PROCEEDINGS OF THE 71ST ANNUAL TUNA CONFERENCE

**Using New Technologies to Update and Validate Life History Studies:
The Times They Are a Changin'**

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Owyn E. Snodgrass – Chair
Stephanie Flores – Coordinator

This year's cover image was taken by Helena Aryafar (Southwest Fisheries Science Center, 2016).

PREFACE

Welcome to the 71ˢᵗ Annual Tuna Conference. The goal of the Tuna Conference is to provide an open and informal forum for scientists, engineers, managers, fishermen, non-governmental organizations and other interested parties from around the world to exchange information and ideas including recent research findings on tunas and "tuna-like" species. The free and open exchange of ideas is key to the Conference's success.

The theme for this year's Tuna Conference will be "Using new technologies to update and validate life history studies: The times they are a changin'." Technologies, fisheries, and marine environments are constantly undergoing change. Subtle changes in life history characteristics and data collection methods can have large impacts on stock assessments that are reliant on accurate and current data. In addition, the dynamics of our marine environments are under constant change from both anthropogenic and natural influences. Despite living in an ever-changing world, many important fisheries management institutions rely on biological or genetic information that may be outdated because they do not account for recent changes or rely on older methods that can now be validated, and/or require time-intensive data collection methods that could benefit from application of improved technologies. Validation of basic life history parameters is important if we strive to provide and produce sound, undeniable, and unbiased science that is incorporated into stock assessment and management decisions. This conference will explore the application of new methods and technologies to collect, update, and validate biological and genetic information on large pelagics who now live in an ever-changing marine environment.

Many of the oral and poster presentations at this year's conference directly relate to the theme and, as always, there is a diverse and interesting series of presentations on the agenda. Over the course of the next three days, there will be 43 oral presentations across 4 sessions. We also have an additional 7 presentations in the poster session. Special thanks to Laurie Barak for her help with the virtual logistics and this year's session moderators: Joseph M. O'Malley, Kelsey James, Tim (Chi H.) Lam, Suzy Kohin, Bryan Keller, Charles Villafana, Catherine Purcell, and John Hyde. We sincerely appreciate their efforts to keep sessions running smoothly.

The abstracts for the oral and poster presentations contained in the Proceedings abstracts are listed as presented. Bold lettering denotes the author giving the presentation. All abstracts are considered reports of preliminary work. If readers are interested in the information presented in the abstracts, they should contact the author(s) directly. No abstract should be cited without prior consent from the author(s).

Several presentations this year will include the scholarship winners from the 2020 Tuna Conference, which was ultimately cancelled due to the Covid pandemic. Many thanks to Leanne Fuller, Kelsey James, Jeanne Wexler, Nick Wegner, John Hyde, and Enrique Mauser for helping to review the 2020 ~ 2021 student application packages. The *Tuna Conference Scholarship* was awarded to Nan Himmelsbach for her talk titled "DNA metabarcoding of stomach contents to assess the diet of bigeye opah (*Lampris megalopsis*) and smalleye opah (*Lampris incognitus*) in Hawaii." A *Manuel Caboz Memorial Scholarship* was awarded to Ryan Logan for his talk titled "High resolution post-release behavior and recovery periods of two highly prized recreational sportfish: blue marlin and sailfish." A *Manuel Caboz Memorial Scholarship* was awarded to Pavel Dimens for his talk titled "Ongoing efforts to understand the tunas in the Western Atlantic Ocean using genomic tools." Géraldine Pérez received the *Wildlife Computers Scholarship* for her talk titled "Impact on tropical tunas ecology of the massive deployment of Fish Aggregating Devices (FADs) by tuna fishery vessels: a modeling approach." Mitchell Lovell received the *American Fisherman's Research Foundation Scholarship* for his talk titled "Seasonal variations in the feeding ecology of yellowfin tuna (*Thunnus albacares*) in the northern Gulf of Mexico."

In addition to support for student scholarships and travel, under normal circumstances, the Tuna Conference benefits from generous donations to support the various "social" functions such as the Sushi Social/Poster
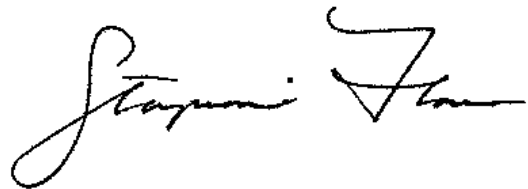
Session, the Tuna Barbecue and Tavern get-togethers. We thank all our past and future donors and look forward to the time when we will be able to resume "normal" functions at the UCLA Conference Center in Lake Arrowhead.

Thanks to graphic designer Chris Patnode put her invaluable help on the Tuna Conference website to make information available to everyone. Finally, our deepest thanks to JoyDeLee Marrow for continuously providing support and guidance through the years; she is an invaluable source to the legacy of the Tuna Conference.

In closing, we would like to thank you all for participating in the first ever virtual Tuna Conference. It is the quality of your presentations and camaraderie that make the Tuna Conference such a great event. We hope you are all well and navigating these unprecedented times safely, and we look forward to seeing you in person next year at the 72nd Tuna Conference!

Owyn Snodgrass
71st Tuna Conference Chair

Stephanie Flores
71st Tuna Conference Coordinator

71st TUNA CONFERENCE AGENDA

Tuesday, 18 May 2021

12:00   Welcome and Introduction

SESSION 1: Life History (Moderator: Joseph M. O'Malley)

12:10   Bombs and Fish – Extending the utility of bomb radiocarbon dating to recently collected pelagic fishes – **Allen H Andrews**, Kei Okamoto, and Keisuke Satoh

12:25   Use of epigenetic markers to estimate billfishes and albacore tuna age– **Louise Helary**, and Marie Roumagnac, Blandine Brisset, Hugues Evano, Jérémie Chanut, Anne-Elise Nieblas, Tristan Rouyer, Serge Bernard, Vincent Kerzerho, Hugues Parrinello, Yann Guiguen, Sylvain Bonhommeau

12:40   Evaluating otolith increment deposition rates in Atlantic Ocean bigeye and yellowfin tuna tagged during the Atlantic Ocean Tropical Tuna Program – Kyne Krusic-Golub, and **Lisa Ailloud**

12:55   Preliminary results of age and growth of California yellowtail (*Seriola dorsalis*) caught in waters of Baja California Sur – **Ulianov Jakes-Cota**, and Sofía Ortega-García, Rubén Rodríguez-Sánchez

13:10   Assessing residency and movement dynamics of Swordfish (*Xiphias gladius*) in the eastern north Pacific Ocean using Stable Isotope Analysis – **Tatiana A. Acosta-Pachón**, Sofía Ortega-García, Brittany Graham

13:25   Larval Atlantic bluefin tuna dispersal in the Gulf of Mexico estimated using octapy, a particle tracking program – **Jason D. Tilley**, James S. Franks, Donald R. Johnson, Barbara A. Muhling, G. Walter Ingram, Jr., Estrella Malca, Dyan P. Gibson, and Anish Narayanan

POSTER SESSION 1: Life History

13:40   Effect of trophic position on daily growth of *Thunnus thynnus* and *Auxis rochei* larvae From the Shelf/ Slope of the Spanish coast – **José María Quintanilla**, Raúl Laiz-Carrión, Ricardo Borrego, Alberto Pastor, Patricio Ahumada, and Alberto García

13:45   Interannual variability of maternal isotopic niche of Atlantic Bluefin Tuna (*Thunnus Thynnus*) estimated by the isotopic signatures of Preflexion larvae of the Gulf of Mexico – **Raúl Laiz-Carrión**, José María Quintanilla, Estrella Malca, Trika Gerard, Rasmus Swalethorp, Mike Stukel, Michael R. Landry, John Lamkin, and Alberto García

13:50   Where do the billfish go? Using recreational catch data to inform local and climate-driven environmental preference – **Danielle Haulsee**, Hannah Blondin, Ryan Logan, and Larry B. Crowder

SESSION 1 continued: Life History (Moderator Kelsey James)

14:00 A metabarcoding of stomach contents to assess the diet of Bigeye Opah (*Lampris megalopsis*) and Smalleye Opah (*Lampris incognitus*) in Hawaii – **Nan Himmelsbach***, Mark Renshaw, and Matthew Iacchei
* Tuna Conference Scholarship

14:15 Seasonal variations in the feeding ecology of yellowfin tuna (*Thunnus albacares*) in the northern Gulf of Mexico – **Mitchell Lovell***, and Michael A. Dance
*American Fisherman's Research Foundation Scholarship

14:30 Variable Atlantic bluefin tuna larval growth in the Gulf of Mexico: Importance of preferred prey – **Estrella Malca**, Akihiro Shiroza, Trika Gerard, Raul Laiz-Carrion, Jose M. Quintanilla, Taylor Shropshire, John Lamkin, Michael R. Landry, Mike Stukel, and Rasmus Swalethorp

14:45 Some like it hot, hungry tunas do not! Implications of temperature and plankton food web dynamics on growth and diet of tropical tuna larvae – **Miram Gleiber**, Su Sponaugle, and Robert Cowen

15:00 Trade-offs between risks of predation and starvation in larvae make the shelf break an optimal spawning location for Atlantic Bluefin tuna – **Taylor A. Shropshire**, Steven Morey, Eric P. Chassignet, Mandy Karnauskas, Victoria J. Coles, Estrella Malca, Raúl Laiz-Carrión, Øyvind Fiksen, Patricia Geglero, Akihiro Shiroza, José M. Quintanilla Hervas, Trika Gerard, john T. Lamkin, Michael R. Strukel

15:15 DNA methylation age predictors for fish – **Benjamin Mayne**, and Oliver Berry, Campbell Davies, Jessica Farley, and Simon Jarman

15:30 New otolith-based age estimates of Bigeye Tuna in the Western and Central Pacific and their impacts on stock status – **Jessica Farley**, Kyne Krusic-Golub, Naomi Clear, Paige Eveson, Francois Roupsard, Caroline Sanchez, Berry Muller, Bradley Phillips, John Hampton, and Simon Nicol

15:45 Close Day One

Wednesday, 19 May 2021

12:00 Open Day Two

SESSION 2: Tagging (Moderator: Tim (Chi H.) Lam and Suzy Kohin)

12:05 Satellite tagging of billfish around the Indian Ocean – **Anne-Elise Nieblas**, S. Bonhommeau, S. Bernard, B. Brisset, M. Bury J. Chanut, R. Coelho5, Y. Colas, H. Evano2, C. Faure7, G. Hervé, V. Kerzerho, Big Game Fishing Réunion, and T. Rouyer

12:20 Tag and release with a difference: a pilot propagation programme for Atlantic Bluefin tuna (*Thunnus thymus*) in Malta **– Christopher R Bridges**, Dimitra Nousdili2, Sarah Kranz-Finger2, Florian Borutta, Stephan Schulz, Shukry Na'amnieh, Robert Vassallo-Agius, Mark Psaila, and Salvu Ellul

12:35 New low-cost electronic tags for marine species using LoRa transmission – **Sylvain Bonhommeaua**, Serge Bernard, Blandine Brisset, Jérémie Chanut, Titouan Etienne, Hugues Evano, Julien Fezandelle, Geoffrey Fournier, Pierre Gogendeau, Andrea Goharzadeh, Vincent Kerzerho, Laurent de Knyff, Anne-Elise Nieblas, Fabien Soulier, Michel Renovell, Tristan Rouyer, Virgil Taillandier

12:50 High resolution post-release behavior and recovery periods of two highly prized recreational sportfish: blue marlin and sailfish – **Ryan Logan*** and Jeremy J. Vaudo, Bradley M. Wetherbee, Christopher G. Lowe, Mahmood S. Shivji
*Manuel Caboz Scholarship

13:05 Movement patterns, utilization distributions, and mixing rates of yellowfin tuna tagged and released with archival tags in six discrete areas of the eastern and central Pacific Ocean – **Kurt M. Schaefer**, and Daniel Fuller

13:20 Horizontal and vertical movements of electronically tagged blue sharks in the Eastern North Pacific Ocean– **Nicole Nasby-Lucas**, Heidi Dewar, Oscar Sosa-Nishizaki, James Wraith, Owyn Snodgrass, John Hyde, Russ Vetter, Jackie King, Barbara Block, Dave Holts, and Suzanne Kohin

13:35 Understanding the movement patterns and incidental mortality rate of bigeye thresher sharks (*Alopias superciliosus*) following capture in a developing deep-set fishery off California – **Scott Albers**, Mike Wang, and Chugey Sepulveda

13:50 Tagging reveals behavioral and habitat partitioning of Atlantic bluefin tuna *Thunnus thynnus*; implications for stock-specific management – **Simon Dedman**, Aalto, E., Stokesbury, M., Schallert, R., Castleton, M., and Barbara. A. Block

POSTER SESSION 2: Tagging

14:05 Biologging: revealing the environmental ecology of yellowfin, bigeye tuna and swordfish in the Western Indian ocean – **Evgeny Romanov**, Philippe S. Sabarros, Loïc Le Foulgoc, Adrien Chevallier & Pascal Bach

14:10 Billfish satellite tracking in the Eastern Tropical Pacific allows inference into horizontal and vertical habitat distributions – **Hannah Blondin,** Danielle Haulsee, Elliott Hazen, & Larry B. Crowder

