

ALMA MATER STUDIORUM Università di Bologna Campus di Ravenna







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TEACHING WEEK 2023 GENETICS AND GENOMICS FOR RESOURCE MANAGEMENT

ALESSIA CARIANI

Lab GenoDREAM - Department BiGeA

ALESSIA CARIANI

BACKGROUND:

- 1998-2009: BSc&MSc&PhD Scienze Ambientali Marine
- 2009-2013: PostDoc from Microarray&Microbes to PopGen in Fish (and AoB!)
- 2013-2019: RTD junior -> RTD senior -> associate professor

NOW:FOCUS ON THE EVOLUTIONARY AND ENVIRONMENTAL DRIVERS OF
BIODIVERSITY IN MARINE TAXA THROUGH INNOVATIVE GENOMIC TOOLS

Main research lines:

- 1. Evolution, systematics and conservation of cartilaginous fish
 - 2. Population genomics and traceability of marine fish

	exploit scientific results in a traceability and management context	eco-compatible management of marine bio-resources	
PRI	IZEFISH & TECHERA (Interreg IT-HR)	MED UNITS; SPELMED (EC EASME/EN	

GBYP (ICCAT) MEDBLUESGEN (EC JRC) FISHBONE; TRANSBORAN (FAO GFC

Lab GenoDREAM - Department BiGeA

Laboratorio di Genetica e **GENO**mica **D**elle **R**isorse **E A**mbiente Marino (GENODREAM) Dip. BiGeA - Campus di Ravenna









Federica P



Elisabetta C - DBC



Ilaria G - DIMEVET



Agostino L



Rachele C Valentina C



Adam J. A



Martina P



Martina S Piergiorgio M





M. Vittoria I



Alexia M

Nicola P

Enrico M. P





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The course will introduce to the potential of genomic approaches, which are increasingly important for understanding evolutionary processes, such as adaptation to the diverse habitats within the marine environment, including fishery-induced evolution.

Recent advances in genome technology will be presented and their implementation from genome assembly to comparative and population genomics.

Examples will be given on how genomics tools can allow tackling several challenges to ensure sustainability and profitability of fisheries management.



WHEN/WHO/WHAT/WHY??? On a Friday afternoon??



Genomic approaches in marine fisheries research: challenges and opportunities LET'S START FROM YOU!



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Genomic approaches in marine fisheries research: challenges and opportunities WORKING GROUP ON APPLICATION OF GENETICS IN FISHERIES AND AQUACULTURE





Genomic approaches in marine fisheries research: challenges and opportunities WORKING GROUP ON APPLICATION OF GENETICS IN FISHERIES AND AQUACULTURE

The Working Group on the Application of Genetics in Fisheries and Aquaculture (WGAGFA)

Promotes the inclusion of genetics and evolutionary concepts and methods as important elements in the management of fisheries and aquaculture.

Establishes a representative, sustained and engaged scientific forum across ICES countries to discuss technological and statistical developments and new ideas in genetics/ genomics, salient opportunities for research consortia, and exchange at the science-policy interface.

New Frontiers

eDNA Microbiomes Transcriptomics Adaptive Diversity Population Sizes Metabarcoding Epigenetics



Contents lists available at ScienceDirect

journal homepage: www.elsevier.com/locate/margen

Marine Genomics



CrossMark

Review

Marine genomics: News and views

Ângela M. Ribeiro ^a, Andrew D. Foote ^b, Anne Kupczok ^c, Bárbara Frazão ^d, Morten T. Limborg ^a, Rosalía Piñeiro ^e, Samuel Abalde ^f, Sara Rocha ^g, Rute R. da Fonseca ^{h,*}

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1.	Introduction
2.	Biodiversity and biogeography
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6.	Aquaculture and bioprospecting
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Ackr	nowledgments
Refe	rences

https://www.ices.dk/community/groups/Pages/WGAGFA.aspx



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Genomic approaches in marine fisheries research: challenges and opportunities WORKING GROUP ON APPLICATION OF GENETICS IN FISHERIES AND AQUACULTURE

How does genetics support fisheries and aquaculture management?

"Applications of genetics and genomics to aquatic resource management is a topical and rapidly growing field of life sciences. In the field of fisheries and aquaculture, genetics is already enabling new genomic approaches to tackling key challenges relating to sustainable exploitation, food security, welfare, and governance of our oceans.

There are two primary levels that genetics have particular application: the first is to provide a source of tools that can be used to designate and monitor individuals, populations/stocks, species and communities, together with elucidating associated biological interactions such as the nature and intensity of predation.

The fact that DNA can be retrieved from whole fish through to highly processed products means that it is possible to trace products and individuals accurately.

Such features, for example enable more effective design of pedigrees in aquaculture, the selection of favourable traits, as well as assigning individuals, stocks and species with unprecedented precision for use in applications from stock assessment through to tackling illegal fishing and promoting eco-certification."



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Professor GARY CARVALHO – ICES INTERVIEW - 8 May 2019

Genomic approaches in marine fisheries research: challenges and opportunities ALSO OUTSIDE EU IN THE MED

GÉNÉTIQUE ET GÉNOMIQUE AU SERVICE DE LA GESTION DE LA PÊCHE ET DE L'AQUACULTURE



Identification taxonomique des espèces : cartographie de leur distribution

 découverte d'espèces cryptiques • reconnaissance des œufs et larves dans le milieu construction des réseaux trophiques pour les modèles écosystémiques de gestion des pêcheries DNA barcoding (mt DNA)

GÉNÉTIQUE ET GÉNOMIQUE POUR

LA GESTION DES PÊCHERIES

ET DE L'AQUACULTURE

Traçabilité des pêcheries pour leur certification et lutte contre la pêche INN

DNA barcoding, SNP, Microsatellites, Nouveaux margueurs

Biosécurité (environnementale et alimentaire) :

• détection des pathogènes détection des blooms d'algues toxiques détection d'espèces invasives DNA barcoding, DNA assays, Nouveaux marqueurs

Sélection génétique pour

l'aquaculture : sélection de géniteurs et des F1 contrôle des croisements suivi du gain génétique Séquençage génomique, gènes

Effets du repeuplement des stocks naturels

Etude des réponses évolutives des espèces face à la pression de pêche : distribution abondance productivité Séquençage génomique, gènes

Evaluation et suivi de la diversité génétique, taille efficace et résilience

Séquençage génomique, gènes fonctionnels

Structure et délimitation des stocks : spatiale

 temporelle stocks mixtes et stocks partagés et détermination de leurs proportions SNP, Microsatellites, Nouveaux marqueurs

Détermination de l'âge des individus (préreguis : taux de diminution de l'ADN télomérique) Telomeric DNA biomarqueur de l'âge

Surveillance des écosystèmes pour

l'approche écosystémique : étude du régime alimentaire pour les réseaux trophiques détection des impacts des facteurs de stress suivi des effets évolutifs du changement climatique DNA barcoding, gènes fonctionnels

Estimation des taux d'exploitation et des abondances

(combiné avec des analyses de capture-marquage-recapture) **DNA fingerprints (Microsatellites)**

des populations



Genomic approaches in marine fisheries research: challenges and opportunities ALSO OUTSIDE EU IN THE MED



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GENETIC VS GENOMIC





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Trends in Ecology & Evolution

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GENETIC & GENOMIC APPLICATIONS

Review

Harnessing the Power of Genomics to Secure the Future of Seafood

Louis Bernatchez,^{1,*,†} Maren Wellenreuther,^{2,3,†} Cristián Araneda,⁴ David T. Ashton,² Julia M.I. Barth,⁵ Terry D. Beacham,⁶ Gregory E. Maes,^{7,8,9} Jann T. Martinsohn,¹⁰ Kristina M. Miller,⁶ Kerry A. Naish,¹¹ Jennifer R. Ovenden,¹² Craig R. Primmer,¹³ Ho Young Suk,¹⁴ Nina O. Therkildsen,¹⁵ and Ruth E. Withler⁶ Trends in Ecology & Evolution, September 2017, Vol. 32, No. 9 STEP 1 STEP 2 STEP 3 STEP 4 Problem New information Do end-users Yes No understand the from genomics Problem not Problem which addresses solution? resolved resolved the problem

Trends in Ecology & Evolution

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QUICK INTRO TO METHODS (QUICK I PROMISE)

Sequencing history



https://the-dna-universe.com/2020/11/02/a-journey-through-the-history-of-dna-sequencing/



QUICK INTRO TO METHODS (QUICK I PROMISE)

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QUICK INTRO TO METHODS (QUICK I PROMISE)

Sequencing history



and-third-generation-sequencing/

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Sequencing history «NEXT» GENERATION SEQUENCING (NGS) PLATFORMS





NGS PLATFORMS -> Illumina Sequencing



https://www.illumina.com/content/dam/illuminamarketing/documents/products/illumina_sequencing_introduction.pdf





NGS PLATFORMS -> Illumina Sequencing



to the flow cell surface. Each bound fragment is amplified into a clonal cluster through bridge amplification.



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NGS PLATFORMS -> Illumina Sequencing

Reads are aligned to a reference sequence with bioinformatics software. After alignment, differences between the reference genome and the newly sequenced reads can be identified.

AGATGGTATTG

GATGGCATTGCAA

ATGGCATTGCAATT AGATGGCATTGCAATTTG

ATGGCATTGCAATTTGACAT TGGCATTGCAATTTG

GCATTGCAATTTGAC

AGATGGTATTGCAATTTGACAT



Sequencing reagents, including fluorescently labeled nucleotides, are added and the first base is incorporated. The flow cell is imaged and the emission from each cluster is recorded. The emission wavelength and intensity are used to identify the base. This cycle is repeated "n" times to create a read length of "n" bases.

