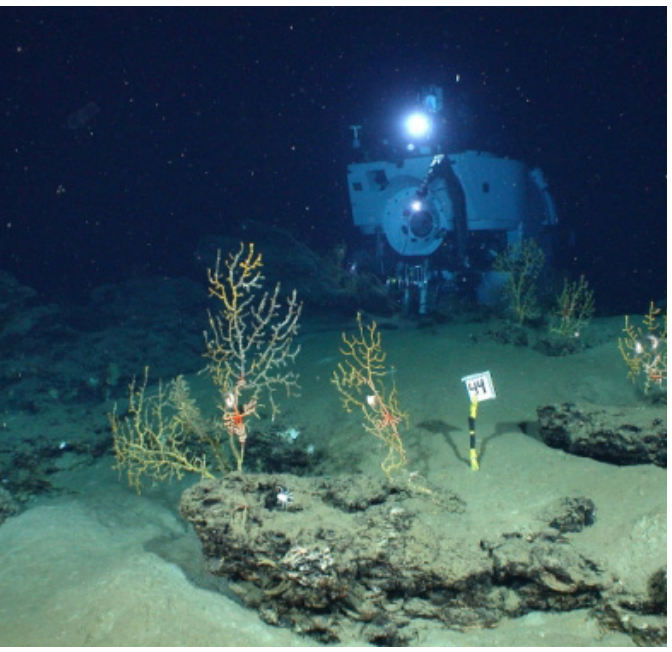
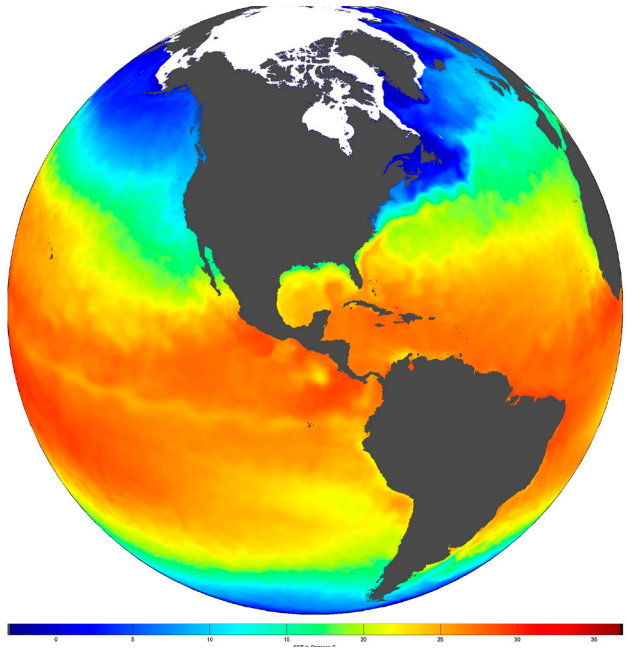




NOAA Scientific Publications Report

SEPTEMBER 7, 2014

HIGHLIGHTED ARTICLE

Global Analysis of mRNA Half-lives and de novo transcription in a dinoflagellate, *Karenia brevis*

Combined effects of climate change and bank stabilization on shallow water habitats of Chinook salmon

Preparation of radiolabeled brevetoxin peptide and lipid metabolites and their blood elimination kinetics

Deep-sea benthic footprint of the Deepwater Horizon blowout

A review of global ocean temperature observations: Implications for ocean heat content estimates and climate change

Influence of temperature and salinity on growth, survival, and biomass productivity of postlarval and early juvenile pink shrimp, *Farfantepenaeus duorarum* (Burkenroad 1939)

ADDITIONAL ARTICLES

Postnesting migratory behavior of loggerhead sea turtles (*Caretta caretta*) from three Florida rookeries

Molecular characterization and quantification of sablefish (*Anoplopoma fimbria*) gonadotropin and their receptors: reproductive dysfunction in female captive broodstock

Definition and densification of the Puerto Rico vertical datum of 2002

Lessons learned from developing integrated ecosystem assessments to inform marine ecosystem-based management in the U.S.

Modeling structured population dynamics using data from unmarked individuals

A Bayesian approach to identifying and compensating for model misspecification in population models

The Pathfinder Atmospheres Extended (PATMOS-x) AVHRR climate data set

Using OPUS for measuring vertical displacements in Houston, Texas

High-throughput sequencing and pathway analysis reveal alteration of the pituitary transcriptome by 17-alpha ethynylestradiol (EE2) in female coho salmon, Oncorhychus kisutch

DNA strand breaks (comet assay) in blood lymphocytes from bottlenose dolphins from Charleston, SC and the Indian River Lagoon, FL

On the spherical and spheroidal harmonic expansion of the gravitational potential of the topographic masses

Evaluating adaptive divergence between migratory and nonmigratory ecotypes of a salmonid fish, *Oncorhynchus mykiss*

Evaluating the precision and accuracy of life history information in FishBase, a global fish database

Predicted transport Of pyrethroid insecticides from an urban landscape to surface water

Bottom side-roll feeding by humpback whales (*Megaptera novaeangliae*) in the southern Gulf of Maine, U.S.A.

Silicon deficiency induces alkaline phosphatase enzyme activity in cultures of four marine diatoms

OPUS use in Alaska: a favored positioning tool from the north slope to the remote Aleutian Islands

Evaluation of single-sample analysis of relaxin combined with progesterone to support pregnancy diagnosis in wild bottlenose dolphins (Tursiops truncatus)

NeEstimator v2.0: re-implementation of software for the estimation of contemporary effective population size (Ne) from genetic data

Ecosystem metabolism and support of freshwater capture fisheries in the Tonle Sap Lake, Cambodia

Seasonal and interannual variation in the extent of hypoxia in the northern California Current from 1998-2012

Spatial variability buffers temporal fluctuations in early juvenile survival for an endangered Pacific salmon

OTHER REPORTS, BOOK CHAPTERS, & INTERNAL PUBLICATIONS

Estimation of Hawaiian monk seal consumption in relation to ecosystem biomass and overlap with fisheries in the main Hawaiian Islands

HIGHLIGHTED ARTICLE

AUTHORS

J. S. Morey and **F. M. Van Dolah (NOS/NCCOS)**

PUBLICATION DATE

Expected Publication Date: 11 June 2013

TITLE

Global Analysis of mRNA Half-lives and de novo transcription in a dinoflagellate, Karenia brevis

JOURNAL

PLoS One

SIGNIFICANCE

- As harmful algal blooms have significant ecological, human health, and economic impacts, this study focused on their molecular biology to better understand the mechanisms underlying bloom dynamics and toxicity for improved coastal management and forecasting.
- In this harmful algal bloom forming dinoflagellate, cellular processes including growth and toxicity appear to be regulated post-transcriptionally. This information allows us to better design appropriate biomarkers for the physiological status of blooms which will contribute to improved bloom monitoring and forecasting bloom impacts.

Karenia bloom

SUMMARY

Dinoflagellates possess many physiological processes that appear to be under post-transcriptional control. However, the extent to which their genes are regulated post-transcriptionally remains unresolved. To gain insight into the roles of differential mRNA stability and de novo transcription in dinoflagellates, we biosynthetically labeled RNA with 4-thiouracil to isolate newly transcribed and pre-existing RNA pools in Karenia brevis. These isolated fractions were then used for analysis of global mRNA stability and de novo transcription by hybridization to a K. brevis microarray. Global K. brevis mRNA half-lives were calculated from the ratio of newly transcribed to pre-existing RNA for 7086 array features using the online software HALO (Half-life Organizer). Overall, mRNA half-lives were substantially longer than reported in other organisms studied at the global level, ranging from 42 minutes to greater than 144 h, with a median of 33 hours. Consistent with well-documented trends observed in other organisms, housekeeping processes, including energy metabolism and transport, were significantly enriched in the most highly stable messages. Shorter-lived transcripts included a higher proportion of transcriptional regulation, stress response, and other response/regulatory processes. One such family of proteins involved in post-transcriptional regulation in chloroplasts and mitochondria, the pentatricopeptide repeat (PPR) proteins, had dramatically shorter half-lives when compared to the arrayed transcriptome. As transcript abundances for PPR proteins were previously observed to rapidly increase in response to nutrient addition, we queried the newly synthesized RNA pools at 1 and 4 h following nitrate addition to N-depleted cultures. Transcriptome-wide there was little evidence of increases in the rate of de novo transcription during the first 4 h, relative to that in N-depleted cells, and no evidence for increased PPR protein transcription. These results lend support to the growing consensus of post-transcriptional control of gene expression in dinoflagellates.

