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UNIVERSITÀ DI BOLOGNA
CAMPUS DI RAVENNA

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FishMed-PhD

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UNIVERSITÀ DI BOLOGNA

Consiglio Nazionale
delle Ricerche

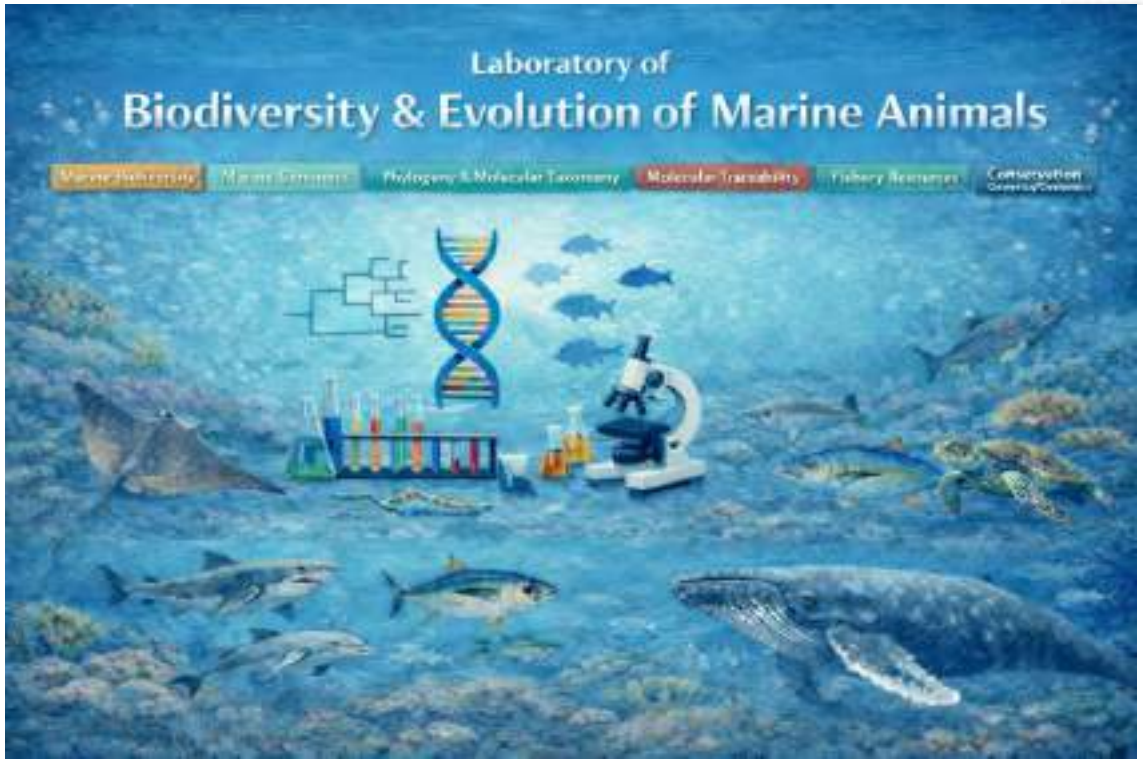
CNR
IRBIM
ISTITUTO PER LE RISORSE BIOLOGICHE E LE BIOTECNOLOGIE MARINE

TEACHING WEEK 2023
GENETICS AND GENOMICS FOR RESOURCE MANAGEMENT

ALESSIA CARIANI

BEAM Lab / GenoDREAM - Department BiGeA

Laboratory of Biodiversity & Evolution of Marine Animals (BEAM) Lab



Marine neo- and archaeogenetics, biomolecular analyses on tissue and environmental samples from marine animals and ecosystems, and bioinformatic analyses for population genetics and genomics. Research on variations in organismal, genetic, and ecological diversity, as well as on the eco-evolutionary impacts of human activities affecting ecosystems, species, and taxonomic groups of marine fauna.