NGS PLATFORMS -> Illumina Sequencing





NEW/NOW GENERATION SEQUENCING (NGS) PLATFORMS AKA THIRD GENERATION SEQUENGING

SINGLE MOLECULE REAL-TIME SEQUENCING



SMRT SOLUTIONS FOR THE WORLD'S MOST INNOVATIVE SCIENTISTS

Advances in sequencing technology have expanded our understanding of biological complexity, but there are still challenges limiting our access to this information. In an effort to overcome these challenges, we have designed a suite of products and services to bring unparalleled depth and accuracy to your sequencing efforts. Our goal is to provide comprehensive solutions that deliver **real insight and real results for real, lasting impact.**

NANOPORE SEQUENCING

NANOPORE

PRODUCTS HOW IT WORKS APPLICATIONS GET STARTED PUBLICATIONS

Scalable, real-time biological analysis technology

Nanopore devices perform DNA/RNA sequencing directly and in real time. The technology is scalable from miniature devices to high-throughput installations.



Min**ION**

- Pocket-sized, portable device for biological analysis
- Up to 512 nanopore channels
- Simple 10-minute sample prep available
- Real-time analysis for rapid, efficient workflows
- Adaptable to direct DNA or RNA sequencing

About MinION Start using MinION



- would like access to sequencing for \$1,000
- want to sequence immediately, not
- wait
 want to sequence outside a lab
- need 10-20Gb per 48 hours
- want to avoid CapEx investments



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NEW/NOW GENERATION SEQUENCING (NGS) PLATFORMS AKA THIRD GENERATION SEQUENGING

SINGLE-MOLECULE REAL-TIME SEQUENCING (SMRT) by Pacific Biosciences

Epifluorescence detection

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Nature Reviews | Genetics

Time

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NEW/NOW GENERATION SEQUENCING (NGS) PLATFORMS AKA THIRD GENERATION SEQUENGING

NANOPORE SEQUENCING

Exonuclease-based 'SEQUENCING BY DECONSTRUCTION' By Oxford Nanopore Technologies 'Strand sequencing' is a technique that passes intact DNA polymers through a protein nanopore, sequencing in real time as the DNA translocates the pore.







- The DNA polymer passes through the nanopore itself
- The nanopore is engineered to allow single-base resolution within the strand
- A DNA polymerase, coupled with a α-hemolysin, synthesizes a new strand of DNA using as a template the polymer coming out of the pore

Video nanopore: http://www.youtube.com/watch?v=_rRrOT9gfpo&feature=related



NEW/NOW GENERATION SEQUENCING (NGS) PLATFORMS AKA THIRD GENERATION SEQUENGING





Oxford Nanopore Long reads



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Illumina sequences:	 STATE STOR
PacBio sequences:	
MinION sequences:	 ALMA MATER STUDIORUM Università di Bologna

Take home message

- High-throughput sequencing, which includes next-generation "short-read" and third-generation "long-read" sequencing methods has brought tremendous opportunities to natural sciences
- Sequencing is becoming cheaper and cheaper and faster
- Sequencing applications are limited only by "imagination" (in reality technical and budget constraints)
 - the whole genome (de novo or resequencing) -> comparative genomics, epigenetics
 - the whole exome
 - the expressed transcriptome -> RNASeq
 - pools of genomes
 - reduced representation of the genome for hundreds of individual -> population genomics (GBS, RADlike...)
 - the same defined target for multiple samples/sources -> metabarcoding/metagenomics



QUICK INTRO TO NGS METHODS All that glitters... Needs Data Analysis!!

CrossMark

Bioinformatic challenges of genomic data



Rute R. da Fonseca^{a,*}, Anders Albrechtsen^a, Gonçalo Espregueira Themudo^c, Jazmín Ramos-Madrigal^b, Ionas Andreas Sibbesen^a, Lasse Maretty^a, M. Lisandra Zepeda-Mendoza^b, Paula F. Campos^{b,d}, Rasmus Heller^a, Ricardo J. Pereira^b







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non-model organisms

GENOMIC CONCEPTUAL FRAMEWORK





Benestan *et al.* 2016

GENOMIC CONCEPTUAL FRAMEWORK

GENOMICS FOR NON-MODEL ORGANISMS

Optimal sequencing method	Minimal Reference Needed
RAD	None
Exome Sequencing	De novo transcriptome**
Low-coverage WGS	Draft genome
RNAseq or TagSeq	None or De novo transcriptome
	Optimal sequencing method RAD Exome Sequencing Low-coverage WGS RNAseq or TagSeq

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Jon Puritz B@G4 2018 https://github.com/jpuritz/Winter.School2018

While (sleepy) fillCup(); drinkCoffee();







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Examples will be given on how genomics tools can allow tackling several challenges to ensure sustainability and profitability of fisheries management.



WHEN/WHO/WHAT/WHY??? On a Friday afternoon??





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FISH and FISHERIES



Ocean's eleven: a critical evaluation of the role of population, evolutionary and molecular genetics in the management of wild fisheries Abstract

Oceans Flagship, CSIRO Marine and Atmospheric B Fisheries, Woolgoolga, NSW, Australia; ⁴Wealth fro Queensland Biosciences Precinct, 306 Carmody Roa Biomedical Sciences, The University of Queensland,

Significant changes have occurred in the well-established partnership between fisheries managers and geneticists over the last 50 years. It is therefore timely to Jennifer R Ovenden^{1,5}, Oliver Berry², David J W review and recalibrate the ways in which genetic technologies can assist the fishing industry to maintain productive and sustainable harvests. Our objective is to ¹Molecular Fisheries Laboratory, Queensland Gover contribute to the mutual understanding of all stakeholders in the genetics-management partnership. Genetic technologies that are relevant to fisheries management are grouped into eleven themes, which are described in plain language for a nonspecialist audience. The role that the genetic information plays in fisheries management is explained, along with an assessment of the challenges and barriers that may be preventing the uptake of the information into the fisheries management process. The compelling conclusion is that genetics offers a diverse collection of versatile and useful tools for informing fisheries managers about issues that have a biological basis. Presently, mainstream use of genetic tools focuses on a narrow set of fisheries management issues, but the diversity of genetic tools and the novel issues they can address indicates that uptake will grow, particularly as communication between geneticists and end-users improves.

Correspondence:

Jennifer Ovenden. Molecular Fisheries Laboratory, School of Biomedical Sciences, University of Queensland, St Lucia, Old 4072, Australia Tel.: +61 7 3346 0806 Fax: +61 7 3365 1766 E-mail: zljovend@uq. edu.au

Received 12 Sep 2012 Accepted 3 Aug 2013

Keywords environmental monitoring, genetic effective population size, genetic ALMA MATER STUD mark-recapture, product provenance, stock structure, unnatural selection





Ocean's eleven: a critical evaluation of the role of population, evolutionary and molecular genetics in the management of wild fisheries

Jennifer R Ovenden^{1,5}, Oliver Berry², David J Welch³, Rik O

¹Molecular Fisheries Laboratory, Queensland Government, PO B Oceans Flagship, CSIRO Marine and Atmospheric Research, Und Fisheries, Woolgoolga, NSW, Australia; ⁴Wealth from Oceans Fl Queensland Biosciences Precinct, 306 Carmody Road, St Lucia, Biomedical Sciences, The University of Queensland, St Lucia, Qu



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WEALTH FROM OCEANS www.csiro.au

UNDERSTANDING THE ATTRIBUTES OF HARVESTED SPECIES

A field genet

A plain-language emerging themes maintenance of p

I. Species identification

Assigning specimens to species ... 2

II. Stock structure

III. Mixed stock analysis

IV. Biomarkers for age

Indexing the age of specimens without otoliths5

V. Ecosystem monitoring

MEASURING THE IMPACT OF FISHING

VI. Harvest rate and abundance

Abundance and other population parameters can be estimated from the recapture of individuals identified with genetic tags......7

VII. Genetic diversity, abundance and resilience

VIII. Evolutionary responses to fishing

IX. Genetic effects of stock enhancement

BIOSECURITY TOOLS

X. Detection of pathogens and invasive species

Genetic assays can diagnose and quantify the incidence of diseases or invasive species in wild fisheries and aquaculture......11

POST-HARVEST REGULATION

XI. Product provenance and fisheries surveillance

Genetic testing can be used to detect product substitution and check accuracy of labeling......12





ATTRIBUTES OF HARVESTED SPECIES

Theme I: Species identification

Why is it important to fisheries management?

- An organism's identity is fundamental to the monitoring, marketing and study of fisheries species.
- DNA analysis is:
 - a rapid, universal and highly accurate tool for assigning a specimen to a species;
 - important when the specimen cannot be identified in any other way; and
 - often the only way to identify cryptic species.

How does it work and what are its limitations?

- DNA analysis for species recognition uses the 'DNA barcoding' approach.
- Species are recognized when a DNA sequence is obtained from the specimen and matched against reference data.
- Accuracy is usually greater than 90%.
- Errors can be due to problems with reference databases or peculiarities in the type of DNA used.
- DNA databases for fisheries species are being established worldwide.

Case studies

- DNA analysis was used to recognize the species identity of fish eggs, larvae and juveniles, and was used to complete the life-cycle of commercially valuable species in Mexican waters of the Caribbean Sea.
- Seabirds killed as bycatch in pelagic longline fisheries were assigned to appropriate source species or populations.





ATTRIBUTES OF HARVESTED SPECIES

Theme I: Species identification

Barriers to uptake

 DNA barcoding is a well established procedure and expertise are widely available. There are no significant technical barriers to uptake by fisheries management.

Future

- Species descriptions will increasingly include DNA sequences as diagnostic characters.
- Reference data per species should consist of DNA sequences from many genes, if possible.
- Accuracy of DNA barcoding assignments will continue to improve as reference databases grow.
- Increasingly DNA-based species recognition will be deployable in the field.

GenoDREAM Experience

- Fish&Chip EU project
- ELASMOMED network
- ABFT larvae and bones ID
- Egg case identification




Theme I: Species identification

GenoDREAM Experience



Which species??