SESSION 2 continued: Tagging (Moderator: Suzy Kohin)

14:15 Connectivity of striped marlin from the central North Pacific Ocean – **Tim (Chi H.)** Lam, Clayward Tam, and Molly E. Lutcavage

14:30 Estimating Natural Mortality in Atlantic Bluefin Tuna with Electronic Tags – **Barbara A. Block,** Becky Whitlock, Robert Schallert and Mike Stokesbury

14:45 Insights into the horizontal movements, migration patterns and stock affiliation of California swordfish – **Chugey Sepulveda**, M. Wang, and S.A. Aalbers

SESSION 3: Modelling, Management, and Monitoring (Moderator: Bryan Keller)

15:00 Review of research activities conducted at the IATTC's Achotines Laboratory from 2019-2021 – **Daniel Margulies**, Vernon Scholey, Susana Cusatti, Enrique Mauser, and Jeanne Wexler

15:15 Environmental preferences and size structure of the silky shark (*Carcharhinus falciformis*) captured by the longline fleet operating in the Mexican Central Pacific– **Natalia Melgar-Martínez**, Sofía Ortega-García, Heriberto Santana-Hernández, and Ulianov Jakes-Cota

15:30 Impact of environmental variability originated by the ENSO on wahoo (*Acanthocybium solandri*) spatial-temporal distribution in the Eastern Tropical Pacific Ocean – **Ramon Cuellar-Peña**, Sofía Ortega-García, and Raúl O. Martínez-Rincón

15:45 How many drifting Fish Aggregating Devices sustain the world largest tuna fishery? – **Lauriane Escalle**, Steven R. Hare, Tiffany Vidal, Maurice Brownjohn, Paul Hamer, and Graham Pilling

16:00 Close Day Two

Thursday, 20 May 2021

12:00 Open Day Three

SESSION 3 continued: Modelling, Management, and Monitoring (Moderator: Charles Villafana)

12:05 Impact on tropical tunas ecology of the massive deployment of Fish Aggregating Devices (FADs) by tuna fishery vessels: a modeling approach – **Géraldine Pérez***, Laurent Dagorn, Jean-Louis Deneubourg, and Manuela Capello
*Wildlife Computers Scholarship

12:20 Management options for reducing dFAD loss and beaching – **Taha Imzilen**, Christophe Lett, Emmanuel Chassot, and David M. Kaplan

12:35 Population genomics for improving management of Indian Ocean bigeye and skipjack tunas and Atlantic bluefin tuna – **Naiara Rodriguez-Ezpeleta**, Natalia Díaz-Arce, Igaratza Fraile, Francis Marsac, Fahmi Z, Campbell R. Davies, Hilario Murua, and Haritz Arrizabalaga

12:50 Comparison of U.S. Pacific Bluefin Tuna Length Sampling Programs: 2014-2020 – **Kelsey C. James**, Liana N. Heberer, and Heidi Dewar

13:05 Driving transparency & sustainability through electronic monitoring – **Craig Heberer and David Itano**

SESSION 4: Genetics and Stock Structure (Moderator: John Hyde and Catherine Purcell)

13:20 Stock-of-origin catch estimation of Atlantic bluefin tuna (*Thunnus thynnus*) based on observed spatial distributions – **Emilius A Aalto**, Francesco Ferretti, Matthew V Lauretta, John F Walter, Michael J W Stokesbury, Robert J Schallert, and Barbara A Block

13:35 Taking Stock of the Population Genetic Structure of Striped Marlin, *Kajikia audax*, in the Central North Pacific Ocean – **Jackson L. Martinez**, Jan R. McDowell, and John E. Graves

POSTER SESSION 3: Genetics and Stock Structure

13:50 Support for the Slope Sea as a major spawning ground for Atlantic bluefin tuna: evidence from larval abundance, growth rates, and particle-tracking simulations – **Christina M. Hernandez**, David Richardson, Irina Rypina, Ke Chen, Katrin Marancik, Kathryn Shulzitski, and Joel Llopiz

13:55 Population genetic structure of mobula rays in the Eastern Pacific Ocean using tuna purse seine bycatch– **Melissa R. Cronin**, Giacomo Bernardi, Michel Guerrero, Jon Lopez, Joshua D. Stewart, and Donald A. Croll

SESSION 4 continued: Genetics and Stock Structure (Moderator: John Hyde and Catherine Purcell)

14:00 Ongoing efforts to understand the tunas in the Western Atlantic Ocean using genomic tools – **Pavel Dimens*** and Eric Saillant
*Manuel Caboz Scholarship

14:15 Adaptive markers distinguish North and South Pacific Albacore amid low population differentiation – **Kathleen G. O'Malley**, Felix Vaux, John R. Hyde, and Sandra Bohn

14:30 PSTBS-IO project: an Indian Ocean basin scale study of population structure of tuna, billfish and sharks. – **Campbell Davies**, Francis Marsac, Hilario Murua, Zulkarnaen Fahmi, Igaratza Fraile, and many others.

14:45 SNP data reveals population structure and connectivity of four key tuna species (albacore, bigeye, skipjack, and yellowfin) fished in the Atlantic, Indian and Pacific oceans – **Peter M. Grewe**, Wudianto, C.H. Proctor, M.S. Adam, A.R. Jauhary, K. Schafer, D. Itano, M.Taufik, J. Hyde, A. Killian, S. Foster, T. Gosselin8, P. Feutry, J. Aulich, R. Gunasekera, M. Lansdell, J. Farley, Mark Fitchett, Joe O'Malley, N. Nikolic, Z. Fahmi, F. Marsac, H.Murua, and C.R. Davies

15:00 Life-history information from Close-Kin Mark-Recapture – **Mark Bravington**

15:15 Close kin mark recapture estimates of abundance for Australian and New Zealand white sharks – Richard Hillary, **Toby Patterson**, Rasanthi Gunasekera, Pierre Feutry, Russell Bradford, Clinton Duffy, Malcolm Francis, Paul Butcher, and Barry Bruce

15:30 Including Close-Kin Mark-Recapture in stock assessments: the Southern Bluefin tuna experience – **Rich Hillary**

15:45 Close Day Three ~ Final Remarks

Abstracts

BOMBS AND FISH – EXTENDING THE UTILITY OF BOMB RADIOCARBON DATING
TO RECENTLY COLLECTED PELAGIC FISHES

Allen H Andrews, PhD[1], Kei Okamoto, PhD[2], Keisuke Satoh, PhD[2], Jessica Farley[3]

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[2]National Research Institute of Far Seas Fisheries, Japan
[3]CSIRO Oceans and Atmosphere, Australia

Pelagic fishes of the tropics are aged using a variety of methods including counts of daily increments and annual growth zones in otoliths or other calcified structures. Some species are being aged beyond the typical lifespan estimates derived from daily increments, and otolith-based annual age reading methods provide estimates approaching and even exceeding 20–30 years. These older ages were supported with bomb radiocarbon (^{14}C) dating for yellowfin (*Thunnus albacares*) and bigeye (*T. obesus*) tuna in the western North Atlantic - Gulf of Mexico. This study exemplifies the extended utility of this age validation method by using the post-peak ^{14}C decline to validate ages for recently collected fishes with shorter lifespans. This method harbors great potential for pelagic tropical and subtropical fishes as various ^{14}C records (typically hermatypic coral) are beginning to converge in recent times, as was demonstrated in a fortuitous study of a 20-year-old blue marlin (*Makaira nigricans*) in the Pacific. At present, the use of the post-peak decline is being explored for tropical tuna of the western and central South Pacific and new coral records across the Pacific support its utility as a temporal reference. Furthermore, 120 young-of-the-year yellowfin and bigeye from the Pacific have been selected from this region covering the post-peak years of 1990 to 2018, to create a verifiable reference that can be compared to ^{14}C measurements from otolith core material (within first year of growth) of aged adults. This line of work holds promise for many other marine organisms of tropical-subtropical seas where questions of age, growth and lifespan remain unanswered.

USE OF EPIGENETIC MARKERS TO ESTIMATE BILLFISHES AND ALBACORE TUNA AGE

Louise Helary[a], Marie Roumagnac[a], Blandine Brisset[a], Hugues Evano[a], Jérémie Chanut[b], Anne-Elise Nieblas[b], Tristan Rouyer[c], Serge Bernard[d], Vincent Kerzerho[d], Hugues Parrinello[e], Yann Guiguen[f], Sylvain Bonhommeau[a]

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[b] COOOL - 61 rue Haute - 97436 Saint Leu - La Réunion
[c] IFREMER MARBEC - av. Jean Monnet 34200 Sète - France
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Sex and age information are critical for fish stock assessment. These information are however difficult to access in the field. Sex identification is based on gonads observation and age determination on reading of otoliths. There is a lack of availability for these tissues which are mostly absent from the fish landed in port. Moreover, for age determination even if otoliths are available, this method is time consuming, expensive with an accuracy issues. Epigenetic has been used recently to determine age of multiple species (fish, mammals, birds) as well as sex. Some studies have also show that epigenetic could be used as an indicator of adaptive divergence and rapid evolutionary response across populations. FLOPPED and TALE projects have both the objective of facilitate information acquirement by using epigenetic in order to obtain age, sex and population structure for billfish and albacore with one sample of muscle or skin. A first pilot study has been done to observe the methylation across DNA of 3 swordfish. Results showed a higher global methylation than mammal species demonstrating methylation presence and the possibility of their use to further study. To date, we have begun to search methylation marks on the DNA of 120 swordfishes to identify age, sex and population structure from them. Later, we will do the same work with albacore tunas and other billfish species (sailfish and marlins) in Indian ocean. At the end, the assessment of multiple parameters needed to estimate stock size will be simplified and may lead to an accurate evaluation of these stocks in the Indian ocean.

EVALUATING OTOLITH INCREMENT DEPOSITION RATES IN ATLANTIC OCEAN BIGEYE AND YELLOWFIN TUNA TAGGED DURING THE ATLANTIC OCEAN TROPICAL TUNA TAGGING PROGRAM.

Kyne Krusic-Golub[1] and **Lisa Ailloud**[2]

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[2]National Marine Fisheries Service, Southeast Fisheries Science Center

The Atlantic Ocean tropical Tuna Tagging Program (AOTTP) provided a unique opportunity to directly validate the otolith increment deposition rates for two important species of tropical tuna. Here we present results on the analysis of a number of bigeye tuna (*Thunnus obesus*) and yellowfin tuna (*Thunnus albacares*) otoliths recovered from samples previously marked with oxytetracycline during a large-scale tag-recapture program run by the AOTTP. Total age and time at liberty were estimated using conventional methods for counting larger macro-increments (presumed annual) and micro-increments (presumed daily) in transverse sections. The counts of annual increments resulted in greater estimates of age than the counts of micro-increments for samples greater than about 55 cm straight fork length at recovery. When compared to known time at liberty, the results indicated that age estimates based on presumed daily increments lead to underestimation of age, while annual increments appeared deposited on an annual basis. Ageing fish accurately is particularly important in the context of tropical tuna stock assessments where data on age and growth play an increasingly important role in informing the population dynamics of the stock.

PRELIMINARY RESULTS OF AGE AND GROWTH OF CALIFORNIA YELLOWTAIL (*Seriola dorsalis*) CAUGHT IN WATERS OF BAJA CALIFORNIA SUR

Ulianov Jakes-Cota[1], Sofía Ortega-García[1, *], Rubén Rodríguez-Sánchez[1,*]

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The California yellowtail *Seriola dorsalis* is a coastal pelagic species distributed in the Northeast Pacific from northern California, U.S.A. to Mazatlan, Sinaloa, Mexico, including the Gulf of California. It feeds mainly of small fish and cephalopods, reaching up to 150 cm fork length and up to 50 kg in weight. This species is captured with purse seine and trawl nets and with line and hook. It is highly prized in both commercial and sport fisheries and also is used in aquaculture in countries, such as Mexico where its sale is usually in fresh, so it is a species that contributes significantly to the economy throughout all its distribution range. Despite its high economic value, particularly in the Mexican Pacific and the Gulf of California, studies on its basic biology, such as age and individual growth parameters, are scarce. These data are the basis of stock assessment models and necessary for the sustainable use of resources. Therefore, this study shows preliminary results of age and individual growth of California yellowtail estimated by counting annual growth marks in sagittae otoliths. From January 2018 to March 2020, 411 organisms (165 males, 126 females and 120 not sexed) were sampled in Cabo San Lucas and La Paz, Baja California Sur. The fork length range for males and females was 43-125 and 36-121 cm, respectively. The length-weight relationship parameters indicated that growth of both males and females was not different from isometric growth. Seven age groups (3 - 9) were sampled, where 4 to 6 were the most abundant. In size-age data, three models of individual growth were adjusted (von Bertalanffy, Gompertz and Logistic), according to the Akaike information criterion values, von Bertalanffy model is the one that better describes individual growth of the species (L_∞ = 123.89, k = 0.14 and t_0 = -0.81).