VISIT THE SCIENTIFIC PUBLICATIONS REPORT ARCHIVE

HIGHLIGHTED ARTICLE

AUTHORS

J. Jorgensen (NMFS/NWFSC), M. McClure (NMFS/NWFSC), M. Sheer (NMFS/NWFSC), and **N. Munn (NMFS/Habitat Conservation Division)**

PUBLICATION DATE

Expected Publication Date: December 2013

TITLE

Combined effects of climate change and bank stabilization on shallow water habitats of Chinook salmon

JOURNAL

Conservation Biology

SIGNIFICANCE

- Evaluated the combined effects of estimated climate change impacts and human habitat alteration (i.e., stabilizing shoreline with large rocks) to Chinook salmon habitats using downscaled climate forecasts.
- Given projected river flows, more than 15% of beach shallow water area was displaced by the rocks, which could restrict salmon feeding, resting, and refuge from predators.
- This approach provides resource managers a wider geographic context for reviewing small projects in concert with climate change, and a method to analyze the cumulative effects of proposed actions and estimate the long-term effects of these actions.

SUMMARY

Significant challenges remain in the ability to estimate habitat change under the combined effects of natural variability, climate change, and human activity. We examined anticipated impacts on shallow water over low-sloped beaches to these combined effects in the lower Willamette River, Oregon, an area highly altered by development. A proposal to stabilize some shoreline with large rocks (riprap) would alter shallow water areas, an important habitat for threatened Chinook salmon (Oncorhynchus tshawytscha), and would be subject to U.S. Endangered Species Act-mandated oversight. In the main stem, subyearling Chinook salmon appear to preferentially occupy these areas, which fluctuate with river stages. We estimated effects with a geospatial model and projections of future river flows. Recent (1999-2009) median river stages during peak subyearling occupancy (April-June) maximized beach shallow water area in the lower main stem. Upstream shallow water area was maximized at lower river stages that have occurred recently. Higher river stages in April-June, resulting from increased flows predicted for the 2080s, decreased beach shallow water area 17- 32%. On the basis of projected 2080s flows, more than 15% of beach shallow water area was displaced by the riprap. Beach shallow water area lost to riprap represented up to 1.6% of the total from the mouth to 12.9 km upstream. Reductions in shallow water area could restrict salmon feeding, resting, and refuge from predators and potentially reduce opportunities for the expression of the full range of life-history strategies. Although climate change analyses provided useful information, detailed analyses are prohibitive at the project scale for the multitude of small projects reviewed annually. The benefits of our approach to resource managers include a wider geographic context for reviewing similar small projects in concert with climate change, an approach to analyze cumulative effects of similar actions, and estimation of the actions' long-term effects.

VISIT THE SCIENTIFIC PUBLICATIONS REPORT ARCHIVE

HIGHLIGHTED ARTICLE

AUTHORS

C. O. Miles and **J. S. Ramsdell (NOS/NCCOS)**

PUBLICATION DATE

Published: June 2013

TITLE

Preparation of radiolabeled brevetoxin peptide and lipid metabolites and their blood elimination kinetics

JOURNAL

Chemical Research in Toxicology

SIGNIFICANCE

- There are vast differences in the toxicity of the three common brevetoxin metabolites in Gulf of Mexico shellfish.
- This research determines that the fatty acid brevetoxin metabolite, previously shown to be ten times more potent than previously thought, also persists in consumers far longer than other brevetoxins.
- More accurately defining exposure risk of brevetoxins strengthens shellfish safety and improves decision-making for shellfish harvesting.

SUMMARY

Brevetoxin B (BTX-B), produced by dinoflagellates of the species Karenia, is a highly reactive molecule, due in part to an α,β-unsaturated aldehyde group at the terminal side chain, leading to the production of metabolites by reduction, oxidation, and conjugation. We have investigated in mice the blood elimination of three common bioactive brevetoxin metabolites found in shellfish, which have been semi-synthesized from BTX-B in radioactive forms. BTX-B was reduced at C42 to yield [3H] dihydro-BTX-B. [3H] S-desoxy-BTX-B2 (cysteine brevetoxin B) was semi-synthesized from BTX-B by conjugation of cysteine at the C50 olefinic group, then [3H] radiolabeled by C42 aldehyde reduction. [14C] N-palmitoyl-S-desoxy-BTX-B2 was prepared using S-desoxy-BTX-B2 as the starting material with addition of the [14C] radiolabeled fatty acid via the cysteine-amide linkage. The elimination of intravenously administered [3H] S-desoxy-BTX-B2, [14C] N-palmitoyl-S-desoxy-BTX-B2, or [3H] dihydro-BTX-B was measured in blood collected from C57BL/6 mice over a 48 hour period. Each brevetoxin metabolite tested exhibited biexponential elimination kinetics and fit a two-compartment model of elimination that was applied to generate toxicokinetic parameters. The rate of transfer between the central compartment (i.e., blood) and the peripheral compartment (e.g., tissue) for each brevetoxin differed substantially, with dihydro-BTX-B exchanging rapidly with the peripheral compartment, and S-desoxy-BTX-B2 eliminating rapidly from the central compartment and N-palmitoyl-S-desoxy-BTX-B2 eliminating slowly from the central compartment. Toxicokinetic parameters were analyzed in the context of the unique structure of each brevetoxin metabolite resulting from a reduction, amino acid conjugation, or fatty acid addition to BTX-B.

VISIT THE SCIENTIFIC PUBLICATIONS REPORT ARCHIVE

HIGHLIGHTED ARTICLE

AUTHORS

P. A. Montagna, J. G. Baguley, **C. Cooksey, I. Hartwell**, L. J. Hyde, **J. L. Hyland**, R. D. Kalke, **L. M. Kracker**, M. Reuscher, and A. C. E. Rhodes **(NOS/NCCOS)**

PUBLICATION DATE

Published: 13 August 2013

TITLE

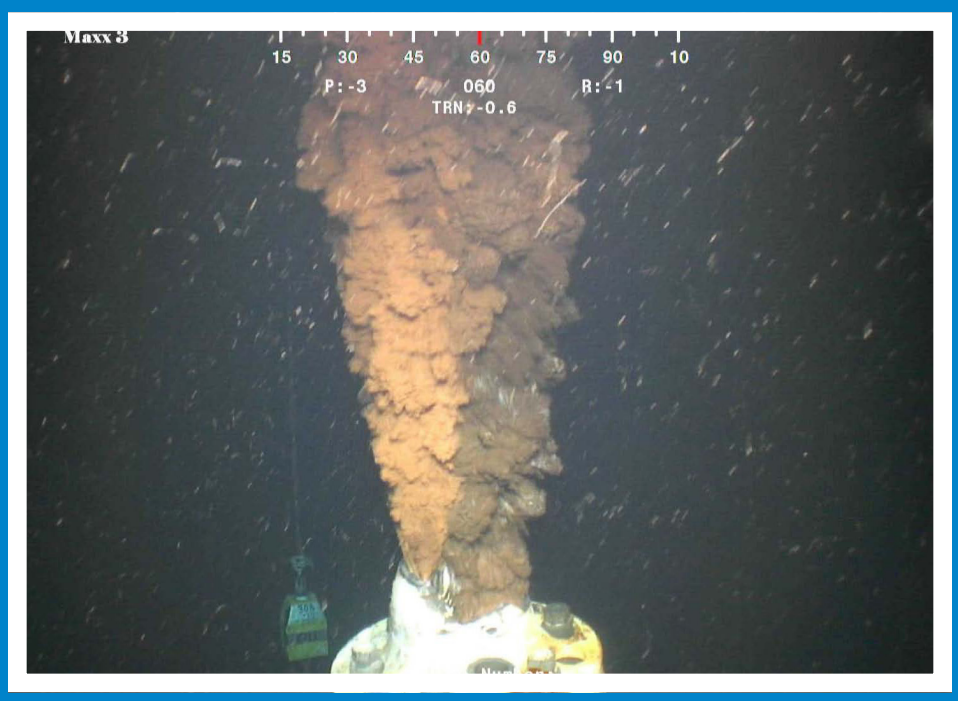
Deep-sea benthic footprint of the Deepwater Horizon blowout

JOURNAL

PLoS ONE

SIGNIFICANCE

- The study provided evidence of DWH-related impacts to the soft bottom benthos in deep-water areas of the Gulf (including reduced diversity and abundances of macrofauna and meiofauna and elevated ratios of pollution-tolerant nematodes relative to pollution-sensitive harpacticoid copepods).
- The most severe impacts extended to 3 km from the wellhead in all directions, covering an area about 24 km2. Moderate impacts were observed up to 17 km towards the southwest and 8.5 km towards the northeast of the wellhead, covering an area 148 km2.
- Benthic impacts were correlated with indicators of oil-spill exposure (including elevated levels of total petroleum hydrocarbons, total polycyclic aromatic hydrocarbons, and barium) and proximity to the wellhead, but not proximity to natural hydrocarbon seeps.
- Recovery rates in the deep sea are likely to be slow, on the order of decades or longer.