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Cogno

Theme I: Species identification











Theme I: Species identification

GenoDREAM Experience







GenoDREAM Experience Fish&Chip EU project



FISH&CHIPS



Towards DNA chip technology as a standard analytical tool for the identification of marine organisms in biodiversity and ecosystem research

OPEN ORCESS Freely available online



Identifying Fishes through DNA Barcodes and Microarrays

Marc Kochzius^{1,2}*, Christian Seidel^{1¤a}, Aglaia Antoniou³, Sandeep Kumar Botla^{1¤b}, Daniel Campo^{4¤c}, Alessia Cariani⁵, Eva Garcia Vazquez⁴, Janet Hauschild^{1¤d}, Caroline Hervet^{6¤e}, Sigridur Hjörleifsdottir⁷, Gudmundur Hreggvidsson^{7,8}, Kristina Kappel¹, Monica Landi^{5¤f}, Antonios Magoulas³, Viggo Marteinsson⁷, Manfred Nölte⁹, Serge Planes^{6¤g}, Fausto Tinti⁵, Cemal Turan¹⁰, Moleyur N. Venugopal¹¹, Hannes Weber¹, Dietmar Blohm¹ September 2010 | Volume 5 | Issue 9 | e12620





GenoDREAM Experience ELASMOMED network

ro		FAO Division
Barcode ID	Morphological ID	(N° of misidentified specimens/N° of barcoded
Pr		specimens)
Dasyatis centroura	Pteroplatytrygon violacea	37.1.3 - Sardina (1/1)
²³ Dasyatis tortonesei	Dasyatis pastinaca	37.2.2 – Ionian (4/4)
Pteroplatytrygon violacea	Dasyatis centroura	37.1.1 - Balearic (1/1)
Leucoraja circularis	Leucoraja fullonica	37.1.3 - Sardinia (2/8); 37.2.2 - Ionian (1/5)
🛯 Raja polystigma	Raja montagui	37.1.1 - Balearic (2/5)
Torpedo marmorata	Torpedo nobiliana	37.3.2 - Levant (3/9)
Torpedo marmorata	Torpedo torpedo	37.2.1 - Adriatic (1/1)
Scyliorhinus canicula	Scyliorhinus stellaris	37.2.1 - Adriatic (4/20)
Mustelus punctulatus	Mustelus mustelus	37.1.1 - Balearic (5/5); 37.2.1 - Adriatic (45/146)
. Centrophorus granulosus	Centrophorus uyato	37.1.1 - Balearic (1/5)
Squalus blainville	Squalus acanthias	37.1.1 - Balearic (2/3); 37.3.2 - Levant (5/5)
🖁 Squalus blainville	Squalus megalops	37.2.2 - Ionian (4/12)
WNLOADS		Jul-06, 2015 05:27 Silvia Messinetti Modify-Specimens (1)
uences		Jul-06, 2015 05:27 Sitvia Messinetti Modify-Specimens (1)
ta Spreadsheets ecimen Labels	Elasmobranchii (class) (978)	Jul-06, 2015 05:26 Silvia Messinetti Modify-Specimens (1) Jul-06, 2015 05:26 Silvia Messinetti Modify-Specimens (1)
<u>ice Files</u>	Hotocephati (class) (17)	Jun-23, 2015 04:32 Silvia Messinetti Move-Records (3)

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GenoDREAM Experience ABFT larvae and bones ID









Rediscovering our relationship with the sea: Unlocking the evolutionary history of the mighty bluefin tuna using novel paleogenetic techniques and ancient tuna remains.



Puncher GN¹, Cilli E¹, Morales A², Onar V³, Massari F¹, Cariani A¹ and Tinti F¹ ¹University of Bologna (IT), ²Autonomous University of Madrid (SP), ³University of Istanbul



RESEARCH ARTICLE

Molecular Identification of Atlantic Bluefin Tuna (Thunnus thynnus, Scombridae) Larvae and Development of a DNA Character-Based Identification Key for Mediterranean **Scombrids**

Gregory Neils Puncher¹*, Haritz Arrizabalaga², Francisco Alemany³, Alessia Cariani¹, Isik K. Orav⁴, F. Saadet Karakulak⁴, Gualtiero Basilone⁵, Angela Cuttitta⁵, Salvatore Mazzola⁵, Fausto Tinti¹

Misidentification of fish larvae: Δ call for caution and taxonomic reform



Bologna, Italy

BOLOGN

Rev Fish Biol Fisheries (2015) 25:485-502 DOI 10.1007/s11160-015-9390-1



REVIEWS

Puncher¹, H

Misidentification of bluefin tuna larvae: a call for caution and taxonomic reform

Gregory Neils Puncher · Francisco Alemany · Haritz Arrizabalaga · Alessia Cariani · Fausto Tinti





GenoDREAM Experience Egg case identification

< <u>S) A11</u>	TORNAL ONLEGO
IDENTIFIERS	
Sample ID:	MEDITS2013C28_C6
Process ID:	ECMR011-16
Institution Storing:	University of Bologna, Genetics for Environmental and Fishery Resources Lab
Field ID:	Medits2013Cala28_C6
Museum ID:	
Collection Code:	
TAXONOMY	
Identification:	Rajidae
Rank:	Family
Identifier	Cecilia Mancusi
Identification Method:	
Identifier Institution:	
Identifier Email:	c.mancusi@arpat.toscana.it
Taxonomy Note:	Unidentified Egg Capsule containing embryo
Rank	Current Record (MEDITS2013C28_C6)
Phylum:	Chordata
Class:	Elasmobranchii
Order:	Rajiformes
Family:	Rajidae
Subfamily:	
Genus:	
Species:	
Veusher Status	
VOLCOM STATUS	

Found of Olarab.
Tissue Descriptor:
Sex:
Reproduction:
Life Stage:
Extra Info:
Note:
Associated Taxa:
Associated Specimens
Reference Link:



License Holder: Unspecified



Strongly structured populations and reproductive habitat fragmentation increase the vulnerability of the Mediterranean starry ray *Raja asterias* (Elasmobranchii, Rajidae)

!	Giusy Catalano ¹	Valentina Crobe ¹ Alice Ferrari ¹ Romano Baino ²
	Daniela Massi ³ ©	Antonino Titone ³ Cecilia Mancusi ² Fabrizio Serena ³
C	Rita Cannas ⁴ 💿 🛛	Laura Carugati ⁴ 🧧 Farid Hemida ⁵ Chiara Manfredi ⁶
	Riccardo Melis ⁴ 💿	Giuseppe Scarcella ⁷ Letizia Sion ⁸ Marco Stagioni ⁶
	Fausto Tinti ¹ 💿 🛛	Alessia Cariani ¹ 💿





Theme II: Fisheries stock structure

How does it work and why is it important?

- Biological stocks, which represent demographically cohesive groups of organisms, are fundamental units of fisheries management.
- Genetics analysis is widely used to determine the spatial extent of biological stocks.
- Genetics detects enduring patterns of stock structure, in contrast to other methods that use characteristics acquired during the lifetime of an individual (e.g. parasite load, chemical composition of otoliths).

How is it used for fisheries management?

- Genetic assays are used to divide the range of a species into discrete demographic units – "stocks".
- Fisheries managers use stock boundaries to assign quotas, model alternative harvesting scenarios and to design monitoring programs.

Case studies

- Genetic stock structure was used to determine if independent or joint management was necessary for shark and snapper species with continuous distributions between northern Australia and Indonesia.
- Sustainable use of salmonid species in North America relies on spatial and temporal genetic stock structure analyses.
- Some fishes, such as the Atlantic Cod, exhibit negligible conventional stock structure, but pronounced regional differences in functional genes.





Theme II: Fisheries stock structure

Barriers to uptake

- A major challenge is whether management can be applied at the appropriate spatial scale revealed by genetic tests.
- Greater communication between geneticists and fisheries scientists and managers is needed to increase the uptake of genetic stock structure information.

Future

- The power of genetic markers to reveal stocks will increase.
- Analyses will increasingly focus on the behaviour of individual organisms on ecological time frames, rather than on the long-term average behaviours of entire populations.
- The availability of genomic resources for fisheries species will increase and enable identification of genetic variants experiencing natural selection. This will increase the power of genetic markers to define stocks and highlight stocks with unique adaptive characteristics.

GenoDREAM Experience

- FishPopTrace EU project
- STOCKMED EU project
- AdriaMED FAO project
- SPELMED EU project
- MED_UNITS EU EU project
- FISHBONE FAO project
- TRANSBORAN FAO project





Theme II: Fisheries stock structure

GenoDREAM Experience FishPopTrace EU project











"GENOME SCAN" APPROACHES TO IDENTIFY "OUTLIER" LOGI









ATTRIBUTES OF HARVESTED SPECIES





Theme II: Fisheries stock structure GenoDREAM Experience FishPopTrace EU project



NEUTRAL LOCI VS OUTLIER LOCI Solea solea



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Theme II: Fisheries stock structure GenoDREAM Experience FishPopTrace EU project



Merluccius merluccius

299 SNPs NEUTRAL

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Theme II: Fisheries stock structure

GenoDREAM Experience STOCKMED EU project



MEDITERRANEAN HALIEUTIC RESOURCES EVALUATION AND ADVICE Specific Contract no 7 - STOCKMED: "Stock units: Identification of distinct biological units (stock units) for different fish and shellfish species and among different GFCM-GSA"

STUDIOR BIOR

Identification of stock units – Vision from different disciplines/criteria *M.Merluccius*







Theme II: Fisheries stock structure GenoDREAM Experience STOCKMED EU project

Identification of stock units and stock boundaries by multi-criteria approach



Merluccius merluccius - Num of stocks = 6 - HAI = 0.95

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Theme III: Resolving mixed-stock fisheries

Why is it important to fisheries management?

- Some fisheries resources consist of aggregations of individuals from several stocks.
- Mixed stock analysis determines the proportion of the harvested aggregation belonging to each stock.
- It allows aggregations to be exploited whilst enabling independent management of breeding stocks.

How does it work and what are the limitations?

- Mixed stock analysis uses baseline (reference) genetic data on component stocks.
- It includes simulations to determine likely accuracy of the analysis.
- Mixed stock analysis requires genetic differences between component stocks.