ASSESSING RESIDENCY AND MOVEMENT DYNAMICS OF SWORDFISH (*Xiphias gladius)* IN THE EASTERN NORTH PACIFIC OCEAN USING STABLE ISOTOPE ANALYSIS

Tatiana A. Acosta-Pachón[1*], Sofía Ortega-García[2], Brittany Graham[3]

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Swordfish are migratory fish that inhabit tropical to temperate waters, but little is known about movement patterns or mixing between subpopulations of this species. This study examines carbon ($\delta^{13}C$) and nitrogen ($\delta^{15}N$) stable isotope ratios in growth rings of the anal fin spine and muscle tissue of swordfish from 3 different areas of the Eastern North Pacific Ocean (ENPO)—off Baja California Sur (Mexico) and California (USA), and in the North Pacific Subtropical Gyre (NPSG)—to assess swordfish movements between these areas. The analysis of $\delta^{13}C$ and $\delta^{15}N$ revealed no relationship between fish size and $\delta^{15}N$, suggesting a consistent consumption of prey items by this species over time. Differences between the anal fin spine and muscle were found, but interpreting these isotopic differences requires information on tissue-specific isotope turnover rates. The spatial pattern suggests that swordfish populations from these areas in the ENPO exhibit a relatively unexpected homing behavior at the temporal scale, according to anal spine and muscle turnover rates. Our findings support that swordfish may show site fidelity, which has important implications for their management and stock assessments.

LARVAL ATLANTIC BLUEFIN TUNA DISPERSAL IN THE GULF OF MEXICO ESTIMATED USING OCTAPY, A PARTICLE TRACKING PROGRAM

Jason D. Tilley[1], James S. Franks[1], Donald R. Johnson[1], Barbara A. Muhling[2,3], G. Walter Ingram, Jr.[4], Estrella Malca[5,6], Dyan P. Gibson[1], and Anish Narayanan[7]

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Larval Atlantic bluefin tuna *Thunnus thynnus* were collected from the Gulf of Mexico to address uncertainties in assessments of the stock. To improve understanding of environmental drivers of recruitment, a particle tracking package, octapy (Ocean Connectivity and Tracking Algorithms in Python), was developed in the Python programming language to estimate larval dispersal and adult spawning locations. The model used 1/25° Hybrid Coordinate Ocean Model (HYCOM) data as inputs with diffusion following a Lagrangian stochastic model. Model performance was validated using skill scores calculated against satellite-tracked mixed-layer drifter trajectories. Skill scores varied by region with an average 3-day skill (s3) of 0.29 (min, 0.0; max 0.92). Using previously aged bluefin larvae (2008, n=25; 2009, n=14; 2010, n=45; 2012, n=138), three hindcast modeling scenarios were run with each particle having 50 replicates: a 2D model at 5 m, a passive 3D model, and a diurnal vertical migration model. Predicted spawning locations were similar among model scenarios, but mean larval dispersal velocities were highly variable among years (5-m surface model: 2008, 41.3 km day-1; 2009, 29.4 km day-1; 2010, 24.1 km day-1; 2012, 20.5 km day-1). Environmental histories were developed for each larva for future analysis of growth. Results suggest that spawned larvae may be retained in distinct hydrodynamic regimes that vary interannually and that adult spawning site selection has a greater effect on larval dispersal than larval vertical migration behavior.

EFFECT OF TROPHIC POSITION ON DAILY GROWTH OF *Thunnus thynnus* AND *Auxis rochei* LARVAE FROM THE SHELF/SLOPE OF THE SPANISH COAST (SW MEDITERRANEAN)

POSTER

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This study examines the relationship between larval growth and early life trophodynamics by analyzing the variability in otolith biometry and bulk stable isotope composition of Atlantic bluefin tuna, *Thunnus thynnus* (ABFT) and bullet tuna, *Auxis rochei* (BT) larvae collected during the ABFT spawning period. Both ABFT and BT larvae were concentrated along the shelf/slope waters along the Levantine coasts of Spain (southwestern Mediterranean). Larvae were collected during the MEDIAS acoustic survey on July 2011 by means of Bongo plankton tows using 90 cm squared mouth equipped with 1mm mesh during night time. Twenty three stations along the shelf/slope waters of the south Mediterranean coasts of Spain (from Cape La Nao to the Gulf of Vera, south of Cape Palos) were selected. A total of 154 postflexion larvae were analyzed: 74 ABFT and 80 BT within the same size range from 5 to 11 mm standard length (SL) for both species. No significant differences were observed in both temperature (T) and salinity (S) at 5 m and 100 m depth. Daily growth, otolith biometrics and trophic position (TP) were determined. Significant differences were observed in somatic (SL and dry weight, DW) and otolith biometrics (radius) variables between species (ANCOVA<0.05). BT showed higher somatic growth than ABFT and its higher growth potential is associated to larger otoliths. Growth variability was studied by a residual analysis, considering both SL and DW, in order to differentiate between optimum (BT+, ABFT+) and deficient (BT-, ABFT-) growth groups. In the interpopulation comparison BT showed higher TP (Mann-Whitney U Test <0.05) than ABFT. This result would relate faster growth with higher TPs. Moreover, this pattern is similar in the intrapopulation analysis between growth contrasted groups defined by the residual analysis. Optimum growth groups presented significantly higher TPs than the deficient ones (Multiple Comparisons z' values <0.05) for both species. Higher TPs values of BT could be associated to its early piscivorous feeding behavior in comparison with ABFT. On the other hand, within the same population, faster larvae would have the possibility to increase their prey size earlier in comparison with slower growing larval cohorts. Therefore, it can be postulated that higher TPs reflect the consequences of greater growth, in such manner that faster growing individuals are able to prey sooner on larger mesozooplankton organisms having higher trophic signatures. These results would imply direct trophic implications on apex species larval growth and survival and consequent recruitment processes with repercussion in management strategies. This study has been financed by ECOLATUN PROJECT CTM2015-68473-R (MINECO/FEDER) and IEO.

INTERANNUAL VARIABILITY OF MATERNAL ISOTOPIC NICHE OF ATLANTIC BLUEFIN TUNA (*Thunnus thynnus*) ESTIMATED BY THE ISOTOPIC SIGNATURES OF PREFLEXION LARVAE OF THE GULF OF MEXICO

POSTER

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The Gulf of Mexico (GOM) is the primary spawning ground for western Atlantic bluefin tuna (ABFT, *Thunnus thynnus* Linnaeus, 1758). ABFT larval studies have focused on distribution, habitat, and trophic ecology, thereby providing valuable early life history information for the rational management of the resource. In the present we use stable isotope analysis (SIA) of larval ABFT to estimate the breeder's isotopic signatures and further evaluate the larval trophic ecology. A maternal transmission model for ABFT combined with yearly specific growth models provided the estimates for the maternal nitrogen and carbon isotopic signatures derived from pre-flexion larvae $\delta^{15}N$ and $\delta^{13}C$ values. SIA of nitrogen and carbon were obtained for 37 and 46 preflexion ABFT larvae collected in the eastern GOM in 2017 and 2018 during the BLOOFINZ-GOM project. The maternal isotopic widths were estimated using a SIBER package (Stable isotope Bayesian ellipses) of SIAR (Stable Isotope Analysis in R). Higher maternal isotopic widths in 2018 suggesting differentiated trophic habits of ABFT breeders between years, with 2018 having a more generalist feeding behavior. Furthermore, maternal isotopic niche overlap between years was observed, indicating a similarity degree in dietary regimes. The Standard Ellipses Area (SEAc) together with trophic niche overlap suggests that although breeders utilize common feeding grounds, the isotopic baseline of the ecosystem is variable between years. These differences may result from variable arrival to the GOM spawning ground and differentiated demographics of ABFT schools. This innovative methodological approach to estimate the nutritional status of spawners from the isotopic signatures of their offspring opens new posibilities for understanding the influence of maternal contribution to larval condition, survival, and growth with a direct effect on recruitment. This study has been financed by ECOLATUN PROJECT CTM2015-68473-R (MINECO/FEDER) funded by the Spanish Ministry of Economy and Competitiveness and National Oceanic and Atmospheric Administration's RESTORE Program Grant.

WHERE DO THE BILLFISH GO?
USING RECREATIONAL CATCH DATA TO INFORM LOCAL
AND CLIMATE-DRIVEN ENVIRONMENTAL PREFERENCE

POSTER

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Recreational fisheries in the Eastern Tropical Pacific (ETP) have increased in popularity since the 1970's, contributing significantly to the economies of many Central American economies through eco-tourism. However, pelagic tropical gamefish face a number of direct and indirect anthropogenic threats which can affect population health and sustainability. Here, we use daily catch logs from three recreational fishing lodges in Guatemala, Costa Rica and Panama as records of change in blue marlin (*Makaira nigricans*) and sailfish (*Istiophorus platypterus*) sightings per unit effort (SPUE) over time. We compared time series of billfish SPUE to the El Niño Southern Oscillation (ENSO) Index and local oceanographic conditions (SST and chl *a*) using cross-correlational analysis to understand how changes in the availability of billfish to recreational fishers is related to environmental conditions at various time lags. Among the three regions, blue marlin were negatively correlated with the ENSO at time lags of 8-22 months, while sailfish were positively correlated with ENSO at time lags of 5-10 months. Cross-correlations with regional oceanographic conditions reflected the seasonal occurrence of these species in each of the three regions. In addition, by comparing catch per unit effort (CPUE) of these two species by the international longline fleet reported to the Inter-American Tropical Tuna Commission (IATTC), to SPUE from the recreational fishers, we show possible offshore movement of fish stocks during the 2016 warming event. In the absence of definitive formal population surveys for these two species, recreational fishing records provide an alternative way to monitor the occurrence of targeted species. Determining responses of these species to regional and ocean basin scale environmental conditions allow us to begin to distinguish the effects of natural variability in the environment, from direct anthropogenic impacts to medium-term (5-10+ years) population trends.

DNA METABARCODING OF STOMACH CONTENTS TO ASSESS THE DIET OF BIGEYE OPAH (*Lampris megalopsis*) AND SMALLEYE OPAH (*Lampris incognitus*) IN HAWAII

Tuna Conference Scholarship

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Bigeye (*Lampris megalopsis*) and smalleye (*L. incognitus*) opah are frequently caught on commercial deep-set tuna longline vessels in the North Pacific Subtropical Gyre. Previous studies have examined the diet of these fishes using traditional morphological techniques to identify prey items, finding opah prey primarily on fishes and squids in the epipelagic and mesopelagic zones. Many of the challenges regarding traditional observational techniques stem from the rigor of identifying fragments of soft-bodied organism and highly digested prey, resulting in classifying prey to family, or labeling as 'unknown'. DNA metabarcoding of stomach contents or feces has emerged as a complementary technique that allows a greater number of prey items to be identified to species than morphological identification alone. This study incorporates DNA metabarcoding to illustrate how utilizing a genetic approach to complement traditional morphological identification of prey may increase the number of organisms detected and identified to species. Stomachs from *L. megalopsis* and *L. incognitus* were collected from opah caught on deep-set tuna longline vessels and landed in Hawaii. Stomachs were dissected and undigested organisms were removed and identified to the lowest taxonomic level. The remaining stomach contents were homogenized and subsampled for DNA extraction. Extracted DNA was amplified at the cytochrome *c* oxidase subunit I (COI) and 12S regions and sequenced on an Illumina MiSeq. This study found that metabarcoding allows the detection of recently consumed prey items to species level even when an individual's stomach contains no distinguishable prey. Furthermore, this study highlights new prey items that have never been reported in opah diets to date. This study provides evidence that DNA metabarcoding expands the diversity of prey species identified and contributes additional life history information to highly migratory pelagic predators for which feeding cannot be directly observed.

SEASONAL VARIATIONS IN THE FEEDING ECOLOGY OF YELLOWFIN TUNA (*Thunnus albacares*) IN THE NORTHERN GULF OF MEXICO

American Fisherman's Research Foundation Scholarship

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Pelagic predators (e.g. tunas, billfish, sharks) play a significant role in the structure and function of marine ecosystems and a better understanding of the food web dynamics that influence predator distribution and movement is essential to improving spatial management and conservation of these species. Here, we employ complementary techniques (gut contents, DNA barcoding, & stable isotopes) to examine seasonal variability in the diets of yellowfin tuna (*Thunnus albacares*) from the northern Gulf of Mexico. Yellowfin tuna (n = 577) were sampled weekly from April 2019 – March 2020 from recreational charter landings and grouped into two size classes based on estimated size at sexual maturity (sub-adult: 70 – 100 cm & adult: 100 – 160 cm). While 114 unique taxa were documented in yellowfin tuna stomachs, prey assemblages varied by season and size class. Carangids (jacks), ommastrephid squids, exocoetids (flyingfishes), and hyperiid amphipods were among the most abundant and frequently encountered prey. Seasonal differences were characterized by squids and flyingfishes in the spring, juvenile fishes (carangids & scombrids) in the summer, coastal fishes during the fall, and an increased consumption of planktonic prey (amphipods & salps) in the winter. DNA barcoding proved to be an effective tool in reducing unidentified prey to < 8% by number. Furthermore, seasonal variability in bulk (white muscle) isotopic signatures (δ13C, δ15N, & δ34S) of yellowfin tuna were also observed. Sub-adult δ13C values were highest during the spring and lowest in the fall, while adult δ13C values were relatively consistent. Seasonal trends in δ15N and δ34S were observed in both size classes and inversely related, with low δ15N (high δ34S) values from late summer to fall and high δ15N (low δ34S) values during late winter/early spring. Finally, Bayesian mixing models were used to estimate the relative contributions of different prey sources (coastal fishes, oceanic fishes & squids, planktonic prey, and sargassum-associated prey) to yellowfin tuna isotopic signatures. Oceanic fishes and squid were the primary contributors to adult yellowfin tuna during all seasons (51.4 – 68.9%), while contribution estimates to sub-adults were seasonally variable. High contribution estimates from planktonic prey to sub-adult yellowfin tuna during summer (44.2%) was in agreement with observed winter peaks in amphipod consumption (~ 6 months for tissue turnover). Additionally, the contribution of coastal fish to sub-adult and adult yellowfin tuna was greatest during the spring (27.2% & 21.7%, respectively), which corresponded with heightened consumption of coastal prey during the fall. Our findings highlight the importance of a suite of seasonally abundant prey resources to yellowfin tuna populations in the northern Gulf of Mexico, and demonstrate the seasonal influence of migratory behavior, prey life cycles, the Mississippi River, and habitat (oil & gas platforms) to the utilization of both inshore and offshore prey resources by yellowfin tuna in this region.