ALESSIA CARIANI

BACKGROUND:

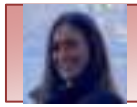
- 1998-2009: BSc&MSc&PhD Scienze Ambientali Marine
- 2009-2013: PostDoc from Microarray&Microbes to PopGen in Fish (and AoB!)
- 2013-2019: RTD junior -> RTD senior -> associate professor

NOW:

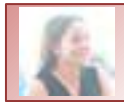
In theory my commitment is:
Understanding the **evolutionary and environmental drivers of biodiversity in marine organisms** by developing and applying **innovative genetic and genomic tools**. Research topics spans from molecular taxonomy to population genomics, and aims to uncover how genetic variation in space and time is shaped by natural forces in marine ecosystems.
Translate research results into real-world applications such as eco-certification, traceability systems, and policy-relevant approaches to sustainable fisheries and marine biodiversity conservation

In practice my commitment is:
Bureaucracy
Admin
Meetings
Reports
Reports
Another reports
Teaching

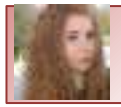
Laboratory of Biodiversity & Evolution of Marine Animals (BEAM) Lab



PhD student
Martina Pasino 38° BCA



PhD student
M.Vittoria Iacovelli 39°BCA



PhD student
Alexia Mazzini 39°FishMed

Fausto Tinti

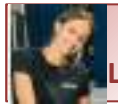
PO
Zoologia
(RS; RDRL)

Archeozoologia e museomica per la biodiversità marina del Mediterraneo

Microevoluzione dei grandi vertebrati marini: cause e impatti antropogenici e climatici

PhD student
Martina Spiga 38°FishMed

PhD student
Piergiorgio Massa 38°STVA



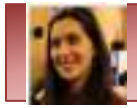
PhD student
Linda Albonetti 40° FishMed

Biodiversità vertebrati marini: tassonomia, sistematica molecolare ed eDNA degli Elasmobranchi *(NBFC-spoke2 research line)*

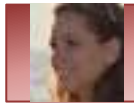
Genomica di popolazione di pesci commerciali: identificazione di stock per la gestione sostenibile

Alessia Cariani

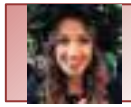
PA
Zoologia



Post-doc
Valentina Crobe



Post-doc
Giusy Catalano



PhD student
Ilaria Melato 40°DIN

Alice Ferrari

RTDa-
PON
Zoologia

Transizione blu: miglioramento della sostenibilità dello sfruttamento delle risorse ittiche del Mediterraneo

Biodiversità vertebrati marini: tassonomia, sistematica molecolare degli Elasmobranchi

Responsabilità Tecnica Lab GenoDREAM

Federica Piattoni

Tecnico D.

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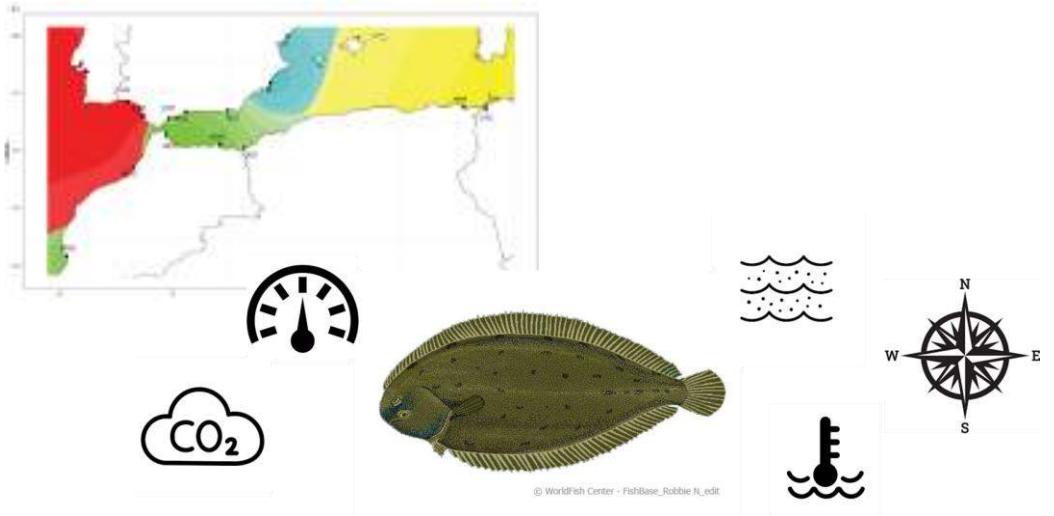
Research @BEAM Lab is…