Case studies

- SNP genetic markers were used to characterize freshwater breeding populations of sockeye salmon from western North America and eastern Russia.
- A large number (35,549) of immature, ocean-going sockeyes were assigned back to breeding populations
- Salmon from North American populations were largely found in the Russian exclusive economic zone.
- Their seasonal route of migration to and from North American breeding locations was determined.





Theme III: Resolving mixed-stock fisheries

Barriers to uptake

- There are no significant technical barriers to uptake. However mixed-stock analysis requires establishment and maintenance of reference datasets.
- The major challenge is balancing the value of the new information with the costs.

Future

- New DNA sqequencing technology will speed the development of DNA markers for mixed-stock analysis, and therefore increase the numbers of species that can be analysed.
- + It may be needed in future for:
 - sharks that have inshore breeding locations (e.g. bull and white sharks); and
 - species whose life cycles alternate between freshwater, estuarine and marine feeding and breeding stages (e.g. mullet).

GenoDREAM Experience

ICCAT GBYP
 consortium 2011-2019





Theme III: Resolving mixed-stock fisheries

GenoDREAM Experience ICCAT GBYP consortium 2011-2019



Subcontractors:

- Dr. Isik Oray
- Univ. Pau (France)
- Univ. Arizona (USA)
- Dr. Toshihide Kitakado (Japan)
- Sgiker/Ibercron (EHU, Spain)
- KaliTuna
- Dr. Massimiliano Valastro

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Fisheries Research Ayency National Research Institute of Far Seas Fisheries







Theme III: Resolving mixed-stock fisheries

GenoDREAM Experience ICCAT GBYP consortium 2011-2019









Theme III: Resolving mixed-stock fisheries

GenoDREAM Experience ICCAT GBYP consortium 2011-2019



Larvae Blue Young-of-the-year Green Medium adult Yellow Large adult Purple

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EMLS110* EMLS130

Theme III: Resolving mixed-stock fisheries GenoDREAM Experience ICCAT GBYP consortium 2011-2019







Theme III: Resolving mixed-stock fisheries

GenoDREAM Experience ICCAT GBYP consortium 2011-2019







Theme III: Resolving mixed-stock fisheries GenoDREAM Experience ICCAT GBYP project still active... ... and TO BE CONTINUED

2004

2006



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2008





Theme III: Resolving mixed-stock fisheries GenoDREAM Experience ICCAT GBYP project still active... ... and TO BE CONTINUED

Check repository at https://www.iccat.int/gbyp/en/biostu.asp





https://doi.org/10.1002/fee.2090





Theme IV: DNA as a biomarker for age

Why is it important to fisheries management?

- Growth estimates are essential for devising harvest strategies. But, growth cannot be estimated without knowing age.
- The age of individuals of some fisheries species can be estimated by counting growth rings in sectioned hard parts (like otoliths in finfish).
- Many fisheries species (e.g. crustaceans) don't have hard parts for sectioning.
- Counting growth rings is lethal, whereas biomarkers can be assayed from tissue taken non-lethally.

How does it work and what are the limitations?

- Telomeric DNA occurs at the end of chromosomes and gets shorter as the animal gets older.
- If the shortening rate of telomeric DNA is known, age can be inferred from the length of a specimen's telomeres.
- Calibrating the rate of telomere attrition is challenging if the species cannot be maintained in captivity or aged in other ways.

Case studies

 A relationship was demonstrated between telomere length and shell size in abalone from Tasmania, but it has not been extended to telomere length and age in this species.





Theme IV: DNA as a biomarker for age

Barriers to uptake

- Little is known about DNA as a biomarker for age in fisheries species.
- Presently cost precludes wide usage.
- Assays for telomere length may need to be developed and calibrated *de novo* for each species and population.

Future

- There are a variety of DNA-based biomarkers for age, but they have received little attention.
- Knowledge about telomeric DNA will increase as genomic resources become available for fisheries species.

GenoDREAM *indirect* Experience

- ICCAT GBYP project
- Methylation patterns in specific genes





Theme IV: DNA as a biomarker for age GenoDREAM *indirect* Experience ICCAT GBYP project

- 7. CALIBRATION EXERCISE IN COLLABORATION WITH GBYP COORDINATION
- Task leader: Enrique Rodríguez-Marín (IEO)

Participants:

GBYP COORDINATOR: Antonio Di Natale

IEO: Pablo Quelle, Marta Ruiz.

CSIRO: Jessica Farley

Gulf Coast Research Laboratory: Patricia Lastra Luque

Hellenic Centre for Marine Research: George Tserpes

IRD/IFREMER/UM2: Fany Sardenne

NOAA: Robert Allman, Ashley Pacicco

NRIFSF: Taiki Ishihara

SABS: Dheeraj Busawon

UNIBO: Marco Stagioni, Ennio Russo

UNICA: Andrea Bellodi, Stefania Vittori

UNIGE: Fulvio Garibaldi, Luca Lanteri, Alessandro Marcone

University of Athens: Persefoni Megalofonou, Niki Milatou

University of Maine/Gulf of Maine Research Institute: Elise Koob



Figure 7.1- CV (%) trend by age and by calcified structure/type of light and reader experience (exp= experienced, inexp= inexperienced).





Theme IV: DNA as a biomarker for age GenoDREAM *indirect* Experience



Research Article 🛛 🔂 Full Access

Inferring chronological age from DNA methylation patterns of human teeth

Cristina Giuliani, Elisabetta Cilli, Maria Giulia Bacalini, Chiara Pirazzini, Marco Sazzini, Giorgio Gruppioni, Claudio Franceschi, Paolo Garagnani 🗙, Donata Luiselli

First published: 15 December 2015 | https://doi.org/10.1002/ajpa.22921 | Cited by: 7

Epigenetic clock in humans

Methylation of ELOVL2 gene as a new epigenetic marker of age

Paolo Garagnani^{1,2}, Maria G. Bacalini^{1,2}, Chiara Pirazzini^{1,2}, Davide Gori³, Cristina Giuliani⁴, Daniela Mari^{5,6}, Anna M. Di Blasio⁷, Davide Gentilini⁷, Giovanni Vitale ^{5,7}, Sebastiano Collino⁸, Serge Rezzi⁸, Gastone Castellani⁹, Miriam Capri^{1,2}, Stefano Salvioli^{1,2} and Claudio Franceschi 1,2,*

Article first published online: 14 OCT 2012 DOI: 10.1111/acel.12005



Issue

Aging Cell

Volume 11, Issue 6, pages 1132–1134, December 2012

Open Acc





published: 17 August 201

dol: f0.3389/lgane.2017.00106

Theme IV: DNA as a biomarker for age

GenoDREAM *indirect* Experience



Epigenetic clock in humans applied to wild animals (mammals)

Measuring Animal Age with DNA Methylation: From Humans to Wild Animals

Ricardo De Paoli-Iseppi^{1,2*}, Bruce E. Deagle², Clive R. McMahon³, Mark A. Hindell¹, Joanne L. Dickinson⁴ and Simon N. Jarman^{5,6}

¹Institute for Menine and Antarctic Studies, University of Tesmania, Hobert, TAS, Australia, ²Australian Antarctic Division, Hobert, TAS, Australia, ^a Sydney Institute of Marine Science, Sydney, NSW, Australia, ⁴ Cancer, Genetics and Immunology Group, Merutes Institute for Medical Research, Hobart, TAS, Australia, ⁹ Trace and Environmental DNA Laboratory, Department of Environment and Agriculture, Curtin University, Parth, WA, Australia, *CSIRO Indian Ocean Marine Research Centre, University of Western Australia, Parth, WA, Australia

AR ECOLOGY

Molecular Ecology (2015) 24, 4826-4847

doi: 10.1111/mec.13367

INVITED REVIEWS AND SYNTHESES Molecular biomarkers for chronological age in animal ecology

SIMON N. JARMAN, * ANDREA M. POLANOWSKI, * CASSANDRA E. FAUX, * JOOKE ROBBINS, † RICARDO DE PAOLI-ISEPPI,** MARK BRAVINGTON§ and BRUCE E. DEAGLE* *Australian Antarctic Division, 203 Channel Highway, Kingston, Tas. 7050, Australia, †Center for Coastal Studies, 5 Holway Avenue, Provincetown, MA 02657, USA, 1Institute of Marine and Antarctic Studies, University of Tasmania, Castray Esplanade, Hobart, Tas. 7000, Australia, §Marine Laboratory, Commonwealth Scientific and Industrial Research Organisation, Castray Esplanade, Hobart, Tas. 7000, Australia

Environomics MINI REVIEW **Future Science** Platform



CSIRO

DNA Ageing: Rapid epigenetic age estimation for animals >

This project aims to advance technical developments and foster a deeper theoretical understanding of the epigenetic changes associated with age.

O SCIENTIFICO-DIDATTICO DI RAVENNA





Theme IV: DNA as a biomarker for age GenoDREAM *indirect* Experience

 Received: 31 May 2019
 Accepted: 22 October 2019

 DOI: 10.1111/1755-0998.13111

RESOURCE ARTICLE

Epigenetic clock in humans applied to wild animals (fishes!)

A clockwork fish: Age prediction using DNA methylation-based biomarkers in the European seabass

WILEY

Dafni Anastasiadi 💿 | Francesc Piferrer 💿

	F	Received: 18 August 2020	Revised: 17 November 2020	Accepted: 26 November 2020
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DOI: 10.1111/mec.15764

ORIGINAL ARTICLE

MOLECULAR ECOLOGY WILEY

Footprints of global change in marine life: Inferring past environment based on DNA methylation and gene expression marks

Dafni Anastasiadi¹ D | Changwei Shao^{2,3} | Songlin Chen^{2,3} | Francesc Piferrer¹





Theme V: Ecosystem monitoring

Why is it important to fisheries management?

- As ecosystem-based management is increasingly adopted, tools to monitor interactions between fisheries and the environment are more in demand.
- Genetic tools can provide unique understandings of ecological processes, including: mapping complex food webs, measuring environmental stressors, and detecting evolutionary effects of climate change.

How does it work and what are the limitations?