DWH well head

SUMMARY

Oil from the Deepwater Horizon blowout contacted and persisted in parts of the bottom of the deep-sea in the Gulf of Mexico. As part of the response to the accident, monitoring cruises were deployed in fall 2010 to measure potential impacts on the two main soft-bottom benthic invertebrate groups: macrofauna and meiofauna. Sediment was collected using a multicorer so that samples for chemical, physical and biological analyses could be taken simultaneously and analyzed using multivariate methods. The footprint of the oil spill was identified by creating a new variable with principal components analysis where the first factor was indicative of the oil spill impacts and this new variable mapped in a geographic information system to identify the area of the oil spill footprint. The most severe relative reduction of faunal abundance and diversity extended to 3 km from the wellhead in all directions covering an area about 24 km2. Moderate impacts were observed up to 17 km towards the southwest and 8.5 km towards the northeast of the wellhead, covering an area 148 km2. Benthic effects were correlated to total petroleum hydrocarbon, polycyclic aromatic hydrocarbons and barium concentrations, and distance to the wellhead; but not distance to hydrocarbon seeps. Thus, benthic effects are more likely due to the oil spill, and not natural hydrocarbon seepage. Recovery rates in the deep sea are likely to be slow, on the order of decades or longer.

VISIT THE SCIENTIFIC PUBLICATIONS REPORT ARCHIVE

HIGHLIGHTED ARTICLE

AUTHORS

J.P. Abraham, M. Baringer, N.L. Bindoff, **T. Boyer (Ocean Cimate Lab/NODC/NESDIS)**, L.J. Cheng, J.A. Church, J.L. Conroy, C.M. Domingues, J.T. Fasullo, J. Gilson, **G. Goni (AOML/OAR)**, S.A. Good, J. M. Gorman, V. Gouretski, M. Ishii, **G.C. Johnson (PMEL/OAR)**, S. Kizu, **J.M. Lyman (JIMAR/UH/PMEL/OAR)**, A. M. Macdonald, W.J. Minkowycz, S.E. Moffitt, M.D. Palmer, A.R. Piola, F. Reseghetti, K. Schuckmann, K.E. Trenberth, I. Velicogna, and J.K. Willis

PUBLICATION DATE

Accepted: 16 August 2013

TITLE

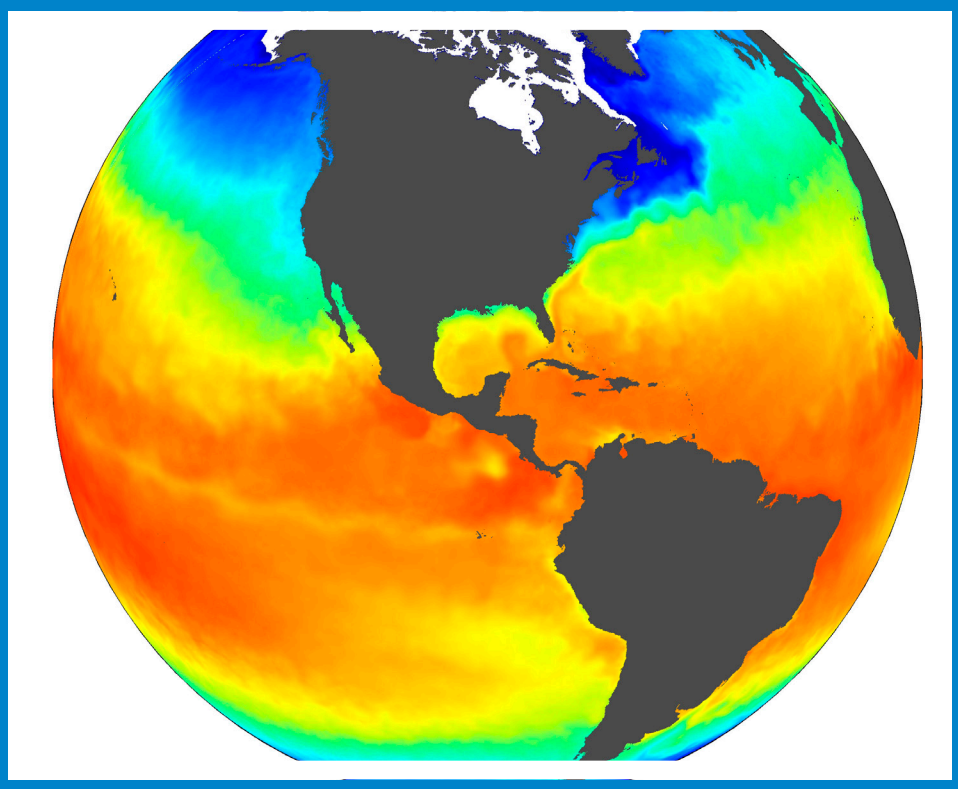
A review of global ocean temperature observations: Implications for ocean heat content estimates and climate change

JOURNAL

Review of Geophysics

SIGNIFICANCE

- Multiple studies show that there has been a multi-decadal increase in the heat content of both the upper and deep ocean regions, which reflect the impact of anthropogenic warming.
- With respect to sea-level rise, mutually reinforcing information from tide gauges and radar altimetry show that presently, sea-level is rising at approximately 3 mm yr-1 with contributions from both thermal expansion and mass accumulation from ice melt.
- In this paper the authors summarize the state of ocean heat content calculations, the importance of these calculations for understanding the global climate system, and the in situ measurements which are used for the calculations in a single coherent manuscript.



Global ocean temperature

SUMMARY

The evolution of ocean temperature measurement systems is presented with a focus on the development and accuracy of two critical devices in use today (expendable bathythermographs and CTDs – conductivity-temperature-depth instruments used on Argo floats). A detailed discussion of the accuracy of these devices and a projection of the future of ocean temperature measurements are provided. The accuracy of ocean temperature measurements is discussed in detail in the context of ocean heat content, Earth's energy imbalance, and thermosteric sea level rise. Up-to-date estimates are provided for these three important quantities. The total energy imbalance at the top-of-atmosphere is best assessed by taking an inventory of changes in energy storage. The main storage is in the ocean; the latest values of which are presented. Furthermore, despite differences in measurement methods and analysis techniques, multiple studies show that there has been a multi-decadal increase in the heat content of both the upper and deep ocean regions, which reflect the impact of anthropogenic warming. With respect to sea-level rise, mutually reinforcing information from tide gauges and radar altimetry show that presently, sea-level is rising at approximately 3 mm yr-1 with contributions from both thermal expansion and mass accumulation from ice melt. The latest data for thermal expansion sea-level rise are included here and analyzed.

LINK TO PAPER

http://onlinelibrary.wiley.com/doi/10.1002/rog.20022/abstract

VISIT THE SCIENTIFIC PUBLICATIONS REPORT ARCHIVE

HIGHLIGHTED ARTICLE

AUTHORS

I. C. Zink, M. M.Criales, and **J. A. Browder (NMFS/SEFSC)**

PUBLICATION DATE

Accepted: 9 August 2013

TITLE

Influence of temperature and salinity on growth, survival, and biomass productivity of postlarval and early juvenile pink shrimp, Farfantepenaeus duorarum *(Burkenroad 1939)*

JOURNAL

Journal of Shellfish Research

SIGNIFICANCE

- The natural productivity of pink shrimp in Florida Bay is depressed by the hypersaline conditions that often prevail in the bay.
- The Comprehensive Everglades Restoration Project, which plans to direct more fresh water to Florida Bay, may increase the production of pink shrimp recruits on nursery grounds by reducing the intensity, frequency, duration, and spatial extent of hypersaline conditions.
- This may increase the productivity of the Tortugas pink shrimp fishery.

SUMMARY

This study investigated the combined effect of salinity and temperature on growth, survival, and biomass productivity of postlarval and early juvenile pink shrimp *Farfantepenaeus duorarum* (Burkenroad 1939). Test subjects were cohorts from a single spawning event. The study had two phases: postlarval (1st 28 d) and early juvenile (2nd 28 d) and used a factorial block design consisting of three salinity treatments (15, 35, 55), each replicated within three temperature treatments (22, 27, 32 °C). Growth was assessed every 7 d by measuring carapace length and wet weight. Survival was assessed at the end of each phase. Biomass, calculated as the product of final wet weight and percent survival relative to initial total weight, increased with temperature and decreased at high salinity. Temperature had a significant positive effect on growth rates in both phases. The effect of salinity on growth became significant in the early juvenile stage. These results suggest that the natural productivity of pink shrimp in Florida Bay is depressed by the hypersaline conditions that often prevail in the bay.

VISIT THE SCIENTIFIC PUBLICATIONS REPORT ARCHIVE

ADDITIONAL ARTICLE

AUTHORS

R. Hardy, S. L. MacPherson, M. Nicolas, and M. S. Coyne

PUBLICATION DATE

Published Online: August 13, 2013

TITLE

*Postnesting migratory behavior of loggerhead sea turtles (*Caretta caretta*) from three Florida rookeries*

JOURNAL

Endangered Species Research

A. M. Foley, **B. A. Schroeder (NMFS/OPR),**

SIGNIFICANCE

- The results from this study provide new information regarding migratory habitats used by adult female loggerheads returning from their nesting beaches to their foraging areas.
- The authors identified four migratory corridors: two on the continental shelf of the Florida Panhandle, one along the northern coast of Cuba, and one along the southeastern coast of Florida.
- These findings provide important information for conservation, management, and recovery implementation, particularly when evaluating the potential effects of anthropogenic activities planned or already occurring within or near these important habitats.