The BEAM Lab focuses on **marine neo-and archaeo-zoogenetics**, implementing biomolecular analysis on marine animal species assessing **space-time changes in biodiversity**, with a focus on relevant marine **fishery resources** as well as taxa of **conservation concern**.
Through the qualitative and quantitative analysis of parameters describing diversity across spatial and temporal dimensions, the results of BEAM's research contribute to defining and supporting strategies and policies for the sustainable use of marine ecosystem and animal resources, and for the biological conservation of species and animal populations at risk of decline or extinction.
The BEAM permanently collaborates with the Ancient DNA Lab at the Cultural Heritage Dept. at Ravenna Campus and is active in several international networks



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Research @BEAM Lab is…

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

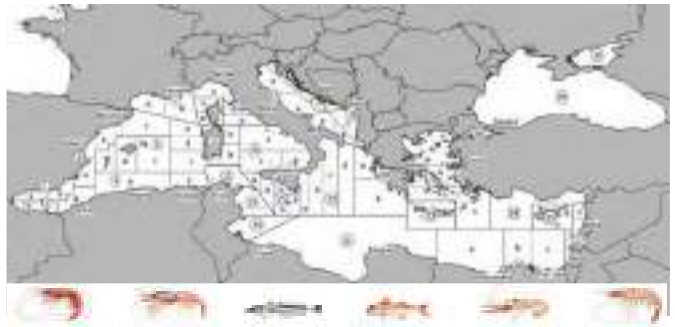
Main research lines:

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

GBYP (ICCAT) *MEDBLUESGEN* (EC JRC)
ELASMODROP (NBFC-SPOKE2)



MED_UNITs; SPELMED (EC EASME/EMFF)
FISHBONE; TRANSBORAN (FAO GFCM)

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Research @BEAM Lab is…

BLUE TRANSITION OF FISHERY ACTIVITIES IN THE ADRIATIC SEA

Main research lines:

1. Challenging the social and cultural valorisation of the Adriatic marine ecosystems
2. Virtuous circle between fishery scientists (biologists, ecologists, economists), fishermen, stakeholders, civil society
3. Increase the sustainability of fishery activities in Adriatic Sea by fostering innovative processes (eco-innovation)

Interreg Italy - Croatia PRIZEFISH EUROPEAN UNION

Interreg Italy - Croatia TECHERA EUROPEAN UNION

Interreg Italy - Croatia 3E-FISHING EUROPEAN UNION

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Research @BEAM Lab is…

CONSERVATION OF THREATENED MARINE SPECIES

1. Improve conservation of elasmobranchs by reducing their bycatch, promoting alternative sustainable resources exploitation and ecotourism activities
2. Cost-effective solutions to reverse the critical status of threatened marine species

LIFE PROMETHEUS PROMoting Elasmobranchs conservation Through by-catch reduction, Ecotourism and alternative sUStainable fisheries

From ancient DNA to modern conservation: : Assessing human impact on Atlantic bluefin tuna Genomes

ELASMODROP - Finding sharks in a drop: leveraging eDNA monitoring to protect elasmobranch biodiversity