- DNA studies can reveal diets in great detail. Dietary studies can be used to understand the indirect effects of fishing on ecosystems.
- Measuring the activity of genes in harvested species can reveal the presence of pollutants and other stressors.
- Functional genetic variants can be tracked though time to detect effects of environmental change.

Case studies

- Comparable diet compositions were obtained from parallel DNA-based and microscopic analyses of Australian fur seal diets. DNA-based analysis was more rapid and more detailed.
- Harvested species including European flounder and mussels are used as biosensors for environmental contaminants.
- Alaskan pink salmon exhibited a genetic change associated with the timing of breeding. This change was in line with expectations under climate change.





Theme V: Ecosystem monitoring

Barriers to uptake

 Technically, these tools are relatively mature. Where there is demand for information to support ecosystembased management, there should be few barriers to adoption of these methods to complement conventional assessment tools.

Future

- Environmental monitoring through DNA analysis is a rapidly growing field driven largely by technological developments such as nextgeneration DNA sequencing.
- Tools to monitor the environment are likely to receive increasing attention for the management of wild fisheries.

GenoDREAM Experience

- INV-CHIP prototype in the framework of Fish&Chip EU project
- Hake diet by gut content metabarcoding
- Water samples metabarcoding (deep sea, fishing activities)



Theme V: Ecosystem monitoring GenoDREAM Experience Hake diet by NGS metabarcoding

Received: 7 May 2018 Reviced: 25 July 2018 Accepted: 8 August 2018

DOI: 10.1002/ece5.4500

ORIGINAL RESEARCH

WILEY Ecology and Evolution

A metabarcoding approach for the feeding habits of European hake in the Adriatic Sea

Giulia Riccioni¹ 💿

| Marco Stagioni¹ | Corrado Piccinetti¹ | Simone Libralato²

¹Department of Siciogical, Geological and Environmental Sciences, University of Sologna, Sologna, Italy

^oChapter of Oceanography, Echo Group, National Institute of Oceanography and Experimental Geophysics - OGS, Triacte, Italy

Correspondence

Giula Riccioni, Department of Biological, Geological and Environmental Sciences, University of Bologna, Bologna, Italy. Email: giuliariccioni@unibo.it

Funding information Italian RITMARE Flagship Project; MEDITS (International Sottom Trawi Survey in the Meditarranean) project Abstract

European hake (Merluccius merluccius) is one of the most economically important fish for the Mediterranean Sea. It is an important predator of deep upper shelf slope communities currently characterized by growth overexploitation: the understanding of hake's diet might support next generation management tools. However, all current European hake diet studies depend on the morphological identification of prey remains in stomach content, with consequent limitations. In this study, we set up a metabarcoding approach based on cytochrome oxidase I PCR amplification and Miseo Illumina paired-end sequencing of M. merluccius stomach content remains and compared the results to classic morphological analyses. A total of 95 stomach contents of M. merluccius sampled in the North-Central Adriatic Sea were analyzed with both the metabarcoding and morphological approaches. Metabarcoding clearly outperformed the morphological method in the taxonomic identification of prey describing more complex trophic relationships even when considering the morphological identification of 200 stomach contents. Statistical analysis of diet composition revealed a weak differentiation among the hake's size classes, confirming an opportunistic feeding behavior. All the analyses performed showed the presence of a core of shared prey among the size classes and a cloud of size-specific prey. Our study highlights the exceptional potential of metabarcoding as an approach to provide unprecedented taxonomic resolution in the diet of M. merluccius and potentially of other marine predators, due to the broad-spectrum of detection of the primers used. A thorough description of these complex trophic relationships is fundamental for the implementation of an ecosystem approach to fisheries.

KEYWORDS Adriatic Sea, European hake, feeding habits, Merluccius merluccius, metabarcoding

scientific reports

DNA metabarcoding suggests dietary niche partitioning in the Adriatic European hake

Giulia Riccioni^{1,5}, Marco Stagioni^{1,2}, Chiara Manfredi^{1,2}, Fausto Tinti³, Corrado Piccinetti¹ & Simone Libralato⁴

The Northern Adriatic Sea (FAO Geographical Sub-Area 17) is one of the most productive fishing areas of the Mediterranean Sea and it includes a broad diversity of habitats. In the Northern Adriatic basin, the Pomo Pit (200–273 m of depth) is one of the most important areas of aggregation for some demersal stocks shared in the Adriatic Sea and it is an important spawning/nursery area of the European hake (*Merluccius merluccius*). Through a metabarcoding approach we investigated the feeding habits of European hake, both inside and outside the Pomo Pit, and their temporal variability comparing samples collected in 2016 and 2014. Our analyses proved the presence of an ontogenetic shift from a diet based mainly on crustaceans in juveniles to a more piscivorous feeding behaviour in adult hakes and suggested the Pomo Pit. The main differences among adult hakes refer to the presence of molluscs in the stomachs of hakes collected within the Pomo Pit and the presence of high depth prey species (i.e., *Micromesistius poutassou*). Metabarcoding revealed the relevant ecological role played by the Pomo Pit in *M. merluccius* feeding behaviour and ontogenetic development, promoting a careful ecosystem-based management of fisheries in this area through focused conservation measures.

https://doi.org/10.1038/s41598-022-05346-0





Theme V: Ecosystem monitoring

Environmental DNA (eDNA) for biodiversity assessments

Ecosystem-based approach to fisheries management

eDNA in Fisheries Management and Ecosystem Monitoring

RESEARCH ARTICLE

Environmental DNA from Seawater Samples Correlate with Trawl Catches of Subarctic, Deepwater Fishes

Philip Francis Thomsen¹*, Peter Rask Møller², Eva Egelyng Sigsgaard², Steen Wilhelm Knudsen², Ole Ankjær Jørgensen^{3,4}, Eske Willerslev^{1,5,6}*

ecology & evolution

Brief Communication | Published: 21 November 2016

Population characteristics of a large whale shark aggregation inferred from seawater environmental DNA

Eva Egelyng Sigsgaard, Ida Broman Nielsen, Steffen Sanvig Bach, Eline D. Lorenzen, David Philip Robinson, Steen Wilhelm Knudsen, Mikkel Winther Pedersen, Mohammed Al Jaidah, Ludovic Orlando, Eske Willerslev, Peter Rask Møller & Philip Francis Thomsen 🐱




ATTRIBUTES OF HARVESTED SPECIES

Theme V: Ecosystem monitoring

Received: 31 August 2017 Accepted: 22 February 2018
DOI: 10.1111/faf.12286

ORIGINAL ARTICLE

WILEY FISH and FISHERIES

The sceptical optimist: challenges and perspectives for the application of environmental DNA in marine fisheries

Brian Klitgaard Hansen¹ | Dorte Bekkevold¹ | Lotte Worsøe Clausen^{1,2} | Einar Eg Nielsen¹

¹Section for Marine Living Resources, National Institute of Aquatic Resources, Technical University of Denmark, Silkeborg, Denmark

²International Council for the Exploration of the Sea (ICES), Copenhagen V, Denmark

Correspondence

Brian Klitgaard Hansen, Section for Marine Living Resources, National Institute of Aquatic Resources, Technical University of Denmark, Silkeborg, Denmark. Email: bihagaqua.dtu.dk

Funding information Danish AgriFish Agency's Green Development and Demonstration Programme (GUDP-VIND): European Union; AtlantOG, Grant/Award Number: 633211; DiscardLeas, Grant/Award Number: 633680

Abstract

Application of environmental DNA (eDNA) analysis has attracted the attention of researchers, advisors and managers of living marine resources and biodiversity. The apparent simplicity and cost-effectiveness of eDNA analysis make it highly attractive as species distributions can be revealed from water samples. Further, species-specific analyses indicate that eDNA concentrations correlate with biomass and abundance, suggesting the possibility for quantitative applications estimating abundance and biomass of specific organisms in marine ecosystems, such as for stock assessment. However, the path from detecting occurrence of an organism to quantitative estimates is long and indirect, not least as eDNA concentration depends on several physical, chemical and biological factors which influence its production, persistence and transport in marine ecosystems. Here, we provide an overview of basic principles in relation to eDNA analysis with potential for marine fisheries application. We describe fundamental processes governing eDNA generation, breakdown and transport and summarize current uncertainties about these processes. We describe five major challenges in relation to application in fisheries assessment, where there is immediate need for knowledge building in marine systems, and point to apparent weaknesses of

precaution against exaggerating the present scope for application of eDNA analysis in fisheries monitoring, but also argue that with informed insights into strengths and limitations, eDNA analysis can become an integrated tool in fisheries assessment and management.

KEYWORDS commercial fisheries, environmental DNA, fisheries management, marine conservation, marine monitorine.

SCIENCE ADVANCES | RESEARCH ARTICLE

ECOLOGY

Environmental DNA illuminates the dark diversity of sharks

Germain Boussarie,^{1,2}* Judith Bakker,³* Owen S. Wangensteen,^{3,4} Stefano Mariani,³ Lucas Bonnin,^{1,2} Jean-Baptiste Juhel,^{1,2} Jeremy J. Kiszka,⁵ Michel Kulbicki,⁶ Stephanie Manel,⁷ William D. Robbins,^{8,9,10} Laurent Vigliola,^{1†} David Mouillot^{2,11†‡}

In the era of "Anthropocene defaunation," large species are often no longer detected in habitats where they formerly occurred. However, it is unclear whether this apparent missing, or "dark," diversity of megafauna results from local species extirpations or from failure to detect elusive remaining individuals. We find that despite two orders of magnitude less sampling effort, environmental DNA (eDNA) detects 44% more shark species than traditional underwater visual censuses and baited videos across the New Caledonian archipelago (south-western Pacific). Furthermore, eDNA analysis reveals the presence of previously unobserved shark species in human-impacted areas. Overall, our results highlight a greater prevalence of sharks than described by traditional survey methods in both impacted and wilderness areas. This indicates an urgent need for large-scale eDNA assessments to improve monitoring of threatened and elusive megafauna. Finally, our findings emphasize the need for conservation efforts specifically geared toward the protection of elusive, residual populations.

e(lasmo)DNA www.marianilab.org





Theme V: Ecosystem monitoring

= > DNA collected from environmental samples

SUBSTRATE Sea water collected directly during fishing activities by METAPROBE (Maiello, et al. 2022)









ATTRIBUTES OF HARVESTED SPECIES

Theme V: Ecosystem monitoring

= > DNA collected from environmental samples

SUBSTRATE Sea water collected directly during fishing activities by METAPROBE (Maiello, et al. 2022)

ICES Journal of Marine Science, 2023, 0, 1–11 DOI: 10.1093/icesjms/fsad022 Review Article



DNA metabarcoding of trawling bycatch reveals diversity and distribution patterns of sharks and rays in the central Tyrrhenian Sea

Linda Albonetti^{1,2,§}, Giulia Maiello ^{(3,4,*,§}, Alessia Cariani ⁽¹⁾, Paolo Carpentieri⁵, Alice Ferrari¹, Alice Sbrana ^{(3,4,*,§}, Peter Shum⁶, Lorenzo Talarico^{2,7}, Tommaso Russo^{2,†} and Stefano Mariani^{6,†}



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Theme VI: Estimating harvest rates and abundance

Why is it important to fisheries management?