VARIABLE ATLANTIC BLUEFIN TUNA LARVAL GROWTH IN THE GULF OF MEXICO: IMPORTANCE OF PREFERRED PREY

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Atlantic bluefin tuna (ABT) are commercially and ecologically important fish that spawn in the Gulf of Mexico (GoM). Larval GoM catches are routinely utilized to link habitat structure to recruitment variability of the western ABT stock by fisheries managers. Larval ABT growth is highly variable during the first weeks of life with unknown mechanisms that link growth to survival. We sampled ABT larval patches for 2-4 days and aged sagittal otoliths from each patch from 10-14 May, 2017 and 15-19 May, 2018. Age, diet and feeding environment were coupled to analyze early life trophodynamics obtained from stomach contents prey field and food limitation estimates. Growth rates were slightly faster in 2018 than 2017, however overall somatic growth was not significantly different between patches. Sagittal otolith microstructure measured from daily increment widths (μm) increased with age (days post hatch) and were larger for 2018 postflexion stages compared to 2017 ($p < 0.05$). In addition, food limitation varied, with 2017 being a more food-limited habitat compared to 2018. A generalized additive model (GAM) was used to relate the variability of observed recent otolith growth with feeding preferences in the GoM's food-limited environment. Our findings suggest that the 2018 ABT patch was in a less food-limited environment, and larvae were able to feed on nutritionally favorable prey, resulting in wider otolith increments during the postflexion stage. Differences between patches are discussed in the context of the BLOOFINZ-GoM project, with linkages to nutrient utilization and survival of older larvae. The observed faster postflexion growth reflected in the otolith increments may improve opportunities for survival during the highly vulnerable larval stages for ABT.

SOME LIKE IT HOT, HUNGRY TUNAS DO NOT! IMPLICATIONS OF TEMPERATURE AND PLANKTON FOOD WEB DYNAMICS ON GROWTH AND DIET OF TROPICAL TUNA LARVAE

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Restricted to low-productivity environments near their thermal maxima, larval tunas may be threatened by warming global temperatures, yet our understanding of how they are constrained is limited. We examined blackfin tuna (Thunnus atlanticus, presumptive) diet and growth in the context of their prey and predators in the Straits of Florida in 2 years with contrasting summer conditions: low temperature (26.7–28.3°C)–high prey and high temperature (28.4–29.0°C)–low prey. In the cooler, high-prey conditions, larvae had 30% faster growth (0.45 mm d−1), fuller guts from predominantly feeding on calanoid copepods, and were 10× more abundant, dominating the larval fish assemblage. In contrast, in warm, low-prey conditions fewer, younger, and slower-growing (0.35 mm d−1) T. atlanticus fed predominantly on nauplii and had less full guts. Modelling individual growth across years revealed that growth peaked at an optimum of 28.5°C (5°C below known thermal maxima in the field) and high densities of predators selectively consumed slower-growing larvae. Low-prey availability may reduce the thermal optima of larvae, as growth and survival are diminished when low prey and high temperature coincide. Our results illustrate the importance of considering food web dynamics with temperature when predicting the response of organisms to ecosystem variability, particularly ongoing climate change.

TRADE-OFFS BETWEEN RISKS OF PREDATION AND STARVATION IN LARVAE MAKE THE SHELF BREAK AN OPTIMAL SPAWNING LOCATION FOR ATLANTIC BLUEFIN TUNA

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Atlantic Bluefin tuna (ABT) (*Thunnus thynnus*) migrate long distances to spawn in Gulf of Mexico which suggests that this region provides unique advantages to offspring survival. To better understand how offspring survival varies within the region, a spatially-explicit, Lagrangian, individual-based model was developed to simulate dispersal and mortality of ABT early life stages during the spawning periods from 1993-2012. The model is forced with realistic spatiotemporally varying predator and prey fields generated by a recently developed biogeochemical model for the region. Model parameterizations are guided by extensive field measurements collected as part of the project BLOOFINZ-GoM (Bluefin Larvae in Oligotrophic Ocean Foodwebs: Investigating Nutrients to Zooplankton in the Gulf of Mexico). The model estimates that starvation is dominant source of mortality driven by an early critical period; however, survival is ultimately limited by elevated predation rates on older individuals. Across the 20-year simulation, larval survival varied by a factor of 2.7 suggesting that early life stage mortality may significantly contribute to ABT recruitment fluctuations. The modeling framework developed here provides a better understanding of factors that influence recruitment during early life stages of ABT and may be useful for better resolving the stock-recruitment relationship.

DNA METHYLATION AGE PREDICTORS FOR FISH

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Age is a fundamental life-history parameter and is used for a variety of purposes in wildlife and fisheries management, including growth assessment, determining survival probabilities, mortality rates, and sustainable harvest. For most fish lethal otolith-based approaches are the only practical approach to determining age. However, lethal methods may not be ideal for high-value and conservation sensitive species, and furthermore, otolith ageing can be labour intensive. In a growing number of species, DNA methylation has been shown to be predictive of age. These studies develop what is referred to as epigenetic clocks. Epigenetic clocks use selected markers in DNA that can be used collectively to predict age. In our research we have developed a comprehensive genome map of age associated sites in caudal fin tissue of zebrafish (*Danio rerio*). We have subsequently performed genome pairwise alignments to identify conserved age-associated sites between zebrafish and other fish species. Our method has shown age can be predicted with high accuracy from DNA in a wide variety of species including but not limited to: Southern bluefin tuna (*Thunnus maccoyii*), Australian lungfish (*Neoceratodus forsteri*), and Murray river cod (*Maccullochella peelii*). These epigenetic clocks provide a non-lethal and rapid approach to age estimation for fish. Epigenetic clocks have the potential to improve the management of fisheries where age is difficult to determine.

NEW OTOLITH-BASED AGE ESTIMATES OF BIGEYE TUNA IN THE WESTERN AND CENTRAL PACIFIC AND THEIR IMPACT ON STOCK STATUS

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Accurate life-history parameters are required for robust stock assessments and management advice. In 2008, the Western and Central Pacific Fisheries Commission recommended that a project on bigeye growth be undertaken to help reduce uncertainty in the parameter estimates to improve the accuracy of the stock assessments. This led to a large collaborative program of work across the Western and Central Pacific Ocean (WCPO) to collect and analyse otoliths for age estimation and growth modelling. We estimated the age of over 1200 bigeye, stratified by length bins and spatial zones, based on counts of daily and annual growth zones. The periodicity of the counts of annual (opaque) growth zones was verified using a combination of direct and indirect methods. A new algorithm was developed to estimate decimal (fractional) age using the counts of opaque zones and otolith measurements. The resulting age estimates were consistent with the daily age data for small/young fish and exhibit low variability in length at age, particularly at young ages. The longevity of bigeye tuna was found to be at least 14 years. The results of fitting growth curves to the length at age data showed that bigeye tuna in the WCPO are considerably smaller-at-age than assumed in previous stock assessments. The inclusion of the new growth data contributed to considerably more optimistic stock status results than when previously assessed.

SATELLITE TAGGING OF BILLFISH AROUND THE INDIAN OCEAN

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Four of the 5 billfish species in the Indian Ocean are overfished or subject to overfishing, but are considered as bycatch of the tuna fisheries, making management measures difficult to develop. Identification of spawning and nursery habitats for marine species is essential to define management measures, but very little is known for these species. One of the highest research priorities laid out by the Indian Ocean Tuna Commission is the identification of areas and seasons of reproduction for billfish in the Indian Ocean. The FLOPPED project aims to investigate the reproduction zones of five billfish species in the Indian Ocean through a comprehensive data collection initiative, including satellite tagging data, biological sampling, genetics, and modeling. Within the framework of this project, 100 satellite tags are being deployed around the Indian Ocean, on blue marlin (*Makaira nigricans*), black marlin (*Makaira indica*), striped marlin (*Tetrapturus audax*), swordfish (*Xiphias gladius*), and sailfish (*Istiophorus platypterus*). Tagging and sampling were originally focused on six study sites around the Indian Ocean, including Réunion Island, Mayotte, Mauritius (Rodrigues), Seychelles, Sri Lanka and Indonesia. However, due to logistical complications resulting from the global COVID-19 pandemic, we included a broader range of sites around the Indian Ocean to maximise the coverage and representativeness of this dataset. Here, we present preliminary results of the initial 46 tags that have been deployed since the start of the project. Tagging data have been converted to a standard NetCDF format and enriched with satellite environmental data using open and generic codes to aid in identifying environmental characteristics of the tagged species' functional habitats. The majority of these tags have been deployed in the Western Indian Ocean (Réunion, Rodrigues, Seychelles and Mayotte), many by local partners of the project trained by IFREMER and COOOL personnel. These tags were deployed on 22 blue marlin, 5 black marlin, 11 sailfish, 1 shortbill spearfish, and 7 swordfish. Thus far, the average duration of tag deployment was about 80 days. Position estimates indicate that fish tagged in the south-western Indian Ocean tend to swim to the north-west Indian Ocean, with little indication of east-west basin travel. Marlin and sailfish inhabit the top 200 meters during the day and restrict their depth range to the upper 100 m at night. In contrast, swordfish in the southern Indian Ocean inhabit the top 600 meters during the day, and restrict their depth range to the top 200 m at night. The results of this tagging project, in combination with the biological information obtained by sampling captured billfish, will help to better identify the habitat and reproductive grounds of these important species in the Indian Ocean.

"TAG AND RELEASE WITH A DIFFERENCE" A PILOT PROPAGATION PROGRAMME FOR ATLANTIC BLUEFIN TUNA (*THUNNUS THYNNUS*) IN MALTA.

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In April 2018 a pilot broodstock cage (30 m in diameter and 20 m deep) containing 48 adult Atlantic bluefin tuna (ABFT) was established 6 km off the coast of Malta and maintained for a period of three years until 2020. When sea water temperatures reached 22°C+, an egg collector net was attached to the downward current side of the cage. On the 21st June 2018 approximately 500,000 eggs were collected and on the following days approximately 1.7 million eggs were collected in total. Pilot experiments were carried out monitoring egg fertilisation, hatching rates and YSL survival after incubation both in the sea and in the laboratory. Eggs incubated in-situ sea incubator nets showed hatching rates between 80 and 90%; corresponding to the laboratory value. YSL survived up to 8 days in the laboratory. Molecular analysis of parental contribution of the egg batches indicated that at least 25 mothers had contributed towards egg production. Based on the figures obtained for egg numbers, hatching rates, the numbers of contributing mothers and the theoretical maximum fecundity approximately 75 million DNA-tagged larvae were released back into the sea in 2018. In the following year 2019 bad weather prevented egg collection on site but the broodstock was maintained throughout the year and we could expect a similar number of tagged larvae were released again. In 2020 conditions had improved and despite the COVID -19 restrictions, approximately 9.6 million eggs were collected and then the tagged larvae release back into the sea . Assuming an egg collection efficiency of 10% then this would equate to the release of 100 million tagged larvae. In October 2020 all 48 fish were sacrificed and endpoint DNA sampling took place for identification and insertion in the databank. It is assumed that if we use the data provided by 2018 we will have placed approximately over 175 million tagged larvae back into the sea by 2020. It now remains to sample the adult population in the coming years from the farmed population. Since the farm population is gathered from all over the Mediterranean then this is a convenient alternative to a sampling programme. It only remains to sample the fish when they are harvested after four months fattening. Initial genetic results have also shown that the spawning site fidelity has occurred with both production cage fish and broodstock fish coming from identical mothers.

NEW LOW-COST ELECTRONIC TAGS FOR MARINE SPECIES USING LoRa TRANSMISSION

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The advent of the Internet of Things has enabled the production of new communication systems to transfer small amounts of data. These transmission modules are low-cost, have low-power consumption, and are small (~ 1.5 cm²). Several transmission systems are available (e.g. SigFOX, NB-IOT, LTE-m, Weightless, …) and Long Range (LoRa) is one of the most prominent transmission protocols for Internet of Things objects. This is due to the fact that LoRa uses license-free radio frequencies, thus no subscription is required, and that LoRa has a broad global network of receiving stations. While LoRa electronic tags have been developed for terrestrial species with GPS tracking (e.g. SmartPark), no current application exists for marine species. Here we show the potential use of this technology for electronic tags with the development of electronic tags for green sea turtles (*Chelonia mydas*) and electronic survival tags developed for a wide range of species and tested on skipjack tuna (*Katsuwonus pelamis*). These tags have undergone successful initial testing. The turtle tags have successfully transferred depth profile data over several months with an average of 30 messages per day. The survival tags deployed on skipjack tuna popped off at the scheduled time and transferred the recorded data. The low direct production costs of these tags is ~$100, which opens the possibility of expanding tagging activities while providing a way of transferring the data at no cost via the LoRa transmission system.