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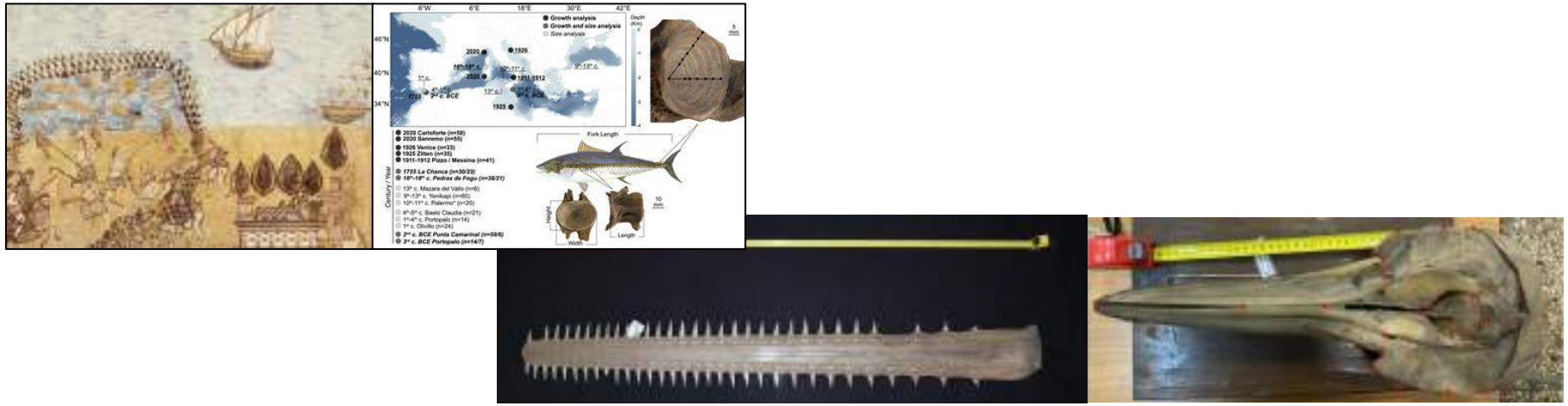
Research @BEAM Lab is…

BLUE MUSEOMICS - CHALLENGING CONSERVATION OF MARINE BIODIVERSITY FROM THE PAST

Main research lines:

1. Historical ecology and species diversity of Mediterranean Marine Apex Predators (small dolphins; angel sharks; sawfishes)
2. Eco-evolutionary consequences of millennial exploitation in the Atlantic bluefin tuna *Thunnus thynnus*



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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.

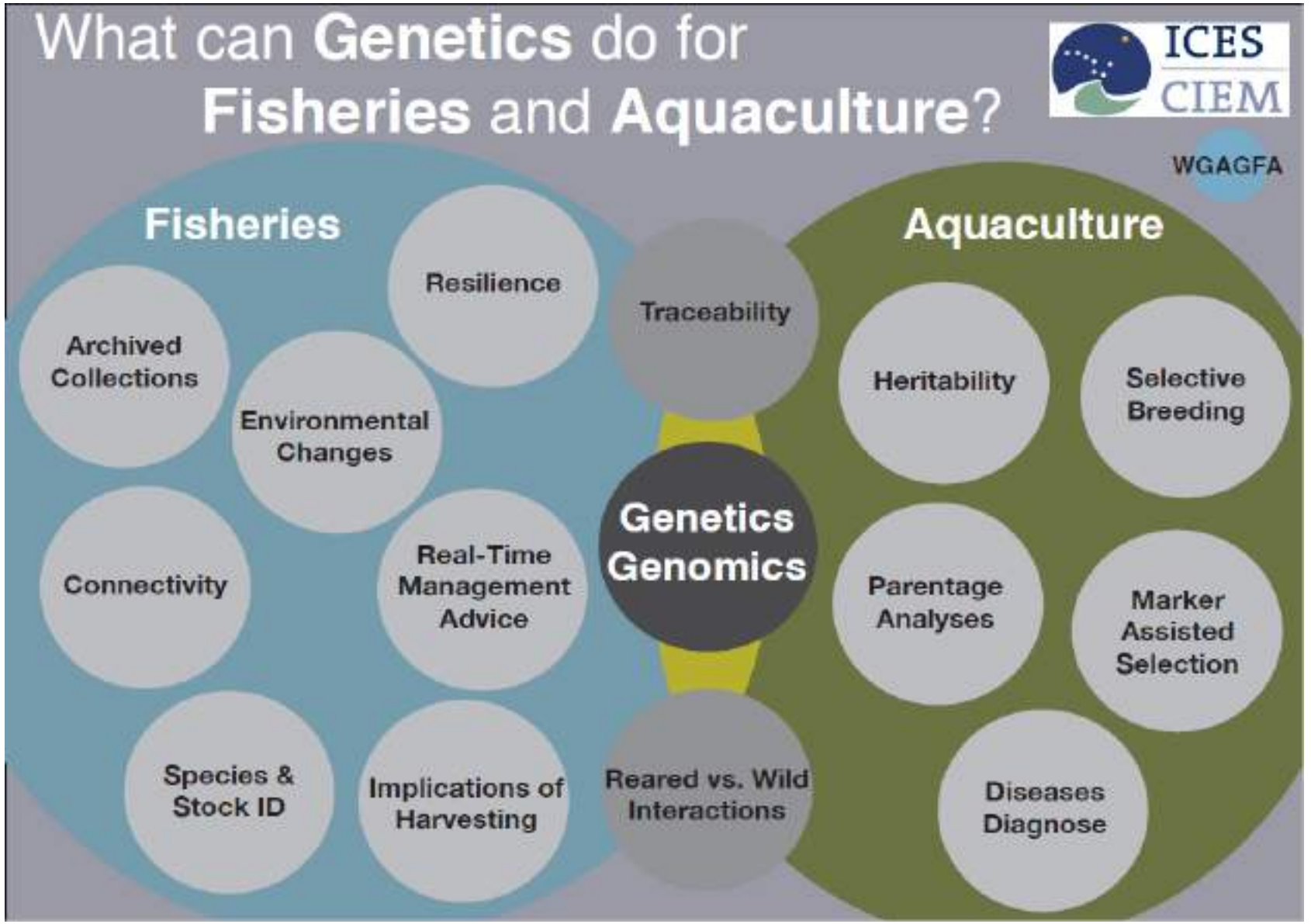
WHEN/WHO/WHAT/WHY???
On a sunny Thursday morning??