SUMMARY

The authors used satellite telemetry to study postnesting migrations of 42 loggerhead sea turtles (*Caretta caretta*) from three Florida rookeries. Postnesting migrations ended in neritic (<200 m) waters of Florida, Alabama, Texas, Mexico, and The Bahamas. Most postnesting migrations were restricted to the continental shelf and were relatively direct. Migrations through oceanic areas (>200 m) tended to be less direct largely due to apparent influences of the Florida Current in the Atlantic and to looping travel paths (often along edges of mesoscale eddies of the Loop Current) in the Gulf of Mexico. The largest loggerheads tended to migrate to foraging grounds that were farthest from the nesting beach. Turtles spent more time near the surface (<3 m) when migrating than they did during residency at foraging sites, and were likely swimming just below the surface. Migrating loggerheads may have been foraging, as evidenced by the substantial amount of time spent near the bottom in neritic areas and by looping travel paths in oceanic areas. Authors identified four migratory corridors. Two were on the continental shelf of the Florida Panhandle, one was along the northern coast of Cuba, and one was along the southeastern coast of Florida. Migrating loggerheads may be uniquely vulnerable to mortality factors because of where they travel and how they behave, particularly if they are concentrated in narrow (perhaps <10 km wide) migratory corridors. Characterizing the behavior and identifying the travel paths of loggerheads during postnesting migrations are necessary steps for implementing successful recovery efforts.

LINK TO PAPER

http://www.int-res.com/articles/esr_oa/n021p129.pdf

ADDITIONAL ARTICLE

AUTHORS

J. M. Guzman, J. A. Luckenbach, and **P. Swanson**
(NMFS/NWFSC)

TITLE

*Molecular characterization and quantification of sablefish (*Anoplopoma fimbria*) gonadotropin and their receptors: reproductive dysfunction in female captive broodstock*

JOURNAL

General and Comparative Endocrinology

SIGNIFICANCE

- In an effort to develop molecular tools to better understand reproductive dysfunction in this marine aquaculture species the authors cloned and sequenced Sablefish gonadotropin subunit and receptor messenger RNAs.
- Captivity associated stress appears to have a profound effect on female reproductive development in sablefish and will need to be addressed in future studies.

SUMMARY

Efforts to establish an aquaculture industry for sablefish (*Anoplopoma fimbria*) are constrained by reproductive dysfunction in wild-caught fish and by lack of reproduction of F1 females. Toward a better understanding of the reproductive dysfunction of captive broodstock, full-length cDNAs encoding the sablefish gonadotropin subunits (fshb, lhb and cga) and their receptors (fshr and lhcgr) were cloned, sequenced and quantitative real-time PCR assays developed. Sablefish gonadotropin subunits display some unique features, such as two additional Cys residues in the N-terminal region of Fshb and a lack of potential N-glycosylation sites in Fshb and Lhb, whereas Fshr and Lhcgr possess conserved structural characteristics described in other vertebrates. Wild females captured in fall completed gametogenesis in captivity the next spawning season, whereas females captured three months earlier, during summer, failed to mature. Interestingly, these wild non-maturing females exhibited similar reproductive features as prepubertal F1 females, including low levels of pituitary gonadotropin and ovarian receptor mRNAs and plasma sex steroids, and ovarian follicles arrested at the perinucleolus stage. In conclusion, this study described the cloning, molecular characterization and development of qPCR for sablefish gonadotropins and their receptors. Rearing conditions may impair vitellogenic growth of ovarian follicles in sablefish, compromising the reproductive success of broodstock.

LINK TO PAPER

http://www.sciencedirect.com/science/article/pii/S0016648013003110

VISIT THE SCIENTIFIC PUBLICATIONS REPORT ARCHIVE

ADDITIONAL ARTICLE

AUTHORS

D. R. Doyle and **D. A Smith (NOS/NGS)**

PUBLICATION DATE

Accepted: 18 July 2013

TITLE

Definition and densification of the Puerto Rico vertical datum of 2002

JOURNAL

Surveying and Land Information Science

SIGNIFICANCE

- This paper defines the datum for Puerto Rico and describes the work leading up to its definition.

SUMMARY

The mission of the National Geodetic Survey (NGS) is to "define, maintain and provide access to the National Spatial Reference System to meet our nation's economic, social, and environmental needs." One component of that mission is to provide accurate geodetic control, including a vertical datum, for all territories of the United States. The islands of the territory of Puerto Rico have had a mixed, patchwork series of geodetic control over the last century, when they have had any geodetic control at all. This has included the lack of a comprehensive vertical datum for the entire territory. In accordance with its mission, NGS underwent an effort beginning in 1993, which has culminated in the Puerto Rico Vertical Datum of 2002.

ADDITIONAL ARTICLE

AUTHORS

J. F. Samhouri (NMFS/NWFSC), A. Haupt (NMFS/NWFSC), P. S. Levin (NWFSC), J. Jason (NMFS/NEFSC), and **R. Schuford (NMFS/OST)**

PUBLICATION DATE

Expected Publication Date: August 2013

TITLE

Lessons learned from developing integrated ecosystem assessments to inform marine ecosystem-based management in the U.S.

JOURNAL

ICES Journal of Marine Science

SIGNIFICANCE

- 8 tenets are proposed to enhance the use of IEAs in implementing EBM.

SUMMARY

Integrated ecosystem assessments (IEAs) were formally defined five years ago to serve as a scientific foundation for ecosystem-based management (EBM) of the ocean in the U.S. As outlined by the U.S. National Oceanic Atmospheric Administration in 2008-2009, an IEA is a stepwise process consisting of setting goals and targets, defining indicators, analyzing status, trends and risk, and evaluating alternative potential future management and environmental scenarios to enhance information needed for effective EBM. These steps are hierarchical, non-prescriptive about technical implementation, and adaptable to existing information for any ecosystem. Despite these strengths and some initial successes, IEAs and EBM have yet to be fully realized. We propose eight tenets that can be adopted by scientists, policymakers, and managers to enhance the use of IEAs in implementing EBM. These tenets include (1) engage with stakeholders, managers, and policy makers early, often, and continually; (2) conduct rigorous human dimensions research; (3) recognize the importance of transparently selecting indicators; (4) set ecosystem targets to create a system of EBM accountability; (5) establish a formal mechanism(s) for the review of IEA science; (6) serve current management needs, but not at the expense of more integrative ocean management; (7) provide a venue for EBM decision making that takes full advantage of IEA products; and, (8) embrace realistic expectations about IEA science and its implementation. With patience, persistence, political will, funding, and augmented capacity, IEAs will provide a general approach for allowing progressive science to lead conventional ocean management to new waters.

VISIT THE SCIENTIFIC PUBLICATIONS REPORT ARCHIVE

ADDITIONAL ARTICLE

AUTHORS

E. F. Zipkina, **J. T. Thorson (NMFS/NWFSC)**, K. See, H. J. Lynch, E. H. C. Granta, Y. Kanno, R. B. Chandler, B. H. Letcher, and J. A. Royle

PUBLICATION DATE

Expected Publication Date: Fall 2013

TITLE

Modeling structured population dynamics using data from unmarked individuals

JOURNAL

Ecology

SIGNIFICANCE

- This research shows that count data from biological surveys can be used in isolation to estimate demographic rates such as survival, recruitment, and migration, as well as detection probabilities.
- However, this is only feasible for species that have high site-fidelity and can be repeatedly measured within a season.

SUMMARY

The study of population dynamics requires unbiased, precise estimates of abundance and vital rates that account for the demographic structure inherent in all wildlife and plant populations. Traditionally, these estimates have only been available through approaches that rely on intensive capture-recapture data. We extend recently developed N-mixture models to demonstrate how demographic parameters and abundance can be estimated for structured populations using only stage-structured count data. Our modeling framework can be used to make reliable inferences on abundance as well as recruitment, immigration, stage-specific survival, and detection rates during sampling. We present a range of simulations to illustrate the data requirements, including the number of years and locations necessary, for accurate and precise parameter estimates. We apply our modeling framework to a population of northern dusky salamanders (*Desomgnathus fuscus*) in the mid-Atlantic region and find that the population is unexpectedly declining. Our approach represents a valuable advance in the estimation of population dynamics using multi-state data from unmarked individuals and should additionally be useful in the development of integrated models that combine data from intensive (e.g., capture-recapture) and extensive (e.g., counts) data sources.

VISIT THE SCIENTIFIC PUBLICATIONS REPORT ARCHIVE

ADDITIONAL ARTICLE

AUTHORS

J. T. Thorson (NMFS/NWFSC), K. Ono, and **S. B. Munch (NMFS/SWFSC)**

PUBLICATION DATE

Expected Publication Date: Fall 2013

TITLE

A Bayesian approach to identifying and compensating for model misspecification in population models

JOURNAL

Ecology

SIGNIFICANCE

- This research develops and tests a new method for building population-dynamics models.
- We show that this process can deal easily with model misspecification, and can also diagnose times when models are misspecified. It therefore has very general applicability throughout fisheries and ecology.