HIGH RESOLUTION POST-RELEASE BEHAVIOR AND RECOVERY PERIODS OF TWO HIGHLY PRIZED RECREATIONAL SPORTFISH: BLUE MARLIN AND SAILFISH

Manual Caboz Scholarship

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The Eastern Tropical Pacific is widely considered to be one of the world's best fishing locations for istiophorid billfish, including blue marlin (*Makaira nigricans*) and sailfish (*Istiophorus platypterus*). As such, substantial recreational fishing effort has developed in the region in recent years, contributing significantly to local economies. As a result, countries in the region have mandated catch-and-release practices to protect recreational billfish fisheries. Although studies thus far have documented low post-release mortality estimates for blue marlin and sailfish, animals in these fisheries are subjected to exhaustive exercise and stress before release, and sublethal injuries may result from repeated jumping during angling, coming into contact with the fishing vessel or being exposed to air for extended periods of time during handling. Therefore, obtaining accurate estimates of post-release recovery time is an important component of assessing the success of catch and release as a management practice. Using a custom-made high-resolution acceleration data logger and video camera tag package, we measured the post-release recovery period and behavior of blue marlin (n = 9) and sailfish (n = 9) off the Pacific coast of Panama for periods of 6–70 h after angling fight times ranging from 4–90 min (mean: 45 ± 30 and 8 ± 3 min for blue marlin and sailfish, respectively). Animal-borne-video enabled the validation of behavioral signatures from acceleration data and recorded interactions with potential prey and conspecifics. Using metrics to quantify tailbeat activity calculated from tri-axial sensor data, results suggest the recovery period for blue marlin and sailfish after catch and release may be shorter than previous estimates using time-depth recorders alone (hours rather than days). This is the first study to use tailbeat activity to estimate the post-release recovery period of billfish and suggests that catch and release can be an effective practice to conserve and sustain billfish populations in the Eastern Tropical Pacific.

MOVEMENT PATTERNS, UTILIZATION DISTRIBUTIONS, AND MIXING RATES OF YELLOWFIN TUNA TAGGED AND RELEASED WITH ARCHIVAL TAGS IN SIX DISCRETE AREAS OF THE EASTERN AND CENTRAL PACIFIC OCEAN

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A total of 1,522 yellowfin tuna, *Thunnus albacares*, were captured, tagged, and released with surgically implanted archival tags (ATs), in six discrete areas of the eastern and central Pacific Ocean, during 2002 through 2019. Of 483 ATs returned (31.7%), 227 ATs from yellowfin (48 to 147 cm in length) at liberty from 32 to 1,846 d ($\bar{x}$ = 300.1 d) provided suitable data sets which were processed using an unscented Kalman filter model with sea-surface temperature measurements integrated (UKFsst), to obtain most probable tracks and movement parameters. Although some differences were observed in the movement patterns for fish from within and among the six release areas, 99% of the 227 fish remained within 1,000 M of their release locations, indicating limited dispersion and fidelity to release locations.

HORIZONTAL AND VERTICAL MOVEMENTS OF ELECTRONICALLY TAGGED BLUE SHARKS IN THE EASTERN NORTH PACIFIC OCEAN

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Between 2002 and 2019, 143 blue sharks (*Prionace glauca*), ranging from 134 to 260 cm fork length, were successfully tagged with SPOT and/or PSAT satellite tags. Sharks were tagged either within the California Current between Baja California, Mexico and Victoria Island, British Columbia, Canada or offshore and to the west of the California Current out towards the Hawaiian Islands. Data were analyzed from 86 SPOT tags with deployment durations of 2 to 740 days (mean 122 ± 117) and 91 PSAT tags with durations of 15 to 360 days (mean 80 ± 78 days), including data from 58 double tagged sharks. Vertical movements for tagged sharks ranged from the surface to more than 800 m with the majority of time spent in the top 50 m. Shark movements were compared by size and age, with juveniles less than 4 years of age, maturing sharks 4 years of age, and mature sharks 5 years of age and greater. The range of horizontal movements of tagged sharks spanned from 51˚N to 4˚N along the coast of North America from the coast of British Columbia, Canada to just south of Puerto Vallarta, Mexico and out to the Hawaiian Islands. The farthest movements to the west (as far as 176˚E) were made by 4 year old, maturing females tagged off the coast of Canada and occurred between 35 - 45˚N in the region of the North Pacific Transition Zone. Among the key findings was the discovery of a high degree of variability in horizontal movement by age and maturity. Our observations of horizontal and vertical movements by season, sex and size will be reported in greater detail.

UNDERSTANDING THE MOVEMENT PATTERNS AND INCIDENTAL MORTALITY RATE OF BIGEYE THRESHER SHARKS (*ALOPIAS SUPERCILIOSUS*) FOLLOWING CAPTURE IN A DEVELOPING DEEP-SET FISHERY OFF CALIFORNIA

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Although frequently caught incidentally in pelagic fisheries throughout the Pacific, bigeye thresher sharks (*Alopias superciliosus*) remain poorly understood. In recent years, bigeye thresher sharks (BETS) have been routinely encountered during exempted fishery trials of deep-set buoy gear (DSBG) and linked buoy gear (LBG), two commercial gear types designed to target swordfish at depth during the daytime. Despite a small domestic market, the majority of BETS are released or discarded to reserve hold space for more valuable catch. Recent fishery authorization of both DSBG and LBG off California reinforces the need to better understand the movement patterns, depth distribution and post-release disposition of BETS following capture on both deep-set gear types. This work plan assessed the survival rate of 28 BETS, ranging in size from 147 to 240 cm FL, following capture on both DSBG and LBG during research and exempted fishery trials from October, 2016 through December, 2019. In addition, transmitted data from satellite-linked survivorship and pop-up archival tags (Wildlife Computers sPATs and miniPATs) were used to evaluate BETS depth distribution. Data were compared with records from tagged swordfish that were at liberty during the same time period to determine if deep-set configurations could be modified to further reduce interaction rates. Overall, BETS were resilient to the acute effects of capture and handling stress on both deep-set gear types, with a combined post-release survival rate of approximately 90% (n=25) following fight times up to 300 min. Of the 3 BETS mortalities, one died immediately and one predation event occurred within 6-h of release on DSBG, and one mortality was recorded upon capture on LBG following branchline entanglement. Similar to swordfish, all surviving BETS exhibited consistent diurnal dive patterns with sharks remaining well below the thermocline during the daytime (mean=365m) and within the mixed layer at night (mean=63m). With the exception of three tags that reported within close proximity (<185 km) to their SCB tagging location, BETS travelled extensively (mean=1,220 km; range=730-1,523 km) to the south (162-228° heading) over the 30-d deployment period. Movements were directed towards a relatively confined area of offshore seamounts along southern Baja California, Mexico (22°-26°N and 114°-126°W), a reported zone of regional importance for other large pelagic sharks of the Eastern North Pacific.

TAGGING REVEALS BEHAVIOURAL AND HABITAT PARTITIONING OF ATLANTIC BLUEFIN TUNA (*Thunnus thynnus*); IMPLICATIONS FOR STOCK-SPECIFIC MANAGEMENT

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Incomplete understanding of the differences between the Gulf of Mexico (GOM) and Mediterranean (Med) stocks of Atlantic bluefin tuna impedes efforts to identify the stock-status of juveniles, improve stock assessments, and preferentially catch the more resilient stock. We used twenty years of electronic tag data to compare the movement behaviours of the stocks over their annual cycles and life histories. Both stocks use the central core area of the US eastern seaboard similarly between November and April, but diverging movement patterns are evident outside these months. The GOM fish expand their range as they age, increasingly pursuing a 'high effort, high reward' strategy that sees them spawn in the GOM then feed in the Gulf of St Lawrence. Contrastingly, Med fish pursue a convenience/trade-off strategy, migrating within a shorter range along the coast, and grazing on lower-calorie prey when on the northern feeding grounds. Discrepant experiences during the first year of life likely result in subtle differences in adult physiology and behavioural preference. Med fish travel from their temperate spawning grounds via the frigid northern North Atlantic to the West Atlantic within their first year, an expansive migration likely leading to a tolerance for cold temperatures. Contrastingly, GOM fish have less need for expansive offshore migrations given their spawning and feeding grounds are on the same coast, while adaptive tolerance to the high temperatures they tolerate as larvae may make them less able to withstand the colder temperatures on the feeding grounds. Using these and other differences, we were able to probabilistically assign unknown-stock fish to stocks, doubling our known-stock-fish dataset, which is highly valuable for stock assessment and many other studies. This approach shows promise as a management tool to allow preferential targeting of the less-imperilled Med stock, buffering impacts to the fishery while protecting the GOM stock.

BIOLOGGING: REVEALING THE ENVIRONMENTAL ECOLOGY OF YELLOWFIN, BIGEYE TUNA AND SWORDFISH IN THE WESTERN INDIAN OCEAN

POSTER

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Habitat and migratory movements of top predators supporting major tropical pelagic fisheries in the Indian Ocean are still poorly known despite decades of research and dedicated large-scale tagging programs. Past tagging efforts mostly based on conventional tags provided a broad idea on the scale of horizontal displacements for principal tuna species, billfish and sharks. However conventional tagging is a fishery-dependent approach broadly describing the extent of the spatial distribution of the resource and its viscosity on the fishing ground. Therefore conventional tagging is not adapted to provide fine-scale migratory behaviour data aiming to describe and explain migratory patterns and habitat use at an individual level. Here we present results of the first large-scale Pop-Up Satellite Tags (PSAT) tagging efforts focused on commercially exploited species in the Indian Ocean: yellowfin tuna (YFT), bigeye tuna (BET) and swordfish (SWO). In the framework of EU-funded projects PROSPER and PELICAN, a total of 41 PSATs were deployed on YFT (26), BET (14) and SWO (1) between November 2014 and December 2015. PSAT deployments took place in the western Indian Ocean: off Reunion Island, on the west border of the Saya-de-Malha Bank, and off the east coast of Madagascar. A total of 36 PSATs surfaced and reported data. During relatively short deployment periods (104 days max at liberty) all species perform large-scale movements throughout the western Indian Ocean reaching South African waters in south and equatorial waters in the north. BET demonstrates less active migratory habits than YFT and SWO suggesting a certain site-fidelity in short-term scale. All species show different vertical habitat occupation patterns during the day but occupy similar habitat at night in the upper layers. During the day YFT stay most of time in the upper mixed layer (0-100 m) while BET and SWO reach colder and deeper layers down to 350-600 m and 500-800 m respectively. BET and SWO spent most of daytime below 200 m depth suggesting that mesopelagic environment is their principal habitat in the western Indian Ocean. Our data also suggest the capacity of BET to explore bathyal depths deeper than 2000 m depth. Regarding dispersion, our results provide first insights on high rates of individuals' horizontal movements at ocean-scale level.

BILLFISH SATELLITE TRACKING IN THE EASTERN TROPICAL PACIFIC ALLOWS INFERENCE INTO HORIZONTAL AND VERTICAL HABITAT DISTRIBUTIONS

POSTER

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Pacific blue marlin (*Makaira nigricans*) and Indo-Pacific sailfish (*Istiophorus platypterus*) are two species of migratory billfish that occupy the epipelagic zone of the world's subtropical and tropical marine waters. Although their Atlantic counterparts are relatively well-studied, far less research has been completed on Pacific populations to date. Both species are top predators and transboundary, particularly within the Eastern Tropical Pacific (ETP) region, meaning they migrate through the Pacific waters of Mexico, Central America, northern South America, and areas beyond national jurisdiction (ABNJ), exposing individuals to a variety of fishing pressures and regulations. Preliminary results from a reanalysis of pop-off satellite archival tags deployed over 17 years in Costa Rica and Panama reveal changes in the seasonal and inter-annual distribution patterns of blue marlin and sailfish in the ETP. Differences in depth preference between the two species are also evident, which suggests differences in vertical habitat use. Using robust statistical models integrating biophysical variables, we can provide insights into the horizontal and vertical distribution of blue marlin and sailfish in the ETP and can infer impacts and responses to local environmental variability, changes in climate, and anthropogenic stressors.

CONNECTIVITY OF STRIPED MARLIN FROM THE CENTRAL NORTH PACIFIC OCEAN

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Striped marlin, *Kajikia audax*, have been in overfished condition in the western and central North Pacific (WCNP). Although the majority of catches of striped marlin are taken by international fleets, namely Japan and Chinese Taipei, a continued decline in the spawning stock biomass could lead to additional catch reductions and management measures for Hawaii-based fleets, even for small boat fisheries and recreation charter vessels. In Hawaii, striped marlin are important to the islands' economy and cultures, and reduction in allowable harvest would be added hardship for fishing communities and seafood consumers. In addition, the prohibition of sales of Hawaii-landed billfish to the US mainland market by the recent amendments to the Billfish Conservation Act of 2012 have established additional economic hardships.