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

What can **Genetics** do for **Fisheries** and **Aquaculture**?

- Assess the correct species – barcode to identify genome region of economic interest
- Health assessment of livestocks
- Selective breeding programmes
- Discriminate stocks
- Assess connectivity of different populations / stocks of vulnerable / exploited species
- Identify migration routes
- Cope with antimicrobial resistance
- Support other techniques in the monitoring

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



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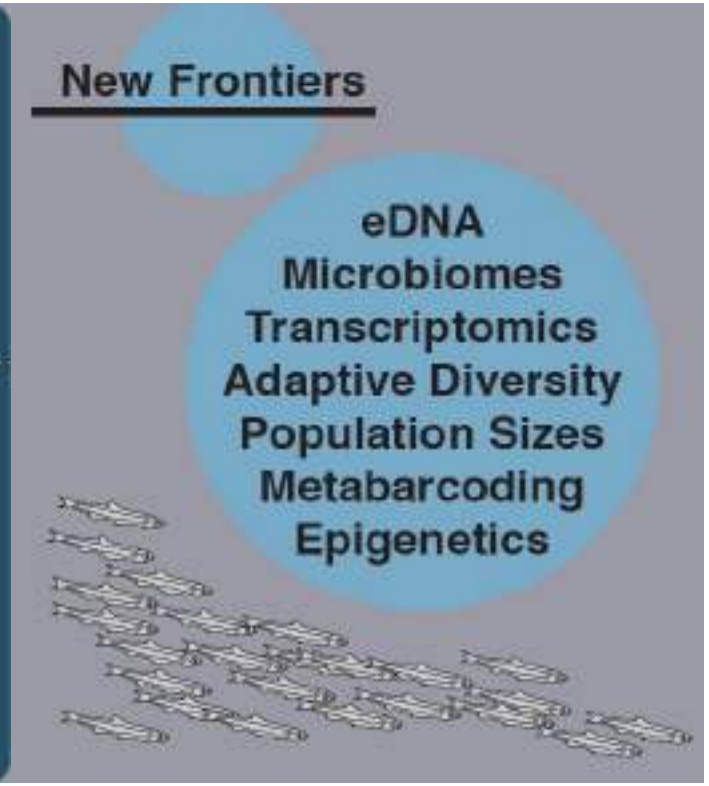
Genomic approaches in marine fisheries research: challenges and opportunities
WORKING GROUP ON APPLICATION OF GENETICS IN FISHERIES AND AQUACULTURE

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.



Contents lists available at ScienceDirect
Marine Genomics
journal homepage: www.elsevier.com/locate/margen

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 [b,*]

Contents

1. Introduction
2. Biodiversity and biogeography
3. Adaptive evolution
4. Effects of anthropogenic-induced changes in marine habitat
5. Genome evolution
6. Aquaculture and bioprospecting
7. Concluding remarks.
Acknowledgments
References

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.”