SUMMARY

State-space estimation methods are increasingly used in ecology to estimate productivity and abundance of natural populations while accounting for variability in both biomass dynamics and measurement processes. However, functional forms for biomass dynamics and density dependence often will not match the true biological process, and this may degrade the performance of state-space methods. We therefore develop a semi-parametric state-space model, which uses a Gaussian process (GP) to approximate the surplus production function (i.e. the functional form of density dependence). We propose that this model offers two benefits for population modeling. First, it allows data to update a specified 'prior' on the surplus production function, while reverting to this prior when data are uninformative. Second, it allows variability in biomass dynamics to be decomposed into random errors around the estimated production function ('process error') and errors due to the mismatch between the specified prior and estimated production function ('model error'). We use simulation modeling to explore the utility of GP methods in state-space dynamical models. Results confirm that the GP model performs similarly to a conventional state-space model when either (1) the prior matches the true process, or (2) data are relatively uninformative. However, GP methods improve estimates of the production function when the function is misspecified, and this in turn improves estimation of other model parameters. Results also demonstrate that estimates of 'model error' can be used to distinguish cases of model misspecification.

ADDITIONAL ARTICLE

AUTHORS

A. K. Heidinger (NESDIS/STAR), M. J. Foster, A. Walther, and **X. Zhao (NESDIS/NCDC)**

PUBLICATION DATE

Accepted: 13 August 2013

TITLE

The Pathfinder Atmospheres Extended (PATMOS-x) AVHRR climate data set

JOURNAL

Bulletin of the American Meteorological Society

SIGNIFICANCE

- The AVHRR has flown since 1978 and continues to provide radiometrically consistent observations with a spatial resolution of roughly 4 km and temporal resolution of four times per day on average.
- The AVHRR dataset is immensely valuable for climate studies and model evaluation.

SUMMARY

The Advanced Very High Resolution Radiometer (AVHRR) Pathfinder Atmospheres Extended (PATMOS-x) data set offers over three decades of global observations from the NOAA Polar Orbiting System (POES) and the EUMETSAT MetOP satellite series. The AVHRR PATMOS-x data provides calibrated AVHRR observations in addition to properties about tropospheric clouds and aerosols, the earth's surface, the earth's radiation budget and relevant ancillary data. To provide three decades of data in a convenient format, PATMOS-x generates mapped and sampled results with a spatial resolution of 0.1° on a global longitude, latitude grid referred to as Level-2b. Level-2b data avoids spatial or temporal averaging of data thus maintaining the flexibility to conduct multi-dimensional analysis. Comparison of Level-2 and Level-2b data within 1°x1° boxes demonstrate Level-2b data reproduces the Level-2 pixel distribution to a high level of accuracy. AVHRR PATMOS-x is comprised of data from 17 different sensors. An examination of cloud amount and cloud optical depth time series demonstrate inter-satellite biases are less than 2%. Comparison of these time-series to data from the ERA-Interim reanalysis demonstrates a high degree of correlation indicating that sensor-to-sensor differences are also not contributing significantly to the observed climate variability in PATMOS-x.

ADDITIONAL ARTICLE

AUTHORS

G. Wang and **T. Soler (NOS/NGS)**

PUBLICATION DATE

Expected Publication Date: August 2013

TITLE

Using OPUS for measuring vertical displacements in Houston, Texas

JOURNAL

Journal of Surveying Engineering

SIGNIFICANCE

- The subsidence experienced by NGS CORS in the Houston area does not considerably affect the accuracy of OPUS vertical results.
- For those users who require a few centimeters of vertical accuracy for daily sessions, OPUS is a good choice, because users do not need to establish any control stations and do not need to install any GPS software packages on their local computers.

SUMMARY

The Houston area has been suffering from subsidence for several decades. Therefore, Continuously Operating Reference Stations (CORS) in this area may have experienced considerable vertical displacements. The Online Positioning User Service (OPUS), provided by the National Geodetic Survey (NGS), uses CORS as references in its data processing. This study investigated what effects, if any, the subsidence experienced by these CORS around Houston contributes to the accuracy of OPUS vertical results. Our OPUS results were determined from three long-term (over 10-year) blocks of continuous data using Global Positioning System (GPS) stations located in different parts of the Houston area. The OPUS results were compared with the vertical measurements from the precise point positioning with single receiver phase ambiguity (PPP-SRPA) solution implicit in the *GIPSY/OASIS 6.1.2* software. This particular study indicates that OPUS achieves 1.0-cm vertical accuracy for daily sessions (24 h) in the region around Houston, which is comparable to the OPUS accuracy previously reported in other investigations. Subsidence as slow as 0.5 cm/year can be detected by analyzing OPUS results spanning 5 or more years of data.

LINK TO PAPER

\http://ascelibrary.org/doi/abs/10.1061/(ASCE)SU.1943-5428.0000103

ADDITIONAL ARTICLE

AUTHORS

L. Harding, I. Schulz, G. Goetz, **J. A. Luckenbach**, G. Young, **F. W. Goetz,** and **P. Swanson (NMFS/NWFSC)**

PUBLICATION DATE

Expected Publication Date: Fall 2013

TITLE

High-throughput sequencing and pathway analysis reveal alteration of the pituitary transcriptome by 17-alpha ethynylestradiol (EE2) in female coho salmon, Oncorhychus kisutch

JOURNAL

Aquatic Toxicology

SIGNIFICANCE

- Low, environmentally relevant, concentrations of ethynylestradiol disrupts expression of hundreds of genes in the pituitary gland of coho salmon, including genes involved in regulating reproduction
- Ethynyl estradiol exposure altered expression of genes involved in circadian rhythms, suggesting environmental estrogens could potentially alter seasonal timing of reproduction in fish.

SUMMARY

Considerable research has been done on the effects of endocrine disrupting chemicals (EDCs) on reproduction and gene expression in the brain, liver and gonads of teleost fish, but information on impacts to the pituitary gland are still limited despite its central role in regulating reproduction. The aim of this study was to further our understanding of the potential effects of natural and synthetic estrogens on the brain-pituitary-gonad axis in fish by determining the effects of 17alpha-ethynylestradiol (EE2) on the pituitary transcriptome. EE2 is a synthetic estrogen used in human contraceptives and is present in sewage effluent. Juvenile coho salmon were exposed to either 0 or 12 ng EE2/L for up to 6 weeks and effects on the pituitary transcriptome of females were assessed using high-throughput Illumina® sequencing, RNA-Seq and pathway analysis. After 1 or 6 weeks, 218 and 670 contiguous sequences (contigs) respectively, were differentially expressed in pituitaries of EE2-exposed fish relative to control. Two of the most highly up- and down-regulated contigs were luteinizing hormone b subunit (241-fold and 395-fold at 1 and 6 weeks, respectively) and follicle stimulating hormone b subunit (-3.4-fold at 6 weeks). Additional contigs related to gonadotropin synthesis and release were differentially expressed in EE2-exposed fish relative to control. These included contigs involved in gonadotropin releasing hormone (GNRH) and transforming growth factor-b signaling. There was an over-representation of significantly affected contigs in 33 and 18 canonical pathways at 1 and 6 weeks, respectively, including circadian rhythm signaling, calcium signaling, peroxisome proliferator-activated receptor (PPAR) signaling, PPARa/retinoid x receptor a activation, and netrin signaling. Network analysis identified potential interactions between genes involved in circadian rhythm and GNRH signaling, suggesting possible effects of EE2 on timing of reproductive events.

ADDITIONAL ARTICLE

AUTHORS

R. F. Lee, K. Brinkley, **J. D. Adams,** M. Peden-Adams, G. D. Bossart, L. King, and **P. A. Fair (NOS/NCCOS)**

PUBLICATION DATE

Accepted: 8 June 2013

TITLE

DNA strand breaks (comet assay) in blood lymphocytes from bottlenose dolphins from Charleston, SC and the Indian River Lagoon, FL

JOURNAL

Marine Pollution Bulletin

SIGNIFICANCE

- This study is the first to carry out the comet assay, one of the most sensitive tests for measuring DNA strand breaks by exposures, on a large number of wild dolphins and thus provides a baseline study of DNA strand breaks in wild dolphin populations.
- Higher DNA strand breaks occurred in the dolphins from Charleston Harbor vs. the Indian River Lagoon, FL, which may be due to higher concentrations of genotoxic agents (e.g. contaminants).

SUMMARY

The comet assay, a measure of DNA strand breaks, was carried out on blood lymphocytes from 71 dolphins from Indian River Lagoon, FL and 51 dolphins from Charleston Harbor area, SC. Kruskal-Wallace multiple comparison test indicated no significant difference in the mean/median comet assay (% DNA in tail) results between the different age and sex categories (juvenile female, juvenile male, adult female, pregnant female, adult male). There was a significant difference in DNA strand breaks between Charleston Harbor dolphins (median - 17.4% DNA in tail) and Indian River Lagoon dolphins (median-14.0% DNA in tail). In addition, there was a strong correlation between T-cell proliferation and DNA strand breaks in dolphin lymphocytes which suggest that dolphins with a high numbers of DNA strand breaks have a decreased ability to respond to infection. Higher concentrations of genotoxic agents (e.g. contaminants, pesticides) in Charleston Harbor compared with Indian River lagoon may have been one of the causes of higher DNA strand breaks in these dolphins.