Despite decades of tagging around Hawaiian waters, movement information on striped marlin is almost nonexistent north of 22 °N and south of 15 °N. To address this knowledge void, 30 popup satellite archival tags (4 X-Tags; Microwave Telemetry, Inc. and 26 MiniPATs; Wildlife Computers Inc.) were deployed on adult striped marlin (60-90 lb whole weight or 138-157 cm EFL) between 2016 and 2019 by Hawaii-based longline vessels. A total of 149 fin clips were also obtained for genetic analyses from the longline fleet during June-August 2017 to coincide with the tagging efforts. Tag mission durations ranged from 1-365 days (median = 69 days). Some of the relatively short missions were due to mechanic failure, i.e., nosecone "pin breaks", for five MiniPATs, providing observational durations between 53 to 99 days.

Tracking results revealed diverse seasonality in striped marlin movements, distributed over a vast area. For instance, in July and August, fish were either tagged in, or occupied areas spanning 8 to 43°N, and "pairs" of fish had similar latitudinal range, despite extensive longitudinal separation. Similarly, in other months the range of tagged striped marlin often exceeded 35° in latitude. A year-long track revealed trans-equatorial and trans-Pacific movement not previously observed for striped marlin. This individual was tagged outside of the WCPFC management area, where it spent four months before migrating southwest across the Central North Pacific to the South East Pacific over five months. It spent the last three months off the Gold Coast of Australia before the tag released on schedule. Our results so far suggest striped marlin movements in the Central North Pacific can be extensive, and their potential connectivity to other regional aggregations may have been previously overlooked due to the lack of long-term (> 9 months) deployments of PSATs. Continued striped marlin tagging efforts in concert with genetic profiling are highly encouraged, and recommended with these initial findings. The use of reliable satellite tags that can achieve minimally a full-year observation period will also be critical to the insightful understanding of pelagic species migration.

ESTIMATING NATURAL MORTALITY IN ATLANTIC BLUEFIN TUNA WITH ELECTRONIC TAGS

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Electronic tagging efforts on Atlantic bluefin tuna (ABT) have utilized a variety of electronic tag types (pop up satellite tags, internal archival and acoustic tags) to better understand the complex spatial distributions and stock structure of these highly migratory fish. We report here on a decade long study to examine the use of externally attached acoustic tags in combination with pop up satellite tags to estimate life history parameters important for stock modeling. Rates of natural mortality are key determinants of productivity for exploited populations, and robust estimates are important for sustainable fisheries management. We have developed a multistate Bayesian mark-recapture model for telemetry data and apply it to estimate the rate of natural mortality for Atlantic bluefin tuna using acoustic tag detections only, and a combination of acoustic tag detections plus estimated positions from pop-up satellite archival tagged animals. ABT were first released in the Gulf of St. Lawrence, Canada with external acoustic tags in the Fall of 2009. The closing of the Cabot Straight with a receiver line and establishment of a second receiver line on the Scotian Shelf by the Ocean tracking Network provided the detection capability for these ABT deployments. Subsequently, ABT were double tagged with acoustic and pop up satellite archival tags. To date a total of ~53,500 detections have been recorded from 6/2010 to 11/2020. To examine mortality estimates, we used 151 tagged ABT, 74 had a single (acoustic) tag, and 77 had both acoustic and pop-up satellite archival tags. We performed a simulation study to investigate the effect of auxiliary information from satellite tagging on mortality rate estimates for a range of acoustic tag detection probability scenarios. We obtained posterior estimates of the annual natural mortality rate across a decade of tagging for Atlantic bluefin tuna of 0.15 yr^{-1}.

INSIGHTS INTO THE HORIZONTAL MOVEMENTS, MIGRATION PATTERNS AND STOCK AFFILIATION OF CALIFORNIA SWORDFISH

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This study reports on the horizontal movements of swordfish (*Xiphias gladius* L.) tagged during deep-set fishery trials off the California coastline. Swordfish position estimates from 123 electronic tag deployments [satellite-linked pop-up tags (n=66), data storage tags (DST) that were recaptured (n=25) and fin-mounted Argos transmitters (n=32)] were used to better understand stock structure and regional affiliation with current boundary hypotheses used to manage swordfish in the Eastern North Pacific. Recent deployments of dorsal fin mounted Argos transmitters have enhanced the capacity to address questions related to annual migration patterns, stock affiliation and seasonal site fidelity. Swordfish tagged off California exhibited movements into both the Eastern Pacific Ocean (EPO) and Western and Central North Pacific (WCNP) management units, with more than half of the individuals tagged within the Southern California Bight (SCB) spending part of the year within the EPO stock boundary area. Seasonal migrations ranged from the Equator (0.8ºN.132.4ºW) to the Hawaiian Islands (17.0ºN/154.2ºW), with annual migration cycles of more than 5,000 km and daily rates of movement exceeding 50 km/d. Argos tracks from individuals at liberty for more than 900 days also revealed that some swordfish transverse both management units over the course of their deployments and routinely exhibit seasonal site fidelity to the SCB. Collectively, this work suggests that SCB swordfish may exhibit a higher level of EPO connectivity than previously proposed and highlights the importance of the SCB foraging grounds. Overall, deployments off California have shown little evidence of trans-equatorial or trans-Pacific crossing and support the need for future inclusion of spatial distribution data in the management of North Pacific swordfish.

REVIEW OF RESEARCH ACTIVITIES CONDUCTED AT THE IATTC'S ACHOTINES LABORATORY FROM 2019-2021

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The Inter-American Tropical Tuna Commission (IATTC) conducts research on the reproductive biology and early life history of yellowfin tuna at the Achotines Laboratory, Republic of Panama. Yellowfin broodstock have been spawning at near-daily intervals since 1996, which represents the only sustained spawning of yellowfin in captivity in the world. The resulting eggs, larvae and early-juveniles are studied in experimental investigations focused on estimation of pre-recruit survival patterns.

Recent patterns of captive spawning of the tank population of yellowfin will be described. During the past 25 years, there have been periodic cessations of spawning in the broodstock group due to either suboptimal water temperatures or low numbers of reproductively active females in the broodstock group. Such a cessation occurred from August 2020 through March 2021. A small group of new broodstock fish was added to the broodstock tank in December 2020, and spawning re-commenced in mid-April 2021.

Pre-recruit research on yellowfin at the Achotines Laboratory has focused on growth and survival dynamics of larvae (the first 3 weeks). Results of recent larval ecology investigations, including studies of growth/survival dynamics and effects of ocean acidification on larval survival, will be presented. Comparative studies of the early life histories of yellowfin and Pacific bluefin are ongoing with Kindai University since 2011 and recent experimental results will be discussed. Ongoing experimental investigations of larval stages in Panama and Japan were suspended due to COVID during 2020 and the first half of 2021, but investigations will be resumed when international travel resumes.

In recent years the research focus on yellowfin at the Achotines Laboratory has expanded to the early-juvenile stages (1-6 months). Growth rates have been estimated for all transformation and early-juvenile individuals reared in land-based tanks or a sea cage; the early-juveniles have ranged from 1.6-28.0 cm in length and up to 158 days after hatch. Juvenile growth investigations planned for 2021-2022 will be summarized.

The Achotines Laboratory also supports research projects of interest to other IATTC scientists. These investigations include pilot studies to test technologies developed to reduce bycatch and detect FADs remotely in the tuna purse seine fisheries. Two recent pilot technology studies were planned at the Achotines Laboratory and have been delayed due to COVID travel restrictions, but there are plans to initiate these studies in either late 2021 or 2022.

ENVIRONMENTAL PREFERENCES AND SIZE STRUCTURE OF THE SILKY SHARK (*Carcharhinus falciformis*) CAPTURED BY THE LONGLINE FLEET OPERATING IN THE MEXICAN CENTRAL PACIFIC

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One of the most important species in the Eastern Pacific Ocean is the silky shark (*Carcharhinus falciformis*), which has been caught by artisanal fisheries, longline fleets, and as bycatch by purse-seine tuna fleet. In Central Mexican Pacific, medium-sized longline fleet based on the Port of Manzanillo, Col. captures this species throughout the year. Database recorded by the shark monitoring program of Instituto Nacional de Pesca y Acuacultura was used to analyze the spatio-temporal distribution of silky shark caught by this fleet from 2003-2017. The fishing information on catch per unit effort was also provided to determine catch /1000 hooks (CPUE). Environmental database, as sea surface temperature (SST), chlorophyll-a concentration (Chl-*a*), and sea surface height (SSH) was derived from satellite images. In addition, bathymetry of the study area was also considered. The effect of environmental variables on the silky shark captures was assessed by means of generalized additive models (GAMs). A total of 19 672 organisms were measured, of which 86% were juvenile individuals. Sex ratio was 0.85:1 F-M. Significant interannual variability in size was found with a decreasing trend during 2003-2006; subsequent years showed a size increase pattern every three to four years. Seasonal variability was also significant; records showed that March and August were the months when sharks with the largest length were caught. No spatial pattern was observed related to shark size and sex distribution. The study area is characterized by SST 24°-30° C, Chl-*a* 0.08-0.48 mg/m^3 and, an SSH -0.12-0.28 m, with a significant inter- and intra-annual variability. A high correlation was observed between CPUE and SST. The best-fit model explained 27.5% of the deviance, which includes spatial variables (latitude, longitude), time (year and month), and environmental factors (SST, Chl-*a*, SSH, and depth). The final model suggested higher catches out of the coast from 2005-2008 and 2014-2016; from April-September in waters with sea surface temperatures from 27-28 °C, low Chl-*a* concentration (0.2 mg/m^3), and in convergence zones with 3000 m in depth.

IMPACT OF ENVIRONMENTAL VARIABILITY ORIGINATED BY THE ENSO ON WAHOO (*Acanthocybium solandri*) SPATIAL-TEMPORAL DISTRIBUTION IN THE EASTERN TROPICAL PACIFIC OCEAN

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The wahoo *Acanthocybium solandri* is a piscivorous, epipelagic and highly migratory species distributed in tropical and subtropical waters worldwide, representing a high economic and ecological value resource. It is caught incidentally mainly by the international tuna fleet that operates in the Eastern Tropical Pacific Ocean, recording a high catch variability. Changes in distribution patterns and abundance of various pelagic species have been related to the presence of climatological events, such as El Niño-Southern Oscillation (ENSO). Investigating and predicting these changes can help to reducing bycatch and conserving species. Therefore, the main objective of this research is to determine ENSO (cold and warm phases) impact, as well as in normal conditions, on wahoo distribution and relative abundance and predict its behavior. The oceanographic variables analyzed were monthly average of Sea Surface Temperature (SST), Chlorophyll-a (Chl-a) concentration and Sea Surface Height (SSH), all derived from satellite remote sensing. As an indicator of ENSO presence, the Oceanic El Niño Index (ONI) was used. Fishing data corresponded to incidental catch recorded by the Inter-American Tropical Tuna Commission (IATTC) Observer Program from 2002-2015. The monthly average incidental catch per unit effort (CIPUE) was determined as an index of relative abundance by one-degree squares. The study area is characterized by average SST values from 24-26 °C, Chl-*a* from 0.16-0.23 mg/m^3 and SSH from 0.007-0.12 m, with a statistically significant interannual and seasonal variability in all the variables. About 99% of the captured organisms were associated with floating objects. The CIPUE values recorded a significant interanual and seasonal variability with minimum values in 2011 and from February-March and maximum values in 2007 and from September-November, respectively. A differential distribution was observed in incidental catches, effort and CIPUE during the three phases with higher CIPUE average values during El Niño. Spatial prediction models showed that the highest incidental wahoo catches takes place in oceanic waters southward from the equator during El Niño phase with sea surface temperatures close to 25 °C and low Chl-*a* concentration (< 0.23 mg/m^3). During La Niña phase spatial distribution was more dispersed.

HOW MANY DRIFTING FISH AGGREGATING DEVICES SUSTAIN THE WORLD LARGEST TUNA FISHERY?

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With the arrival of new technological developments to track drifting Fish Aggregating Device (dFAD) locations such as satellite and echo-sounder buoys, dFADs are now a major fishing mode for tropical tuna purse seine fisheries worldwide. However, the extent of dFAD use remains poorly understood. Such information is however key for designing adequate management measures. In the Western and Central Pacific Ocean (WCPO), the tuna commission (WCPFC) will review the tropical tuna Conservation and Management measure this year, which includes a limit in the number of active buoys monitored by a vessel, at any given time, at 350. Better knowledge in the current use of dFADs in the WCPO is therefore needed.

We used novel approaches for estimating annual dFAD deployments and number of dFADs monitored by individual vessels across the entire WCPO between 2011 and 2019. The estimation procedures were based on observer and logbook data, combined with the Parties to the Nauru Agreement (PNA) dFAD tracking data. Estimates ranged between 20,300 and 47,000 deployments per year, depending on the methodology. The median number of active buoys monitored per vessel per day ranged from 45 to 75 depending on the year, well below the current management limit of 350. These results provide a basis for improved monitoring and management of dFAD use in the WCPO, with applicability for other regions.