Professor GARY CARVALHO – ICES INTERVIEW - 8 May 2019

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

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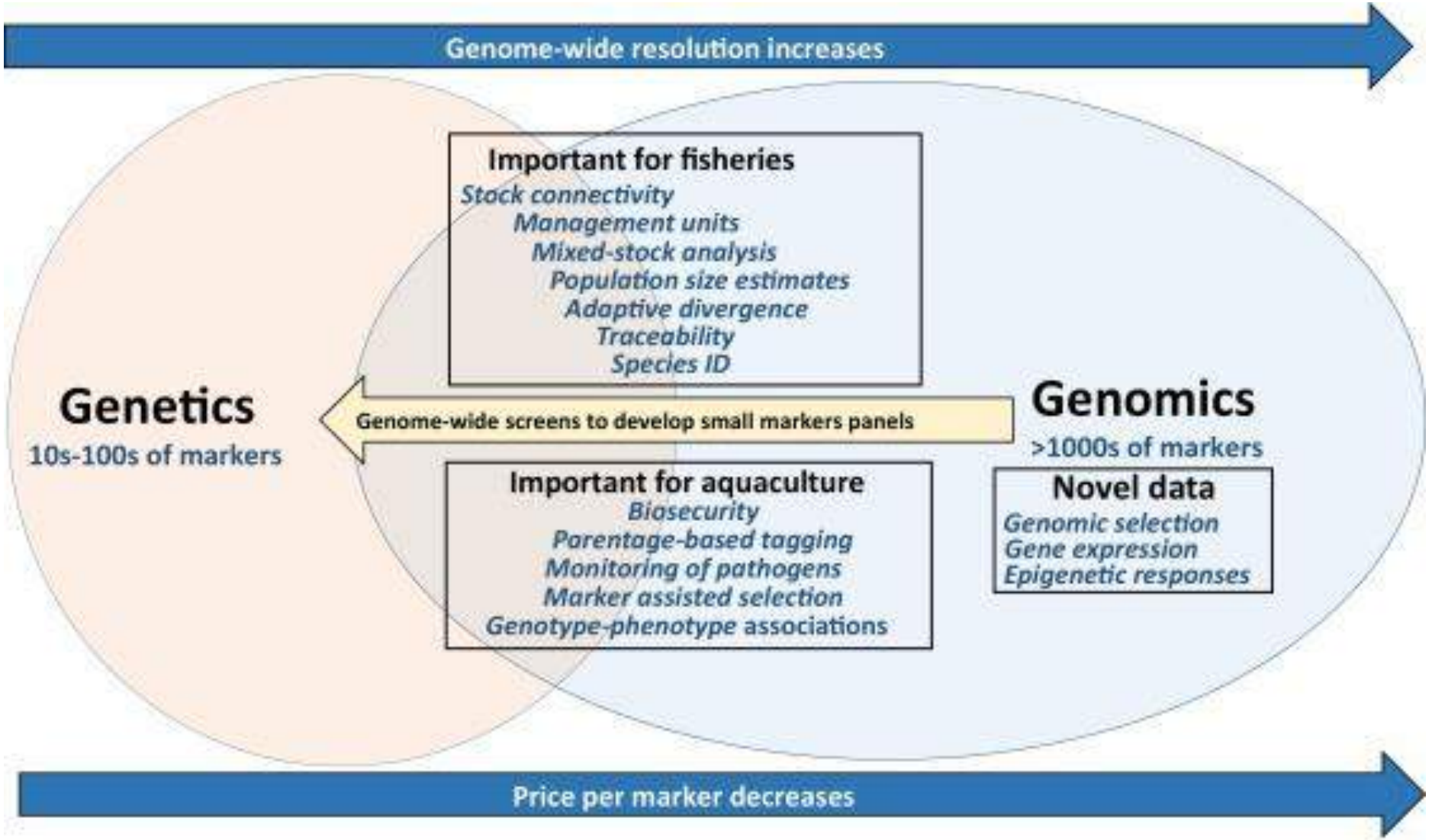
Genomic approaches in marine fisheries research: challenges and opportunities ALSO OUTSIDE EU IN THE MED