ADDITIONAL ARTICLE

AUTHORS

Y. M. Wang (NOS/NGS) and X. Yang

PUBLICATION DATE

Pre-published online 6 August 2013

TITLE

On the spherical and spheroidal harmonic expansion of the gravitational potential of the topographic masses

JOURNAL

Journal of Geodesy

SUMMARY

This paper is devoted to the spherical and spheroidal harmonic expansion of the gravitational potential of the topographic masses in the most rigorous way. Such an expansion can be used to compute gravimetric topographic effects for geodetic and geophysical applications. It can also be used to augment a global gravity model to a much higher resolution of the gravitational potential of the topography. A formulation for a spherical harmonic expansion is developed without the spherical approximation. Then, formulas for the spheroidal harmonic expansion are derived. For the latter, Legendre's functions of the first and second kinds with imaginary variable are expanded in Laurent series. They are then scaled into two real power series of the second eccentricity of the reference ellipsoid. Using these series, formulas for computing the spheroidal harmonic coefficients are reduced to surface harmonic analysis. Two numerical examples are presented. The first is a spherical harmonic expansion to degree and order 2700 by taking advantage of existing software. It demonstrates that rigorous spherical harmonic expansion is possible, but the computed potential on the geoid shows noticeable error pattern at Polar Regions due to the downward continuation from the bounding sphere to the geoid. The second numerical example is the spheroidal expansion to degree and order 180 for the exterior space. The power series of the second eccentricity of the reference ellipsoid is truncated at the eighth order leading to omission errors of 25nm (RMS) for land areas, with extreme values around 0.5mm to geoid height. The results show that the ellipsoidal correction is 1.65m (RMS) over land areas, with maximum value of 13.19m in the Andes. It shows also that the correction resembles the topography closely, implying that the ellipsoidal correction is rich in all frequencies of the gravity field and not only long wavelength as it is commonly assumed.

VISIT THE SCIENTIFIC PUBLICATIONS REPORT ARCHIVE

ADDITIONAL ARTICLE

AUTHORS

M. Hale, **F. Thrower (NMFS/AFSC), E. Berntson (NMFS/NWFSC),** M. Miller, and **K. M. Nichols (NMFS/NWFSC)**

PUBLICATION DATE

Expected Publication Date: August 2013

TITLE

Evaluating adaptive divergence between migratory and nonmigratory ecotypes of a salmonid fish, Oncorhynchus mykiss

JOURNAL

Genes, Genomes, Genetics

SIGNIFICANCE

- This article illustrates the use of genome-wide SNPs for evaluating adaptive divergence between ecotypes of this specific salmonid.

SUMMARY

Next generation sequencing and the application of population genomic and association approaches have made it possible to detect selection and unravel the genetic basis to variable phenotypic traits. Using the two approaches in parallel is an especially attractive approach in non-models organisms that lack a sequenced and annotated genome, but only works well when population structure is not confounded with the phenotype of interest. Herein, we use population genomics in a non-model fish species, rainbow trout (*Oncorhynchus mykiss*), to better understand adaptive divergence between migratory and non-migratory ecotype, and to further our understanding about the genetic basis of migration. RAD tag sequencing was used to identify Single Nucleotide Polymorphisms (SNPs) in migrant and resident *O. mykiss* from two systems, one in Alaska and the other in Oregon, USA. A total of 7,920 and 6,755 SNPs met filtering criteria in the Alaska and Oregon, data sets respectively. Population genetic tests determined that 1,423 SNPs were candidates for selection when loci were compared between resident and migrant samples. Prior linkage mapping studies using RAD tag SNPs were available to determine the position of 1,990 markers. Several significant SNPs are located in genome regions that contain QTL for migratory related traits, reinforcing the importance of these regions in the genetic basis of migration/residency. Annotation of genome regions linked to significant SNPs revealed genes involved in processes known to be important in migration (such as osmoregulatory function). This study adds to our growing knowledge on adaptive divergence between migratory and non-migratory ecotypes of this species; across studies, this complex trait appears to be controlled by many loci of small effect, with some in common, but many loci not shared between populations studied.

VISIT THE SCIENTIFIC PUBLICATIONS REPORT ARCHIVE

ADDITIONAL ARTICLE

AUTHORS

J. T. Thorson (NMFS/NWFSC), J. M. Cope (NMFS/NWFSC), and **W. S. Patrick (NMFS/OSF)**

PUBLICATION DATE

Expected Publication Date: Winter 2013

TITLE

Evaluating the precision and accuracy of life history information in FishBase, a global fish database

JOURNAL

Ecological Applications

SIGNIFICANCE

- Globally-available life history information (e.g., growth, size, and natural mortality information) were collected and evaluated for their potential use in stock assessments and productivity assessments.
- This analysis showed that available life history data are generally unbiased, but that estimates from certain global data sets (i.e., FishBase) are less reliable.

SUMMARY

Single-species life history parameters are central to the research and management of environmental systems, and are increasingly stored in centralized and global databases. However, there has been little independent evaluation of the precision and accuracy of the values in these databases. We therefore develop a Bayesian error-in-variables model that compares database entries with estimates from local experts, and illustrate this process by comparing entries in FishBase, a global fish database, with life history estimates compiled by local experts through the U.S. We do not assume that local experts have perfect information, but instead that they have obtained unbiased parameter estimates on average. This model distinguishes biases among seven life history parameters, two types of information available in FishBase (i.e. published values, or those estimated from other parameters) and two taxa (i.e. bony vs. cartilaginous fishes) while accounting for additional variance caused by sex- and region-specific life history traits. For published values in FishBase, the model identifies a small positive bias in natural mortality and negative bias in life span, perhaps caused by unacknowledged fishing mortality. For values calculating from other parameters, the model identifies large and divergent biases. It also demonstrates greatest precision for body size parameters, decreased precision for values derived from geographically distant populations, and greatest between-sex differences in age at maturity. We recommend that parameter estimates be used in future error-in-variables models as a prior on measurement errors. We hope that this independent evaluation will be replicated for other global databases, and that it will encourage further development and improvements in FishBase, which remains an indispensible tool for marine research.

VISIT THE SCIENTIFIC PUBLICATIONS REPORT ARCHIVE

ADDITIONAL ARTICLE

AUTHORS

B. Jorgenson, E. Fleishman, **K. H. Macneale**, D. Schlenk, **N. L. Scholz, J. A. Spromberg**, I. Werner, D. P. Weston, Q. Xiao, T. M. Young, and M. Zhang **(NMFS/NWFSC)**

PUBLICATION DATE

Accepted: 1 August 2013

TITLE

Predicted transport pyrethroid insecticides from an urban landscape to surface water

JOURNAL

Environmental Toxicology and Chemistry

SIGNIFICANCE

- The authors developed a simple screening-level model of exposure of aquatic species (including salmon) to pyrethroid insecticides for the lower American River watershed (California, USA).
- This study is important because it helps us understand how emerging pesticides in California may influence salmon habitat quality.
- The model also accurately predicts how various mitigation methods will affect the concentration of the pesticides in the surface water, although the predicted concentration of some pyrethroid pesticides would continue to exceed chronic aquatic life criteria

SUMMARY

The model incorporated both empirically derived washoff functions based on existing, small-scale precipitation simulations and empirical data on pyrethroid insecticide use and watershed properties for Sacramento County, California. We calibrated the model to in-stream monitoring data and used it to predict daily river pyrethroid concentration from 1995 through 2010. The model predicted a marked increase in pyrethroid toxic units starting in 2000, coincident with an observed watershed-wide increase in pyrethroid use. After 2000, approximately 70% of the predicted total toxic unit exposure in the watershed was associated with the pyrethroids bifenthrin and cyfluthrin. Pyrethroid applications for above-ground structural pest control on the basis of suspension concentrate categorized product formulations accounted for greater than 97% of the predicted total toxic unit exposure. Projected application of mitigation strategies, such as curtailment of structural perimeter band and barrier treatments as recently adopted by the California Department of Pesticide Regulation, reduced predicted total toxic unit exposure by 84%. The model also predicted that similar reductions in surface water concentrations of pyrethroids could be achieved through a switch from suspension concentrate categorized products to emulsifiable concentrate categorized products without restrictions on current use practice. Even with these mitigation actions, the predicted concentration of some pyrethroids would continue to exceed chronic aquatic life criteria.