IMPACT ON TROPICAL TUNAS ECOLOGY OF THE MASSIVE DEPLOYMENT OF FISH AGGREGATING DEVICES (FADS) BY TUNA FISHERY VESSELS: A MODELING APPROACH

Wildlife Computers Scholarship

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Understanding the effects of increasing FAD densities on the movements and ecology of tropical tunas is key to provide science-based advices on the limits of the total number of FADs. Previous electronic tagging studies conducted on different arrays of FADs allowed characterizing the time spent by tuna associated with FADs and out of them. In this work, we combined these data with a model of tuna motion in an array of FADs. This model, simulating the movements of a single tuna, was built upon three main assumptions: (1) tunas show a random-search behaviour in an array of FADs, (2) tunas can orient themselves straight to a FAD when the FAD is located within a given orientation radius and (3) during nighttime tuna do not associate with FADs. Tunas search behaviour was simulated by a correlated random walk depending on a sinuosity parameter. The distance from which tunas are able to detect a FAD is characterized by the orientation radius parameter, and a loss parameter accounts mortality (natural or fishing) and departure of individuals from the FAD array. These three parameters were calibrated using acoustic tagging data recorded for yellowfin tuna (60 to 80 cm fork length) within two different arrays of anchored FADs (Hawaii and Mauritius) characterized by distinct FAD densities. Finally, the model was used to build scenarios on the impact of increasing numbers of FADs on tuna behavior, in terms of the time spent associated and away with/from FADs.

MANAGEMENT OPTIONS FOR REDUCING dFAD LOSS AND BEACHING

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Debris from fisheries pose significant threats to coastal marine ecosystems worldwide. Tropical tuna purse seine fisheries contribute to this problem via the construction and deployment of thousands of man-made drifting fish aggregating devices (dFADs) annually, many of which end up lost out of fishing grounds or beaching in coastal areas. In this study, we analyzed a large number of trajectories of French dFAD tracking buoys deployed throughout tropical tuna fishing grounds in the Indian and Atlantic Oceans to identify where and when dFAD loss and beaching occur. We found that there is tremendous promise for reducing beaching events by prohibiting deployments in areas most likely to lead to a beaching. For example, our results indicate that around 40% of beachings can be prevented if deployments are prohibited in areas in the south of 8°S latitude, the Somali zone in winter, and the western Maldives in summer for the Indian Ocean, and in an elongated strip of areas adjacent to the western African coast for the Atlantic Ocean. In both oceans, the riskiest areas for beaching are not coincident with areas of high dFAD deployment activity, suggesting that these closures could be implemented with relatively minimal impact to fisheries. We also found that more than 40% of dFADs ultimately drifted away from fishing grounds and were lost in the open ocean. However, a significant number of these dFADs passed close to ports along their drift, indicating that dFAD recovery programs from ports could be effective measures to reduce dFAD loss.

POPULATION GENOMICS FOR IMPROVING MANAGEMENT OF INDIAN OCEAN BIGEYE AND SKIPJACK TUNAS AND ATLANTIC BLUEFIN TUNA

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Effective fisheries management relies in appropriate definition of management units (stocks) on which assessment is performed. These management units are assumed to constitute naturally isolated populations (groups of sexually interbreeding individuals) whose parameters such as growth, recruitment and natural and fishing mortality are intrinsic and not dependent on emigration or immigration rates. Yet, mismatches between management and biological units are common in fisheries management, in part due to the difficulty to identify reproductively isolated populations, which is especially challenging for large migratory fishes such as tunas. For example, within the Indian Ocean, the bigeye (Thunnus obesus) and the skipjack (Katsuwonus pelamis) tunas are assessed as one stock respectively despite uncertainties regarding to their population connectivity. Likewise, the Atlantic bluefin tuna (Thunnus thynnus) is assessed as two stocks, one at each side of the Atlantic Ocean, whose delimitation is challenged by the ability of this species to perform transoceanic migrations. Here, we have studied the population connectivity of these three species by assembling, for each, a dataset of tens of thousands genome-wide Single Nucleotide Polymorphisms (SNPs) from more than five hundred individuals of different age classes covering the distribution of the species and several years of sampling. Our results support a single genetically homogeneous bigeye population within the Indian Ocean, endorsing the single-stock based assessment. For skipjack, our results reveal presence of genetically differentiated groups within the Indian Ocean that co-occur in different proportions from north to south; this challenges the single stock-based assessment while demanding additional analyses to better understand connectivity of this species. On Atlantic bluefin tuna, our results support presence of two genetically differentiated ancestral populations, mainly spawning in the Mediterranean and Gulf of Mexico, that interact through east to west unidirectional transatlantic gene flow and a mixed spawning area in the Slope Sea; this challenges the two-stock based assessment and has important implications on the conservation of the species. Altogether, these results highlight the benefits of genomics-informed management and conservation strategies in tunas.

COMPARISON OF U.S. PACIFIC BLUEFIN TUNA LENGTH SAMPLING PROGRAMS: 2014-2020

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Pacific bluefin tuna (PBF) in the Eastern Pacific Ocean have been fished since at least the 1950s; however, declines in the U.S. commercial catch have resulted in recreational fishing emerging as the larger sector of the U.S. PBF fishery since the early 2000s. The U.S. recreational fishery is dominated by commercial passenger fishing vessels (CPFVs). The size selectivity of the CPFV fleet was historically mirrored to the U.S. commercial fleet in stock assessments before 2020, but the current length composition of the recreational fleet may not reflect the length composition of the historical (1950s-1980s) commercial catch. The National Oceanic and Atmospheric Administration (NOAA) conducts both the Pacific Bluefin Tuna Port Sampling Program and supports the Sportfishing Association of California (SAC) Fisheries Sampling Program to determine the length composition of the CPFV fleet. The NOAA Sampling Program opportunistically measures whole PBF unloaded in port from CPFV trips. The SAC Program is implemented by CPFV fleet crew during regular fishing trips and serves as a data collection method that does not rely on personnel resources outside of the fishery. The length compositions collected by these programs were compared to investigate their overlap, potential bias, and how representative they were of the CPFV fleet. The length compositions between the programs were similar, but the NOAA Sampling Program generally sampled larger PBF (median = 97.1 cm FL) likely due to their port sampling methods. In contrast, the SAC Program was able to measure smaller PBF (median = 92.0 cm FL) often filleted at sea and unavailable for port sampling. The SAC Program generally sampled fewer vessels than the NOAA Sampling Program, but a subsampling simulation demonstrated that this did not drastically affect the length composition. The NOAA Sampling Program measured 4.5% of the CPFV fleet between 2014 and 2019, while the SAC Program measured 3.8% of the CPFV fleet between 2015 and 2020; both programs were representative of the CPFV landings of PBF. While the potential of sampling design bias needs to be considered, both programs produced comparable data that are likely more representative of current CPFV landings than the historical data previously used for the U.S. recreational fleet.

DRIVING TRANSPARENCY & SUSTAINABILITY THROUGH ELECTRONIC MONITORING

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Background: For the past 5+ years, TNC has been working collaboratively with a range of stakeholders, including industry and government partners, to transform tuna longline fisheries monitoring through the procurement and placement of automated onboard electronic monitoring (EM) video camera systems. We have engaged with over 15 countries and several globally significant seafood companies to help design, finance, and implement EM projects. The COVID-19 pandemic has provided opportunities to highlight EM as a "fit for purpose" monitoring and surveillance tool that can be used when human observation is not feasible (health/safety) or practical (increasing the observer coverage in tuna longline fisheries). This presentation will provide an update on TNC's EM work, highlight existing data gaps/challenges, and share recent innovations and emerging projects and opportunities.

Challenge: While the image of illegal, unreported, and unregulated (IUU) fishing activities is often portrayed as being conducted by dark vessels operating outside of RFMO scrutiny, the reality is that the majority of IUU activities are undertaken by vessels legally licensed to fish. Yet we don't have the basic granular on-the-water information to combat IUU and sustainably manage global tuna fisheries and associated ecosystem components or the transparent and verifiable compliance monitoring information to ensure that fishers are playing by the established rules. EM can deliver that information if we can provide the tool at scale in a cost-effective, trusted, and efficient manner.

Innovations and Opportunities:
- Machine Learning and Artificial Intelligence: TNC is helping to catalyze investments in machine learning and artificial intelligence (AI) tools to address the back-end inefficiencies and high costs of manually annotating EM data and to decrease the large time lags between fishing events/data collection and recording/reporting useful information for management and enforcement. With the advent of more cost effective wireless and satellite technologies, the potential to compress and transmit EM data to the cloud provides an opportunity to deliver faster data while reducing EM costs. In addition, we continue to manage and add to our public facing Fishnet.AI library which currently contains ~86,000 labeled EM images with over 400,000 bounded box entries to support open source AI development.
- Using EM Video Clips for Training - (Case Study Oceanic Whitetip Shark Initiative): Images and video clips from our EM projects are being used for training and standardization of catch identification protocols and best handling and safe release practices. EM data from an Indian Ocean project recently showed landing and retention of oceanic whitetip sharks, a violation of regional measures and regulations for a species in serious global decline. TNC is designing a proof of concept project with Microsoft's AI Team to create a detection model for quickly scanning EM records to identify oceanic whitetip shark encounters to highlight these events for use by fisheries managers and compliance officers. If successful, this detection model approach could be applied to other bycatch species of concern including marine turtles and seabirds.
- Using EM to Increase Transparency – (Case Study Tunago EM Carrier Project): TNC, in partnership with among others, Thai Union and the Taiwanese Fishing and Shipping Company Tunago, is leading the testing of an EM system onboard a frozen tuna transshipment carrier operating in the Western Central Pacific Ocean. One of the objectives is to install and operate a motion-compensated crane scale with digital data outputs to be ingested into the EM system and transmitted via satellite to project partners.

- Thai Union Partnership: In April 2021, TNC announced a partnership with Thai Union, one of the world's largest seafood companies, to raise the standard of tuna transparency worldwide, aiming to implement on-the-water monitoring across the company's vast supply chain by 2025. This new initiative will deploy EM systems or employ human observers on all partner vessels. TNC is working with Thai Union to design a bulk procurement initiative for EM monitoring, which will address preferential cost savings at scale and outline system performance specifications, data requirements, and roles/responsibilities across stakeholders.

STOCK-OF-ORIGIN CATCH ESTIMATION OF ATLANTIC BLUEFIN TUNA (*Thunnus thynnus*) BASED ON OBSERVED SPATIAL DISTRIBUTIONS

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Atlantic bluefin tuna, *Thunnus thynnus,* are a large, highly migratory fish distributed throughout the North Atlantic ocean and adjacent seas currently managed as two discrete stocks, western and eastern. Both stocks forage in the North Atlantic and a high degree of intermixing occurs, which combined with limited single-stock survey data makes it difficult to assess the abundance and status of individual populations. In this study, we used movement patterns from a multi-decadal tagging dataset to create monthly distribution maps for these two major stocks. We then used these maps to separate the overall catch records into stock-specific catch (CPUE) time series. We identified an increase in the past two decades in the proportion of catch estimated to come from the eastern stock, attributable to a decrease in CPUE in regions dominated by the western stock, relative to other regions. The stock-specific catch series can be used to improve the accuracy of stock assessments and inform spatial management.

TAKING STOCK OF THE POPULATION GENETIC STRUCTURE OF STRIPED MARLIN (*Kajikia audax)* IN THE CENTRAL NORTH PACIFIC OCEAN

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Relative to many highly migratory fishes, striped marlin (*Kajikia audax)* exhibit considerable stock structure. At least four genetically distinct stocks of striped marlin have been resolved throughout the Pacific and Indian oceans with stock overlap occurring in some regions. However, stock composition in the central North Pacific (CNP) remains unclear. Genetic evidence from some studies indicates that CNP striped marlin are part of a single North Pacific stock comprising individuals from Japan, Taiwan, Hawaii, and California, but the presence of an additional stock in the CNP has been suggested in two recent studies. The goals of this research were to 1) resolve the genetic stock structure of striped marlin in the CNP and 2) intensively study the stock composition of striped marlin caught in the Hawaii-based pelagic longline fishery (HBPLLF) over a 12-month period. Fishery observers collected 418 samples of striped marlin from the HBPLLF from 2019-2020. Of these, 85 samples underwent genotyping-by-sequencing and the data were co-analyzed with over 61,000 sequences from individuals collected throughout the species' range and reported in a previous study. Clustering analyses, which included the new samples, strongly supported a single CNP stock. Samples from the HBPLLF clustered with either the North Pacific or Oceania (New Zealand, Eastern Australia, Western Australia, and Hawaii sample locations) stocks, indicating mixing of the two stocks in the region. Currently, a panel comprised of single nucleotide polymorphisms (SNPs) with the highest power to discriminate between the two stocks is in development and will be used to assign an additional 333 individuals sampled from the HBPLLF with known capture date and location, size, sex, and reproductive condition to their stock of origin in an effort to better understand striped marlin stock dynamics within the HBPLLF.