- Estimating the abundance of harvested species is a key requirement for determining sustainable yields or environmental impacts.
- Capture-mark-recapture analysis of harvested organisms is used to estimate abundance, but for many species capture leads to high mortality rates.
- "Genetic tagging" combines capture-recapture analysis frameworks with natural genetic tags.
- Tagging can be achieved without capturing organisms.
- Genetic tagging avoids some difficulties associated with conventional capturerecapture, such as tag loss and high mortality.

How does it work and what are the limitations?

- Genetic tags are unique DNA fingerprints that are obtained by sampling organisms and assaying variable DNA markers. For analyses they function in the same manner as conventional tags.
- Abundance and other population parameters can be estimated from the recapture of individuals identified with genetic tags.
- New panels of genetic tags must be developed for each new species.
- Users must ensure genetic tags are read without error.

Case studies

- Genetic tagging was first applied to humpback whales in the North Atlantic. Estimates of abundance based on photo records were subsequently shown to be underestimates.
- The 'genetag' project used a unique hook design to remotely take tissue biopsies from Australian Spanish mackerel for an assessment of harvest mortality.
- A 'close-kin' approach was used for Australian southern bluefin tuna. Parent-offspring pairs were detected through parentage analysis and analysed as recaptures. Results were incorporated into the assessment of the fishery.





Theme VI: Estimating harvest rates and abundance

Barriers to uptake

- There are biological and financial barriers to uptake of these novel methods by fisheries management.
- Costs per tag are higher than conventional tagging methods, but other costs (such as deployment, resampling and analysis) are similar.
- Similar to conventional tagging, large populations of mobile and dispersed species require extensive effort to obtain sufficient recaptures for accurate and precise parameter estimation.

Future

 Genetic tagging is a relatively new in the marine environment, but has been widely adopted for monitoring terrestrial fauna.

GenoDREAM *indirect* Experience

 ICCAT launched multiple calls for close-kin tagging on Bluefin Tuna, but...





Theme VI: Estimating harvest rates and abundance GenoDREAM *indirect* Experience ICCAT launched multiple calls for close-kin tagging on Bluefin Tuna

Madrid, 10 June 2015

ICCAT CIRCULAR # 03646/2015

SUBJECT: TERMS OF REFERENCE – CALL FOR TENDERS – ICCAT GBYP (07/2015) ADVICE ON CLOSE-KIN GENETIC TAGGING STUDY (ICCAT GBYP Phase 5)

I have the honour to transmit to you the attached Call f on Close-Kin Genetic Tagging Study" of the ICCAT. Tuna (ICCAT GBYP).

Madrid, 16 June 2015

ICCAT CIRCULAR # 03792/2015

SUBJECT: CORRECTED TERMS OF REFERENCE – CALL FOR TENDERS – ICCAT GBYP (07/2015) ADVICE ON CLOSE-KIN GENETIC TAGGING STUDY (ICCAT GBYP Phase 5)

ALMA MATER STUDIORUM - I have the honour to re-transmit to you the attached Call for Tenders ICCAT GBYP 07/2015 for "Advice on Close-Kin Genetic Tagging Study" of the ICCAT Atlantic-Wide Research Programme on Bluefin Tuna (ICCAT GBYP). The previous version (Circular # 3646) contained a small error in the deliverables section. Please excuse any inconvenience caused.





ICCAT launched multiple calls for close-kin tagging on Bluefin Tuna,

But...

Fishery-independent estimate of spawning biomass of Southern Bluefin Tuna

through identification of close-kin using genetic markers

Mark V. Bravington, Peter M. Grewe and Campbell R. Davies

FRDC Project No. 2007/034 March 2014



Campbell Davies visit to JRC under the scope of the a4a initiative Ispra, 16-18/December/2013 and 07-10/January/2014

The method was tested and used in southern bluefin tuna [3] and performed very well and is now being considered as a method for routine long-term monitoring of the spawning stock. The method requires that the stock structure is well known and that juveniles from known spawning populations can be collected. This is likely to be a constraint of the application of the approach for for most European stocks that show a large overlap between spawner and juveniles. However, an interesting application may be for stocks of deep sea species, which have a more local behaviour and and are unlikely to be amenable to traditional stock assessment methods, due to the long time series required. Cephalopod stocks may be another potential candidate because the biology of these species makes it very difficult to use the traditional stock assessment methods.





JRC TECHNICAL REPORTS				
Deep Sea – Close Kin: A Genetic Approach for Improved Fisheries Management				
Close Kin Analysis based on Genetics in Support of Improved Management under the Common Fisheries Policy – A Feasibility Assessment				
Jann Th. Martinsohn Ernesto Jardim Ilaria Coscia Francis Neat 2015				





ww.nature.com/scientificreports

SCIENTIFIC REPORTS

Genetic relatedness reveals total population size of white sharks in eastern Australia and New Zealand

R. M. Hillary¹, M.V. Bravington², T. A. Patterson¹, P. Grewe¹, R. Bradford¹, P. Feutry¹, R.Gunasekera¹, V. Peddemors³, J. Werry⁴, M. P. Francis⁵, C. A. J. Duffy⁶ & B. D. Bruce¹

Conservation concerns exist for many sharks but robust estimates of a bundance are often lacking. Improving population status is a performance measure for species under conservation or recovery plans, yet the lack of data permitting estimation of population size means the efficacy of management actions can be difficult to assess, and achieving the goal of removing species from conservation listing challenging. For potentially dangerous species, like the white shark, balancing conservation and public safety demands is politically and socially complex, often leading to vigorous debate about their population status. This increases the need for robust information to inform policy decisions. We developed a novel method for estimating the total abundance of white sharks in eastern Australia and New Zealand using the genetic-relatedness of juveniles and applying a dose-kin mark-recapture framework and demographic model. Estimated numbers of adults are small (ca. 280–650), as is total population size (ca. 2,500–6,750). However, estimates of survival probability are high for adults (over 90%), and fairly high for juveniles (around 73%). This represents the first direct estimate of total white shark abundance and survival calculated from data across both the spatial and temporal life-history of the animal and provides a pathway to estimate population trend. Received: 20 January 2021 Revised: 23 August 2021 Accepted: 27 August 2021

DOI: 10.1111/faf.12615

FIRE and PERSONNELS

ORIGINAL ARTICLE

Close-kin methods to estimate census size and effective population size

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Funding information Frolich Feellowship; NOAA Fisheries Office of Science and Technology

Abstract

The last two decades have witnessed rapid developments and increasing interest in use of: (1) genetic methods to estimate effective population size (N_) and (2) close-kin mark-recapture (CKMR) methods to estimate abundance based on the incidence of close relatives. Whereas N, estimation methods have been applied to a wide range of taxa, all CKMR applications to date have been for aquatic species. These two fields of inquiry have developed largely independently, and this is unfortunate because deeper insights can be gained by joint evaluation of eco-evolutionary processes. In this synthesis, we use simple analytical models and simulated pedigree data to illustrate how various factors (life-history traits; patterns of variation in individual reproductive success; experimental design; stochasticity; marker type) can affect the performance of the estimators. We show that the Ne/N ratio and the probability of a close-kin match both depend on a vector of parental weights that specify relative probabilities that different individuals will produce offspring. Although age-specific vital rates are central to both methodologies, for CKMR they can potentially bias abundance estimates unless properly accounted for, whereas they represent the signals of genetic drift that N, estimation methods depend upon. Coordinating N, and CKMR estimation methods using the same or overlapping datasets would facilitate joint evaluation of both the ecological and evolutionary consequences of abundance.

KEYWORDS

abundance, genetics, mark-recapture, parentage analysis, reproductive skew, siblings





Low levels of sibship encourage use of larvae in western Atlantic bluefin tuna abundance estimation by close-kin mark-recapture

Jan R. McDowell¹, Mark Bravington², Peter M. Grewe², Matthew Lauretta³, John F. Walter III³, Shane M. Baylis², Thierry Gosselin⁴, Estrella Malca^{3,5}, Trika Gerard³, Akihiro Shiroza^{3,5}, John T. Lamkin³, Ellen E. Biesack¹, Glenn Zapfe³, Walter Ingram³, Campbell Davies² & Clay Porch³

Globally, tunas are among the most valuable fish stocks, but are also inherently difficult to monitor and assess. Samples of larvae of Western Atlantic bluefin tuna *Thunnus thynnus* (Linnaeus, 1758) from standardized annual surveys in the northern Gulf of Mexico provide a potential source of "offspring" for close-kin mark-recapture (CKMR) estimates of abundance. However, the spatial patchiness and highly skewed numbers of larvae per tow suggest sampled larvae may come from a small number of parents, compromising the precision of CKMR. We used high throughput genomic profiling to study sibship within and among larval tows from the 2016 standardized Gulf-wide survey compared to targeted sampling carried out in 2017. Full- and half-siblings were found within both years, with 12% of 156 samples in 2016 and 56% of 317 samples in 2017 having at least one sibling. There were also two pairs of cross cohort half-siblings. Targeted sampling increased the number of larvae collected per sampling event but resulted in a higher proportion of siblings. The combined effective sample size across both years was about 75% of the nominal size, indicating that Gulf of Mexico larval collections could be a suitable source of juveniles for CKMR in Western Atlantic bluefin tuna.