VISIT THE SCIENTIFIC PUBLICATIONS REPORT ARCHIVE

ADDITIONAL ARTICLE

AUTHORS

C. Ware, **D. N. Wiley (NOS/ONMS)**, A. S. Friedlaender, M. Weinrich, **E. L. Hazen (NMFS/SWFSC)**, A. Bocconcelli, S. E. Parks, A. K. Stimpert, **M. A. Thompson (NOS/ONMS)**, and K. Abernathy

PUBLICATION DATE

Expected Publication Date: August 2013

TITLE

Bottom side-roll feeding by humpback whales (Megaptera novaeangliae) *in the southern Gulf of Maine, U.S.A.*

JOURNAL

Marine Mammal Science

SIGNIFICANCE

- Synchronous motion and acoustic recording tags (DTAGs) were employed to provide the first detailed kinematic descriptions of humpback whales using bottom side-rolls (BSRs) to feed along the seafloor
- Three distinct classes of behavior were identified: simple side-roll, side-roll inversion, and repetitive scooping
- This behavior also leads to vulnerability to entanglement in bottom-set fishing gear, which is a major mortality factor for this species

SUMMARY

Humpback whales (*Megaptera novaeangliae*) are known for the variety and complexity of their feeding behaviors. Here we report on the use of synchronous motion and acoustic recording tags (DTAGs) to provide the first detailed kinematic descriptions of humpback whales using bottom side-rolls (BSRs) to feed along the seafloor. We recorded 3,505 events from 19 animals (individual range 8–722). By animal, mean BSR duration ranged from 14.1 s to 36.2 s.; mean body roll angle from 80º to 121º, and mean pitch from 7ºto 38º. The median interval between sequential BSRs, by animal, ranged from 24.0 s to 63.6 s and animals tended to maintain a consistent BSR heading during long BSR series encompassing multiple dives. BSRs were most frequent between 2200 and 0400. We identify three classes of behavior: simple side-roll, side-roll inversion, and repetitive scooping. Results indicate that BSR feeding is a common technique in the study area and there is both coordination and non-coordination between animals. We argue that this behavior is not lunge feeding as normally characterized, because animals are moving slowly through the event. The behavior also leads to vulnerability to entanglement in bottom-set fishing gear, a major mortality factor for the species.

VISIT THE SCIENTIFIC PUBLICATIONS REPORT ARCHIVE

ADDITIONAL ARTICLE

AUTHORS

S. Fuentes, G.H. Wikfors, and **S. Meseck (NMFS/NEFSC)**

PUBLICATION DATE

Accepted: 5 August 2013

TITLE

Silicon deficiency induces alkaline phosphatase enzyme activity in cultures of four marine diatoms

JOURNAL

Estuaries and Coasts

SIGNIFICANCE

- Alkaline phosphatase activity (APA) - important for growth - is widely used as an indicator of phosphate deficiency in phytoplankton.
- This study shows that other stressors, like silicon deficiency, can also activate alkaline phosphatase, so APA may indicate other important deficiencies, not just phosphate limitation.
- Therefore, alkaline phosphatase activity (APA) should be used cautiously as an indicator of phosphate limitation.

SUMMARY

Alkaline phosphatase (AP) was detected using ELF-97® in silicon-starved *Pseudo-nitzschia multiseries* cells, thus we tested two, alternative hypotheses: *Pseudo-nitzschia multiseries* has a high phosphate demand, showing signs of phosphate deficiency even when concentrations of orthophosphate are high, or silicate deficiency can stimulate the AP enzyme in this species. We also studied the effect of silicon deficiency on AP in three other common marine diatoms: *Thalassiosira pseudonana, Nitzschia pusilla,* and *Nitschia closterium.* Each of the species tested showed a different pattern of AP regulation. AP levels, however, increased in the four diatoms as a result of silicon deficiency, suggesting that AP may be involved in a variety of intracellular processes related to silicon deficiency. Additionally, the results of this study indicate that AP could be stimulated by stressors other than phosphate deficiency, such as silicon deficiency; therefore, it should be used cautiously as an indicator of phosphate limitation.

VISIT THE SCIENTIFIC PUBLICATIONS REPORT ARCHIVE

ADDITIONAL ARTICLE

AUTHORS

N.D. Weston, and **T. Soler (NOS/NGS)**

PUBLICATION DATE

Published: In 2013

TITLE

OPUS use in Alaska: a favored positioning tool from the north slope to the remote Aleutian Islands

JOURNAL

Proceedings for the 10th International Symposium on Cold Regions Development, held in Anchorage, Alaska June 2 to 5, 2013

SIGNIFICANCE

- This article discusses recent Continuously Operating Reference Stations (CORS) improvements performed in Alaska and the importance of keeping track of changing National Geodetic Survey (NGS) published coordinates.

SUMMARY

Since 2002, the National Geodetic Survey (NGS) has made available to the general engineering and surveying community a web-based GPS processing software named the Online Positioning User Service (OPUS). The popularity of this free service has steadily increased over time and Alaskan GPS users were no exception in quickly adopting this simple-to-use positioning tool. This article discusses recent CORS improvements performed in Alaska and the importance of keeping track of changing NGS published coordinates which is crucial to all GPS surveys in a region with crustal dynamics as active as Alaska. The status of the Continuously Operating Reference Stations (CORS) network in Alaska will also be reviewed. More CORS sites in the state will undoubtedly help the use of other newly developed versions of OPUS, such as OPUS-RS, OPUS-Net and OPUS-Projects. Each one of these flavors contains its own specific applications; therefore, they expand the OPUS arsenal with a variety of alternatives making the culmination of surveying engineering and mapping projects more user-friendly.

LINK TO PAPER

http://ascelibrary.org/doi/abs/10.1061/9780784412978.030

ADDITIONAL ARTICLE

AUTHORS

D.R. Bergfelt, B.G. Steinetz, J.S. Reif, A.M. Schaefer, G.D. Bossart, M.S. Mazzoil, and **P.A. Fair (NOS/NCCOS)**

PUBLICATION DATE

Accepted: 4 May 2013

TITLE

Evaluation of single-sample analysis of relaxin combined with progesterone to support pregnancy diagnosis in wild bottlenose dolphins (Tursiops truncatus)

JOURNAL

Aquatic Mammals

SIGNIFICANCE

- The present study provides preliminary results for hormonal diagnosis of pregnancy status in wild bottlenose dolphins based on single-sample analysis of progesterone and relaxin above (pregnant) or below (non-pregnant) respective baseline concentrations.
- Preliminary results indicated that relaxin may have limited value in pregnancy diagnosis when used alone. However, in combination with an elevation of progesterone in a single-sample analysis, a pregnancy-specific elevation of relaxin can clarify that progesterone is pregnancy-related.
- Thus, use of both hormones may have application in increasing certainty to support pregnancy diagnosis in wild animals for which only single samples can be collected.

SUMMARY

The present study is a preliminary evaluation of the potential for an elevation in relaxin to clarify an elevation of progesterone in wild bottlenose dolphins as pregnancy-related, since relatively high progesterone in a single-sample analysis is not necessarily pregnancy-specific. Blood samples were collected from adult female dolphins in estuaries of Charleston, SC and the Indian River Lagoon, FL. Serum progesterone and relaxin concentrations were analyzed in the same samples (n=74) with respective RIAs. Diagnosis of pregnancy was based on concentrations of progesterone and relaxin >6.0 and >11.2 ng/mL, respectively, whereas non-pregnancy was based on respective hormone concentrations less than or equal to baseline concentrations. Progesterone was observed at elevated concentrations considered diagnostic of pregnancy in 20 and relaxin in 12 dolphins. In a contingency table analysis with progesterone as the conventional standard for pregnancy diagnosis, there was a 60% positive correspondence with relaxin (12 relaxin- out of 20 progesterone-diagnosed pregnancies) and 40% negative correspondence (8 relaxin-diagnosed non-pregnancies out of 20 progesterone-diagnosed pregnancies). Kappa analysis indicated good agreement (κ= 74%) between relaxin- and progesterone-diagnosed pregnancies. Contingency table results were verified based on known pregnancies of 9 cow-calf pairs observed through photo-identification subsequent to health assessments. Concordance between hormone diagnosed and observed pregnancies was 9 of 9 (100%) for progesterone and 7 of 9 (78%) for relaxin. In conclusion, preliminary results indicated that relaxin may have limited value in pregnancy diagnosis when used alone. However, in combination with an elevation of progesterone in a single-sample analysis, a pregnancy-specific elevation of relaxin can clarify that progesterone is pregnancy-related and, thus, confirm the diagnosis of pregnancy in wild dolphins.

ADDITIONAL ARTICLE

AUTHORS

C. Do, R. Waples, D. Peel, M. Macbeth, B. Tillett, and J. Ovenden **(NMFS/NWFSC)**

PUBLICATION DATE

Accepted: 25 July 2013

TITLE

NeEstimator v2.0: re-implementation of software for the estimation of contemporary effective population size (Ne) from genetic data

JOURNAL

Molecular Ecology Resources

SIGNIFICANCE

- Effective population size (Ne) is one of the most important parameters in conservation and evolution but is difficult to estimate in natural populations.
- We have completely rewritten and updated the most popular software for estimating Ne based on genetic data.
- The new software includes several new methods and can handle the large genomics datasets (tens of thousands of genetic markers) now being produced for non-model species.