SUPPORT FOR THE SLOPE SEA AS A MAJOR SPAWNING GROUND FOR ATLANTIC BLUEFIN TUNA: EVIDENCE FROM LARVAL ABUNDANCE, GROWTH RATES, AND PARTICLE-TRACKING SIMULATIONS

POSTER

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The life history of Atlantic bluefin tuna (*Thunnus thynnus*) offers several open questions that complicate the international management of the species, including stock mixing across the Atlantic and the extent of spawning occurring outside of the historically recognized spawning grounds. Recent collections of bluefin tuna larvae in the Slope Sea off the Northeast United States have opened questions about how this region contributes to population dynamics. We analyzed larvae collected in the Slope Sea and the Gulf of Mexico in 2016 to estimate larval abundance and growth rates, and used a high-resolution regional ocean circulation model to estimate spawning locations and larval transport. Using detailed otolith analyses, we did not detect a regional difference in growth rates, but found that in 2016 Slope Sea larvae were larger than Gulf of Mexico larvae prior to exogenous feeding. Slope Sea larvae generally backtracked to locations north of Cape Hatteras and would have been retained within the Slope Sea until the early juvenile stage. We also discuss the spatial and temporal extent of larval collections in the Gulf of Mexico, Mediterranean Sea, and the Slope Sea, and calculate a larval index for the Slope Sea in 2016. Overall, our results provide supporting evidence that the Slope Sea is a major spawning ground that is likely to be important for population dynamics. Further study of larvae and spawning adults in the region should be prioritized to support management decisions.

POPULATION GENETIC STRUCTURE OF MOBULA RAYS IN THE EASTERN PACIFIC OCEAN USING TUNA PURSE SEINE BYCATCH

POSTER

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Manta and devil rays (the family *Mobulidae*) are a charismatic but poorly understood group of ten widely-ranging, filter-feeding elasmobranch species. Mobulids are threatened by incidental capture fisheries (referred to here as "bycatch") in at least 30 fisheries in 23 countries, with the highest bycatch rates reported from gillnets and purse seiners. However, the extent of this bycatch remains unknown, in large part due to the lack of data about genetic stock structure for these species. This study aims to characterize mobulid population structure in the Eastern Pacific Ocean using genetic tools to make species-specific identifications, as well as to infer population demographic information that will directly inform fisheries management and mobulid conservation. Working in collaboration with the Inter-American Tropical Tuna Commission and technicians, we sampled pelagic Mobula rays caught by tuna purse seine vessels, and combined these with samples from research collections and coastal fisheries in Nicaragua, Guatemala, Peru, Mexico, and Ecuador. We used fractional genome sequencing (RAD-Seq), a method that allows for high-coverage genome sequencing for multiple samples simultaneously. We tested for population structure and effective population size among >200 samples, and present preliminary results of this ongoing research. This study is part of an ongoing project to increase our understanding of mobulid population structure and stock structure within Mobula species; information critical to inform management on mobulid population viability in the region.

ONGOING EFFORTS TO UNDERSTAND THE TUNAS IN THE WESTERN ATLANTIC OCEAN USING GENOMIC TOOLS

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Large migratory pelagic marine fishes have long been hypothesized to show a high degree of connectivity across wide areas up to entire oceanic basins, but this idea has been challenged by recent studies based on high-density genome scans that revealed cryptic structure could occur within areas previously thought to be genetically homogeneous. In this work, the connectivity and structure of two exploited tropical tunas, the Atlantic yellowfin tuna (*Thunnus albacares*) and the Atlantic blackfin tuna (*Thunnus atlanticus)* is revisited using a genomic approach. Initial efforts focused on developing draft reference genomes for the two species using Illumina and PACBIO SMRT sequencing. The current blackfin tuna genome assembly based on Illumina reads spans ~63% of the species genome in 74,166 contigs over 1,000bp. The yellowfin tuna hybrid genome assembly currently spans ~94% of the genome in 5,100 contigs over and is being scaffolded by a high-density linkage map developed based on genotypes from a single-pair cross produced in captivity. These resources are being applied to interpret the results of high-density genome scans based on Single Nucleotide Polymorphism markers genotyped using double-digest Restriction Associated DNA sequencing in populations of both species sampled over multiple years across their Atlantic ranges. Results obtained in blackfin tuna currently indicate minimal divergence among geographic sites across the entire sampled range. Ongoing research addressing the structure of the popular yellowfin tuna in the Atlantic Basin and the composition of US fisheries catches is discussed.

ADAPTIVE MARKERS DISTINGUISH NORTH AND SOUTH PACIFIC ALBACORE AMID LOW POPULATION DIFFERENTIATION

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Though much work has been done to understand stock structure of albacore globally, research in the Pacific Ocean has been coarse in nature and has raised a number of questions. For example, tagging data have shown no movement of albacore across the equator and yet previous genetic data have shown a surprisingly poor ability to discriminate between the currently managed North and South Pacific stocks. On a more local scale, tagging studies have shown that the migratory behavior of juvenile albacore varies regionally and seasonally with limited mixing between the northern and southern fishery areas in the Northeast Pacific. However, it is uncertain whether the two migratory groups represent two genetically distinct stocks or fish from the same stock that exhibit different foraging behaviors.

To help resolve some of these uncertainties, we used double digest restriction site-associated DNA sequencing to survey genomic variation in 308 albacore previously collected from 10 sample areas in the North Pacific and 2 sample areas in the South Pacific. We identified two categories of single nucleotide polymorphisms (SNPs) referred to as neutral and putatively adaptive. While both types of SNPs provide information on population structure, the latter has the potential to identify patterns of selection. We analyzed the 308 samples in two ways. First, we grouped individuals based on the 12 sample areas and identified 6,446 SNPs, 32 of which were identified as putatively adaptive. Second, we grouped individuals based on the North Pacific (n = 234) and South Pacific (n = 74) and identified 12,872 SNPs, 84 of which were identified as putatively adaptive.

For the 12 sample area dataset, we found that most sample areas could not be distinguished from one another based on variation at the 6,446 SNPs. However, the two South Pacific sample areas, New Caledonia and Tasmania, were significantly different from the 10 North Pacific sample areas. Correspondingly, the 32 putatively adaptive SNPs primarily distinguished these North and South Pacific groups. In addition, we found evidence for at least two F1 hybrid individuals between the North and South Pacific groups, and results also indicated that a small number of albacore sampled in the North Pacific may be migrants from the South Pacific. For the North vs. South Pacific dataset, we found that albacore could be distinguished from one another based on variation at the 12,872 presumed neutral SNPs. However, the genetic differentiation was largely attributed to variation at the 84 putatively adaptive SNPs.

Altogether these genomic results support the distinction of separate stocks of albacore in the North and South Pacific, but a relatively small proportion of the genome is responsible for the differentiation between these groups. The majority of genetic differentiation between the North and South Pacific is potentially adaptive, which may be important for future management and conservation efforts. Contrary to previous tagging data, the genomic evidence also indicates that migration and interbreeding occurs between these populations, which may matter particularly for fisheries management close to the equator.

PSTBS-IO PROJECT: AN INDIAN OCEAN BASIN SCALE STUDY OF POPULATION STRUCTURE OF TUNA, BILLFISH AND SHARKS.

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In 2017, CSIRO in collaboration with AZTI Tecnalia (Spain), IRD (France) and CFR (Indonesia) commenced a 3-year collaborative project on population structure of tuna, billfish and sharks of the Indian Ocean funded by the European Union and the consortium partners (PSTBS-IO). The project aimed to describe the population structure and connectivity of 12 priority tuna and tuna-like species for the Indian Ocean Tuna Commission, as well as blue and scalloped hammerhead sharks. Genetic analysis of new and archived tissue samples was the primary method, complimented by microchemical analysis of otoliths. The project also aimed to extend collaborative research networks and contribute to technical capacity building in participating coastal states. Sampling was completed between late 2017 and early 2019 with a total of 5,767 tissue samples and 3,010 otoliths collected or made available to the project from partner archives. Of these, 3,610 tissue samples were genotyped and 689 otoliths analysed for microchemistry. The final data coverage for each species across their range within the Indian Ocean varied among the study species and between genetics and microchemistry methods. For genetics, good sample coverage was achieved for the six neritic and tropical tuna species and swordfish; while the coverage for albacore, the two other billfish species and blue shark limited the power of analyses to examine population structure within the Indian Ocean. The sample coverage for otolith microchemistry was often less complete for each species than for genetics due to the logistic difficulty in obtaining otoliths, relative to tissue samples, particularly in the case of larger, more valuable adults. Good coverage was achieved for kawakawa and Spanish mackerel and the three tropical tunas, whereas the lack of otolith samples from the south-east Indian Ocean for albacore limited the scope of inferences that could be made based on microchemistry for this species. The project has provided a sound foundation for exploring specific hypotheses on population structure related to stock assessment and management purposes for the majority of the study species and a good foundation for extending the coverage for the remainder. This presentation provides a summary of the population structure results for each species and recommendations on the next steps to be taken by the IOTC Scientific Committee in considering their implications for assessment and management of these important regional stocks.

SNP DATA REVEALS POPULATION STRUCTURE AND CONNECTIVITY OF FOUR KEY TUNA SPECIES (ALBACORE, BIGEYE, SKIPJACK, AND YELLOWFIN) FISHED IN THE ATLANTIC, INDIAN AND PACIFIC OCEANS.

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Current stock assessments and management arrangements for tropical and temperate tuna assume large panmictic stocks confined to boundaries within regional fishery management organisations (RFMOs). More specifically, they assume a single, well mixed spawning stock generates the recruitment for subsequent generations across the region of the assessment. Recent advances in high throughput sequencing methods have been used to provide greater genetic resolution to address questions of stock structure and provenance. Results from studies of yellowfin tuna suggest there may be more structure in populations of tropical tuna than previously thought. In this paper we summarise results from research spanning 10-year period that provides a global perspective into genetic structure of albacore tuna, bigeye tuna, skipjack tuna, and yellowfin tuna. Comparison of data among these four species reveals a lack of genetic connectivity between ocean basins. We also found evidence of within Ocean basin genetic population differentiation among current sampling sites demonstrating that population structure of these species is more complex than previously thought. Further sampling will confirm temporal stability of these results and will help illuminate the causal mechanisms responsible for observed differentiation such as: i) isolation by distance; and ii) strong bio-geographic barriers; iii) or loci under differential selection among areas in a way that is consistent with global patterns in biogeography. Sustainable management practices for these species should benefit from improved understanding of stock structure and connectivity in these species but this will require further investigation with careful consideration regarding extension of sampling coverage (both temporal and spatial), quality control of tissue collection, and consistent application of genetic methods.

LIFE-HISTORY INFORMATION FROM CLOSE-KIN MARK-RECAPTURE

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CKMR is a fairly new technique that can directly estimate absolute abundance, based simply on genetic comparisons of tissue-samples taken e.g. from fishery catches. While abundance-estimation is the feature that has attracted most attention, CKMR also gives estimates of several important life-history parameters which are between-hard-and-impossible to estimate in any other way--- including true effects of size on fecundity, natural mortality, and connectivity. In this talk, I will give a non-technical explanation of why this works, drawing on examples from various CKMR projects at CSIRO and beyond.

CLOSE KIN MARK RECAPTURE ESTIMATES OF ABUNDANCE FOR AUSTRALIAN AND NEW ZEALAND WHITE SHARKS

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We detail updated results on abundance and population dynamics for the East Australian/New Zealand and Southern-Western Australiana white shark (*Carcharodon carcharias*) populations. Importantly, these estimates do not rely on the highly uncertain historical catch data for this species. To our knowledge, no similar study has been conducted worldwide. The results and methods employed, represent a step-change in capacity to assess otherwise difficult to monitor species, such as white sharks. A larger dataset, and the inclusion of mitochondrial DNA (which is inherited solely from the mother) permitting the exploration of both male and female adult shark population dynamics, enabled a substantial update to previous estimates of both adult and total population size using ancillary juvenile survival estimates. In the east we estimated an adult population of 750 (range: 470 - 1,030) and total abundance 5,460 (range 2,909 – 12,802). Results on adult survival by sex and adult sex ratio are discussed. In addition, sufficient genetic samples have also accrued from to enable the first estimate of adult abundance for the southern-western population. In the southern-western population, adults were estimated to be 1,460 (uncertainty range 760 to 2,250). We also provide estimates of adult survival and population trend from CKMR and statistical design results that allow us to determine how potential future sample collection rates will reduce uncertainty.

INCLUDING CLOSE-KIN MARK-RECAPTURE IN STOCK ASSESSMENTS: THE SOUTHERN BLUEFIN TUNA EXPERIENCE

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Arguably the most important role of a stock assessment is to try and figure out how many adults there are in the population and how many are there now relative to when/if we were not fishing. Some form of this metric forms the stock status advice, and as a result drives the management advice, for the vast majority most of the major assessed tuna populations. Reality often means we have little to no direct data on this part of the population – often we have only fisheries dependent data on the juvenile and sub-adult populations with some coverage of a portion of the mature part of the population. Close-Kin Mark Recapture (CKMR) is a way of using modern genetics and mark-recapture modelling concepts to solve this shortfall. We look for Parent Offspring (POP) and Half-Sibling (HSP) pairs in juvenile-adult and juvenile-juvenile comparisons, respectively and use them within a mark-recapture modelling framework to estimate adult abundance, mortality and population trend. The first successful application of this to a pelagic stock assessment was for Southern Bluefin tuna (SBT) and we outline the CKMR approach and the difference it made to the assessment and management of this stock.

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