Sci Rep **12**, 18606 (2022). https://doi.org/10.1038/s41598-022-20862-9 INTERNATIONAL COMMISSION FOR THE CONSERVATION OF ATLANTIC TUNAS CON

COMMISSION INTERNATIONALE POUR LA CONSERVATION DES THONIDES DE L'ATLANTIQUE

COMISION INTERNACIONAL PARA LA CONSERVACION DEL ATUN ATLANTICO

Madrid, 21 February 2023

ICCAT CIRCULAR # G-0194/2023

SUBJECT: GBYP WORKSHOP ON BLUEFIN TUNA CLOSE-KIN MARK-RECAPTURE (CKMR), INCLUDING BIOLOGICAL SAMPLING COORDINATION (hybrid/Madrid (Spain), 14-16 March 2023)

I am pleased to inform you that the *GBYP Workshop on Bluefin Tuna Close-Kin Mark-Recapture (CKMR)*, including Biological Sampling Coordination will be held between 14 and 16 March 2023.

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Why is it important to fisheries management?

- Genetic diversity refers to the diversity of genetic variants in a species' gene pool.
- Diversity is reduced by prolonged reductions in population size and changes to connections between populations.
- Metrics of genetic diversity can provide indications of the abundance of a species, as well as its capacity to evolve in response to environmental change.

How does it work and what are the limitations?

- Genetic effective population size is a convenient way to summarize and standardize changes in genetic diversity across taxa.
- There are two types; contemporary (short-term) and historical (long-term).
- Estimates are independent of catch-per-unit-effort.
- Genetic effective population size:
- is relevant to time-scales over which harvesting has occurred;
- has potential for indexing virgin biomass that predates harvesting; and
- plays a key role in monitoring changes in genetic diversity associated with fisheries enhancement via restocking (theme IX).
- Effective population size is typically smaller than the census population size.

Case studies

- The short and long-term genetic effective population size of tiger prawns in south-east Queensland were similar, implying harvest rates have been sustainable.
- Genetic effective population size and the spawning population size of sandbar sharks on east coast of US were similar.





Barriers to uptake

 Uptake will increase as the challenges of translating effective population size to census population size are better resolved.

Future

- Comparisons between estimates of effective size from genetic and demographic data will help to understand how they are related.
- Comparisons between genetic effective population size and estimates of abundance from other systems where genetic markers are used (e.g. mark-recapture studies, theme VII) will assist both fields.

GenoDREAM Experience

 Ne estimates (contemporary and long term) in Bluefin Tuna and other species





GenoDREAM Experience Ne estimates (contemporary and long term) in Bluefin Tuna and other species

Spatio-temporal population structuring and genetic diversity retention in depleted Atlantic Bluefin tuna of the Mediterranean Sea

Giulia Riccioni^{a,1}, Monica Landi^{b,1,2}, Giorgia Ferrara^b, Ilaria Milano^b, Alessia Cariani^b, Lorenzo Zane^c, Massimo Sella^{d,3}, Guido Barbujani^a, and Fausto Tinti^{b,4}

2102–2107 | PNAS | February 2, 2010 | vol. 107 | no. 5

www.pnas.org/cgi/doi/10.1073/pnas.0908281107





GenoDREAM Experience Ne estimates (contemporary and long term) in Bluefin Tuna and other species

MOLECULAR ECOLOGY

Molecular Ecology (2011) 20, 3555–3568

doi: 10.1111/j.1365-294X.2011.05196.x

Temporal genetic stability and high effective population size despite fisheries-induced life-history trait evolution in the North Sea sole

E. L. CUVELIERS,* F. A. M. VOLCKAERT,*A. D. RIJNSDORP,†‡ M. H. D. LARMUSEAU*§¶ and G. E. MAES*





GenoDREAM Experience Ne estimates (contemporary and long term) in Bluefin Tuna and other species

Ancient DNA SNP-panel data

sugge Genomic stability through time despite decades of tuna exploitation in cod on both sides of the Atlantic despit

Malin L. Pinsky^{a,1}, Anne Maria Eikeset^b, Cecilia Helmerson^b, Ian R. Bradbury^c, Paul Bentzen^d, Corey Morris^c, Agata T. Gondek-Wyrozemska^b, Helle Tessand Baalsrud^b, Marine Servane Ono Brieuc^b, Olav Sigurd Kjesbu^e, Jane A. Godiksen^f, Julia M. I. Barth^{b,g}, Michael Matschiner^{b,h,i}, Nils Chr. Stenseth^{b,j,1}, Kjetill S. Jakobsen^b, and N. Sissel Jentoft^b, and Bastiaan Star^{b,1}

Adam J. Andrews^{1,2,11^{III}}, Gregory N. Puncher^{1,3,11^{III}}, Darío Bernal-Casasola⁴, Antonio Di Natale⁵, Francesco Massari¹, Vedat Onar⁶, Nezir Yaşar Toker⁶, Alex Hanke⁷, Scott A. Pavey³, Castrense Savojardo⁸, Pier Luigi Martelli⁸, Rita Casadio⁸, Elisabetta Cilli², Arturo Morales-Muñiz⁹, Barbara Mantovani¹⁰, Fausto Tinti¹ & Alessia Cariani¹





Theme VIII: Evolutionary responses to fishing

Why is it important to fisheries management?

- Fishing has the potential to introduce undesirable evolutionary changes to harvested populations, ultimately altering their distribution, abundance and productivity.
- Understanding these processes would enable fisheries managers to adapt practices to prevent or reduce their impacts on productivity.

How does it work and what are the limitations?

- Evolutionary changes in functional genes underlying traits of interest can be directly monitored through time or in space.
- A significant challenge for this approach is our incomplete understanding of the genetic basis of most traits in wild fishes.

Case studies

 Heavily exploited North Atlantic cod have shifted towards earlier and smaller maturation in spite of environmental conditions favouring the opposite.





Theme VIII: Evolutionary responses to fishing

Barriers to uptake

- Few fisheries have adopted strategies to guard against evolutionary responses to fishing.
- This may reflect a lack of awareness of the issue, lack of compelling local examples, or greater focus on more immediate and conventional fishing pressures.
- Underpinning this is the difficulty of making clear links between environmental change, selection, and evolutionary responses, and then extending the inference to meaningful impacts on fisheries productivity.

Future

 Genomic resources are increasingly becoming available for fisheries species and will provide a means to understanding adaptive traits, including those associated with environmental change.

GenoDREAM Experience

- FInE EU Project
- ATGC-TUNA UNIBO FARB Project
- ICCAT GBYP Data Recovery Project
- MSCA ITN SeaChanges





Theme VIII: Evolutionary responses to fishing GenoDREAM Experience FInE EU Project







Theme VIII: Evolutionary responses to fishing GenoDREAM Experience it all started in this building...

Massimo Sella Archive



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Andrews et al. 2022, ICES J Marine Sciences. Jan 2022 Editor's Choice









UIO: Centre for Ecological and Evolutionary Synthesis University of Oslo

Adam Andrews, MSCA PhD Fellow / PostDoc adam@palaeome.org **Morphology:** Size reconstructions Inferring growth using annul



WG sequencing: Demography Structure Adaptive responses





 δ^{13} C, δ^{15} N, δ^{34} S stable isotopes: Diet and habitat use dynamics





Unlocking ecological history using fish remains

Eco-evolutionary consequences of exploitation in the Atlantic bluefin tuna

measurements over **two millennia** showed that

- 21st c. ABFT age 1-2 grew significantly faster than in the 20th c. and 16-18th c.,
- 20th c. ABFT age 1-2 grew significantly faster than the 16-18th c.
- 3. coincides with stepwise SST and NAO increases
- 4. decrease in growth at age 4-6 between the 20th and 21st c.



1-3. Climate-Change Evolution 4. Fishery - Induced Evolution

Andrews et al. 2023, ICES J Marine Sciences Mar 2023 Editor's Choice





Theme IX: Genetic consequences of stock enhancement

Why is it important to fisheries management?

- Stock enhancement overcomes recruitment failure by the release of captive-bred individuals.
- Interbreeding between local and introduced individuals leads to hybrids, which may have lower fitness than wild fish.
- Unfit hybrids can reduce the productivity of the population and increase the reliance on enhancement.

How does it work and what are the limitations?

- Genetic consequences can be avoided by releasing individuals that are compatible with the local environment and wild populations.
- This is challenging, despite quality assurance programs for hatcheries.
- Genetics can be used to monitor:
 - hatcheries for changes to genetic attributes; and
 - post-release survival and detect hybridization.

Case studies

- The reproductive success of offspring of captive-bred steelhead trout in the wild was 40% below that of wild conspecifics.
- This suggested the overall fitness of the enhanced population would progressively decrease.





Theme IX: Genetic consequences of stock enhancement

Barriers to uptake

 A balance is needed between the requirement for enhancement and its potentially detrimental consequences.

Future

- Managers need guidelines describing the likelihood of genetic consequences, and how to minimise them.
- Two areas need attention:
 - how to produce captive-bred individuals with sufficient fitness for survival after release; and
 - quantifying the extent and success of mixed spawning in enhanced populations.
- Countries like Australia that are trialing enhancement need to plan in advance for genetic consequences.