SUMMARY

NeEstimator v2.0 is a completely revised and updated implementation of software that produces estimates of contemporary effective population size, using several different methods and a single input file. NeEstimator v2.0 includes three single-sample estimators (updated versions of the linkage disequilibrium and heterozygote-excess methods, and a new method based on molecular co-ancestry), as well as the two-sample (moment-based temporal) method. New features include the following: 1) An improved method for accounting for missing data; 2) Options for screening out rare alleles; 3) Confidence intervals for all methods; 4) The ability to analyze datasets with large numbers of genetic markers (10,000 or more); 5) Options for batch processing large numbers of different datasets, which will facilitate cross-method comparisons using simulated data; and 6) Correction for temporal estimates when individuals sampled are not removed from the population (Plan I sampling). The user is given considerable control over input data and composition, and format of output files. The freely-available software has a new JAVA interface and runs under MacOS, Linux and Windows.

ADDITIONAL ARTICLE

AUTHORS

E. J. Ward (NMFS/NWFSC)

PUBLICATION DATE

Accepted: 1 July 2013

TITLE

Ecosystem metabolism and support of freshwater capture fisheries in the Tonle Sap Lake, Cambodia

JOURNAL

PLoS ONE

SIGNIFICANCE

- This study used a state-space oxygen mass balance model and continuous dissolved oxygen measurements from four locations to provide the first estimates of gross primary productivity (GPP) and ecosystem respiration (ER) for the Tonle Sap.
- Repeated hypoxia was observed at most sampling sites along with persistent net heterotrophy (GPP)
- Because the majority of fishing is indiscriminate (not targeting particular species), it may be that humans have shifted the food web toward smaller, faster growing species.

SUMMARY

The Tonle Sap Lake in Cambodia is a dynamic flood-pulse ecosystem that annually increases its surface area by over 600% with monsoon-driven rains and is part of one of the largest and most diverse freshwater fisheries in the world. This flooding is thought to structure many of the critical ecological processes, including aquatic primary and secondary productivity. The lake also has a large fishery that supports the livelihoods of nearly 2 million people. Management of fisheries is hindered by a lack of scientific knowledge, in particular ecological data relevant to fish production. We used a state-space oxygen mass balance model and continuous dissolved oxygen measurements from four locations to provide the first estimates of gross primary productivity (GPP) and ecosystem respiration (ER) for the Tonle Sap. GPP averaged 4.1 ± 2.3 g O2 m-3 d-1 with minimal differences among sites. There was a negative correlation between monthly GPP and lake level (r=0.45) and positive correlation with turbidity (r=0.65). ER averaged 24.9 ± 20.0 g O2 m-3 d-1 but had >6-fold variation among sites and minimal seasonal change. Repeated hypoxia was observed at most sampling sites along with persistent net heterotrophy (GPP). Because the livelihoods of millions of people depend on the fishery, understanding impacts of climate, dams, and humans on the ecosystem are extremely important (and extendable to other ecosystems).

VISIT THE SCIENTIFIC PUBLICATIONS REPORT ARCHIVE

ADDITIONAL ARTICLE

AUTHORS

J. O. Peterson, C. A. Morgan, and **W. T. Peterson**
(NMFS/NWFSC)

PUBLICATION DATE

Expected Publication Date: Fall 2013

TITLE

Seasonal and interannual variation in the extent of hypoxia in the northern California Current from 1998-2012

JOURNAL

Limnology and Oceanography

SIGNIFICANCE

- The presence and magnitude of hypoxia in the northern California Current varies seasonally and inter-annually.
- Hypoxic regions have covered up to 62% of the shelf (15,600 km2) in some years.

SUMMARY

This study addresses the occurrence, severity, and extent of hypoxia over the continental shelf of the northern California Current (40 – 48.5° N Latitude) from 1998 to 2012. Clear seasonal trends exist in the timing and duration of hypoxia. The highest bottom-water dissolved oxygen concentrations occurred from November to March, and levels below the 1.4 mL L-1 hypoxia threshold were detected during the upwelling season (May through October). Regions of hypoxia tended to occur north of 42°N latitude and were most severe over the widest areas of the continental shelf. Hypoxic waters covered up to 62% (15,600 km2) of the continental shelf during some years (2002, 2007, 2008), and < 10% in others (2003, 2010-2011). There are seasonal and inter-annual shifts in both the depth and oxygen content of upwelled waters. Years with the greatest extent and severity of hypoxia had the lowest concentration of dissolved oxygen in upwelling source waters. The dissolved oxygen concentration of source waters showed a gradual decline from 1998 through 2007, with a subsequent increase from 2008-2010 before leveling off in 2011 and 2012.

VISIT THE SCIENTIFIC PUBLICATIONS REPORT ARCHIVE

ADDITIONAL ARTICLE

AUTHORS

J. T. Thorson, M. D. Scheuerell, E. R. Buhle, and T. Copeland **(NMFS/NWFC)**

PUBLICATION DATE

Expected Publication Date: Fall 2013

TITLE

Spatial variability buffers temporal fluctuations in early juvenile survival for an endangered Pacific salmon

JOURNAL

Journal of Animal Ecology

SIGNIFICANCE

- We conclude that spatial diversity decreases interannual variability in juvenile salmon production, which suggests that conservation and restoration of spatial diversity will improve population persistence for this metapopulation.
- However, the exact magnitude of spatial buffering depends upon demographic parameters such as adult survival that may vary among populations, and is proposed as an area of future research using hierarchical life cycle models.
- We recommend that future sampling of this metapopulation employ a repeated-measure sampling design to improve estimation of early juvenile carrying capacity.

SUMMARY

Spatial, behavioral, and genetic diversity at relatively small scales can buffer species against large-scale processes such as climate change that tend to synchronize populations and increase temporal variability in overall abundance or production. This so-called portfolio effect generally results in improved biological and economic outcomes for managed species. Previous evidence for the portfolio effect in salmonids has arisen from examinations of time series of adult abundance, but we lack evidence of spatial buffering of temporal variability in demographic rates such as survival of juveniles during their first year of life. We therefore use density-dependent population models with multiple random effects to represent synchronous (similar among populations) and asychronous (different among populations) spatial variability as well as temporal variability in survival. These are fitted to 25 years of survey data for breeding adults and surviving juveniles from 15 demographically distinct populations of Chinook salmon (Oncorhynchus tshawytscha) within a single metapopulation in the Snake River. Model selection identifies the most support for a model that includes both synchronous and asynchronous temporal variability. Asynchronous variability (log-SD = 0.55) was approximately equal in magnitude to synchronous temporal variability (log-SD = 0.67), but much lower than spatial variability (log-SD = 1.11). We therefore find evidence for spatial buffering of temporal variability in early juvenile survival, although between-population variability that persists over time is also large.

VISIT THE SCIENTIFIC PUBLICATIONS REPORT ARCHIVE

AUTHORS

R. Sprague, **C. Littnan,** and **J. Walters (NMFS/PIFSC/PIRO)**

PUBLICATION DATE

Published: August 2013

TITLE

Estimation of Hawaiian monk seal consumption in relation to ecosystem biomass and overlap with fisheries in the main Hawaiian Islands

JOURNAL

NOAA Technical Memorandum-NMFS-PIFSC

SIGNIFICANCE

- Current data indicate that monk seals in the main Hawaiian Islands do not have greater effects on other species in the ecosystem than do other apex predators or fisheries.
- Authors estimate that the current population of ~200 Hawaiian monk seals in the main Hawaiian Islands consumes ~1300 kg/day, which is a maximum of 0.009% of the estimated available prey biomass.
- Recreational and commercial fisheries in the main Hawaiian Islands (excluding pelagic species) are estimated to land ~3 times more nearshore marine resources than are consumed by monk seals.

SUMMARY

As the Hawaiian monk seal population has increased in the main Hawaiian Islands (MHI), it has resulted in increased marine resource use overlap between monk seals and commercial, recreational, and subsistence fisheries. This has understandably led to questions and concerns about the potential impact of Hawaiian monk seals on the nearshore ecosystem and in particular, on populations of marine species consumed by humans. In this analysis, the authors estimated food consumption by the current Hawaiian monk seal population in the MHI. To put this consumption into context, they also estimated biomass of nearshore fishes, including apex predators, herbivores, secondary consumers, and planktivores, and the biomass consumption by apex fish predators and humans (i.e., fishery landings). Finally, they compared the families of fish found in the monk seal diet and those targeted by fisheries. They estimate that the current population of about 200 Hawaiian monk seals in the MHI consumes around 1300 kg/day (2900 lbs/day, or about 15 lbs/day per seal), which is a maximum of 0.009% of the estimated available prey biomass. The biomass of apex predatory fish in the MHI nearshore marine ecosystem is estimated to be more than 80 times the biomass of the Hawaiian monk seal population, and apex predatory fish likely consume at least 50 times more biomass daily than the monk seal population. Recreational and commercial fisheries in the MHI (excluding pelagic species) together are estimated to land ~ 3 times more nearshore marine resources than are consumed by monk seals. An estimated 27% of commercial fishery landings and 39% of recreational fishery landings (by weight, excluding pelagic species) are from fish families found in the monk seal diet.

LINK TO PAPER

http://www.pifsc.noaa.gov/library/pubs/tech/NOAA_Tech_Memo_PIFSC_37.pdf