GenoDREAM Experience

- AQUAGEN EU Tender
- AQUATRACE EU Project





AQUAGEN EU Tender & AQUATRACE EU Project

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				FP7 AquaTrace: the development of tools for tracing and evaluating									
				the genetic impact of fish from aquaculture									



AQUAGEN EU Tender & AQUATRACE EU Project

Trends in world aquaculture production: major species groups



Note: NEI = not elsewhere included. FAO 'State of World Fisheries and Aquaculture-2010' report



AQUAGEN EU Tender & AQUATRACE EU Project



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AQUAGEN EU Tender & AQUATRACE EU Project



Sole: 96 SNP

Figure 4: Pedigree reconstruction of the two aquaculture families drawn by Pedigree viewer (Kinghorn, 1990-2010). Left: based on 21SNPs. Right: based on 50 SNPs. Blue: candidate mothers, red: candidate fathers. Notice the two misassigned individuals, caused by bad DNA quality (leading to genotyping errors/missing values).









Vol. 8: 131-145, 2016

doi: 10.3354/



AQUACULTURE ENVIRONMENT INTERACTIONS Aquacult Environ Interact Published February 25

Evaluating genetic traceability methods for captive-bred marine fish and their applications in fisheries management and wildlife forensics

Jonas Bylemans^{1,2,*}, Gregory E. Maes^{1,3}, Eveline Diopere¹, Alessia Cariani⁴, Helen Senn⁵, Martin I. Taylor⁶, Sarah Helyar⁷, Luca Bargelloni⁹, Alessio Bonaldo⁹, Gary Carvalho¹⁰, Ilaria Guarniero⁹, Hans Komen¹¹, Jann Th. Martinsohn¹², Einar E. Nielsen¹³, Fausto Tinti⁴, Filip A. M. Volckaert¹, Rob Ogden¹⁴







Theme X: Detection of pathogens and invasive species

Why is it important to fisheries management?

- Pathogens and invasive species represent major threats to the productivity of wild fisheries.
- Genetic assays can diagnose and quantify the incidence of diseases or invasive species in wild fisheries and aquaculture.
- Rapid diagnosis of disease or invasive species enables a targeted response, which is likely to increase its effectiveness.

How does it work and what are the limitations?

- Genetic tools for detecting biosecurity risks in wild fisheries rely on the polymerase chain reaction (PCR) which copies scarce DNA molecules until they are abundant enough for diagnositic tests.
- PCR enables highly sensitive detection of target organisms from tissue samples as well as environmental samples including water and sediment.
- Novel tests need to be developed for each new pathogen or invasive species.

Case studies

- A disease caused high mortality in wild populations of abalone (Haliotis spp.) along the southeast Australian coastline
- A genetic assay for the disease in farmed and wild abalone was developed and deployed in southern Australia. A code of practice was subsequently developed to control the disease in the commercial, recreational, aquaculture and processing sectors.
- DNA analysis of water samples in a large river and canal complex in the northeastern USA have been used to delimit the range of two species of invasive carp with greater sensitivity and lower cost than conventional surveys.





Theme X: Detection of pathogens and invasive species

Barriers to uptake

 There are few technical barriers to the use of this technology for pathogen or invasive species detection.

Future

- The potential for the spread of disease into wild populations will rise as more species are farmed within their natural ranges.
- Environmental change (e.g. increasing water temperature) may change the ranges of pathogens and the way in which pathogens and hosts interact.

GenoDREAM Experience

MICRO(BI)ARRAY Project

Tuesday afternoon Gian Marco Luna, National Research Council Safety of fish products; microbial food webs and teleost microbiome.





POST-HARVEST REGULATION

Theme XI: Product provenance and fisheries surveillance

Why is it important to fisheries management?

- Genetic tools can be used to test samples to see if they belong to individuals, families, populations, or species of interest.
- Accurate identification is important for:
- powerful and economical enforcement and surveillance; and
- ensuring consumer safety and confidence.
- The technology is typically used for post-harvest analyses, such as the detection of product substitution and checking accuracy of labeling.

How does it work and what are the limitations?

- Generally, a 'DNA barcoding' approach is used to assign specimens to a species through comparison to a reference database of DNA sequences.
- Specimens can also be assigned to biological stocks or individual carcasses.
- Establishing reference samples requires a coordinated effort ahead of application of the technology.

Case studies

- In 2011, 10 30% of smoked Atlantic cod products tested in United Kingdom were mislabeled.
- An Australian fisher was fined for possessing female mud crabs allegedly caught in the Northern Territory, but were genetically assigned to a Queensland population where females are protected.





POST-HARVEST REGULATION

Theme XI: Product provenance and fisheries surveillance

Barriers to uptake

 Establishment and maintenance of reference databases requires long-term planning and funding.

Future

- Seafood producers may use genetic provenance testing to accredit their product and protect their commercial interest and reputation.
- Increasingly, specimen identifications
 will need to stand up to crossexamination within the legal system.

GenoDREAM Experience

FISHPOPTRACE EU
 Project





TRACEABILITY EU LABELING REGULATION: EC 104/2000 AND 2065/2001



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FRAUDS RELATED TO:

- PROTECTED AREAS
- CLOSURE TO FISHING (LOCAL/SEASONAL)
- EXCEEDING TAC
- CERTIFICATIONS (ECO/GREEN LABEL)







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Journal of Fish Biology (2016) 89, 2755-2767 doi:10.1111/jfb.13151, available online at wileyonlinelibrary.com

The role of genetics in fisheries management under the E.U. common fisheries policy^a

J. CASEY*, E. JARDIM AND J. TH. MARTINSOHN





European Commission, Directorate-General Joint Research Centre (JRC), Dire D-Sustainable Resources, Unit D.02-Water and Marine Resources, TP051-Bldg Journal of Fish Biology (2016) 89, 2505-2518 Enrico Fermi 2749, 21027, Ispra, VA, Italy doi:10.1111/jfb.13129, available online at wileyonlinelibrary.com

Can estimates of genetic effective population size contribute to fisheries stock assessments?^a

J. R. Ovenden*†, G. M. Leigh‡, D. C. Blower*§, A. T. Jones*||, A. Moore¶, C. Bustamante***, R. C. Buckworth††, M. B. Bennett** and C. L. Dudgeon***



Briefings in Functional Genomics, 2016, 1-6



doi: 10.1093/bfgp/elw006 Review paper

How fisheries management can benefit from genomics?

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Abstract

Fisheries genomics is an emerging field that advocates the application of genomic tools to ad management. Genomic approaches bring a new paradigm for fisheries management by mak adaptive diversity to understand fundamental aspects of fisheries resources. Hence, this revi of genomic approaches to solve fisheries-specific questions. Particularly the detection of ada vides unprecedented opportunity to understand bio-complexity, increased power to trace pr enforcement and the potential to understand bio-complexity patterns will be the cornerston fisheries and genomics. These studies will help stakeholders anticipate the potential effects the resilience of fisheries stocks; consequently, in the near future, fisheries sciences might ir with fisheries management.

Key words: fisheries; genomics; next-generation sequencing; fisheries management; adaptiv

EuroMarine

Foresight Workshop - Horizon scanning



The application of population genomics to fisheries management

Faro, Portugal: 8th - 10th May 2017



Review

Harnessing the Power of Genomics to Secure the Future of Seafood

Louis Bernatchez,^{1,*,†} Maren Wellenreuther,^{2,3,†} Cristián Araneda,⁴ David T. Ashton,² Julia M.I. Barth,⁵ Terry D. Beacham,⁶ Gregory E. Maes,^{7,8,9} Jann T. Martinsohn,¹⁰ Kristina M. Miller,⁶ Kerry A. Naish,¹¹ Jennifer R. Ovenden,¹² Craig R. Primmer,¹³ Ho Young Suk,¹⁴ Nina O. Therkildsen,¹⁵ and Ruth E. Withler⁶

Trends in Ecology & Evolution, September 2017, Vol. 32, No. 9



Trends in Ecology & Evolution



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DOI: 10.1111/faf.12343

GHOTI

WILEY FISH and FISHERIES

DNA-analysis to monitor fisheries and aquaculture: Too costly?

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Funding information

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Abstract

Evidence from DNA-analysis is commonplace in human criminal investigations, and while it is increasingly being used in wildlife crime, to date, its application to control and enforcement activities in fisheries and aquaculture has only been sporadic. Contemporary DNA-analysis tools are capable of addressing a broad range of compliance issues, species identification, mislabelling of fish products, determining the origin of catches and the farm of origin of aquaculture escapees. Such applications have the potential to ensure traceability along the fish product supply chain and to combat consumer fraud and Illegal, Unreported and Unregulated fishing, Nevertheless, DNAanalysis is not yet used routinely in investigations into compliance with fisheries and aquaculture legislation. One potential reason for this is that DNA-analysis techniques may have been regarded as too expensive. However, costs have plummeted over the past decade prompting us to objectively assess whether the costs associated with routine use of DNA-analysis techniques for fisheries and aquaculture control and enforcement activities do constitute an impediment. Based on a number of recent fisheries and aquaculture compliance investigations that incorporated DNA-analysis, our results indicate that the use of genetic analysis was justified and worthwhile in all cases examined. We therefore conclude that the costs associated with DNA-analysis do not represent a barrier to the routine adoption of DNA-analysis techniques in fisheries and aquaculture compliance investigations. Thus, control and enforcement agencies should be encouraged to use such techniques routinely.

KEYWORDS

control, costs, enforcement, genetics, genomics, marine resource management

Genomic approaches in marine fisheries research: challenges and opportunities

The course will introduce to the potential of genomic approaches, which are increasingly important for understanding evolutionary processes, such as adaptation to the diverse habitats within the marine environment, including fishery-induced evolution.

Recent advances in genome technology will be presented and their implementation from genome assembly to comparative and population genomics.

Examples will be given on how genomics tools can allow tackling several challenges to ensure sustainability and profitability of fisheries management.



WE DID IT!!



Genomic approaches in marine fisheries research: challenges and opportunities THE MOST POWERFUL DEVICES





Genomic approaches in marine fisheries research: challenges and opportunities THE MOST POWERFUL DEVICES

SPECIES/COMMUNITIES BARCODING/ METABARCONDING

POPULATION/STOCKS POPGEN IN SPACE AND TIME





Genomic approaches in marine fisheries research: challenges and opportunities



ALMA MATER STUDIORUM Università di Bologna Campus di Ravenna