GENETIC VS GENOMIC



Trends in Ecology & Evolution

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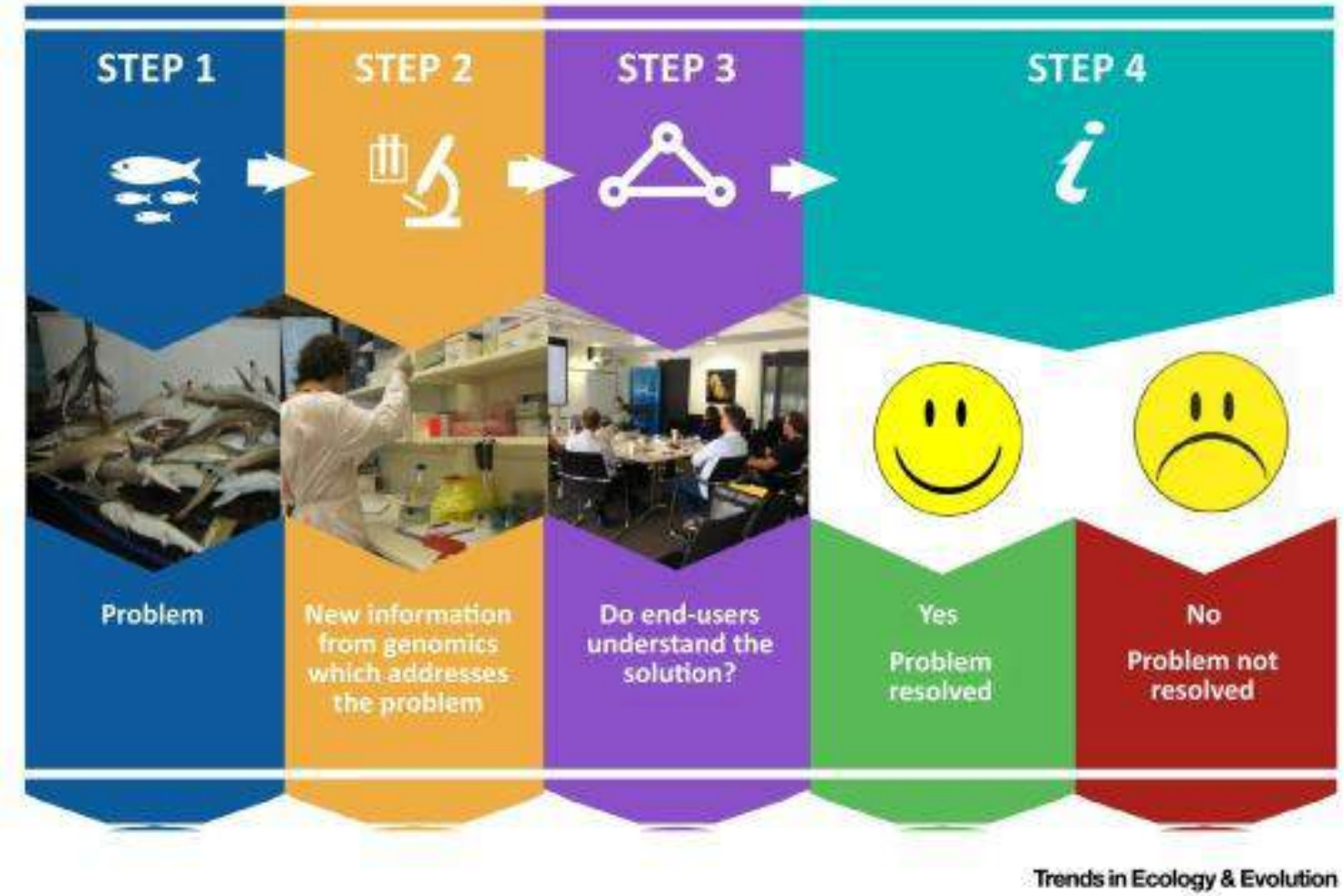
GENETIC & GENOMIC APPLICATIONS

Review

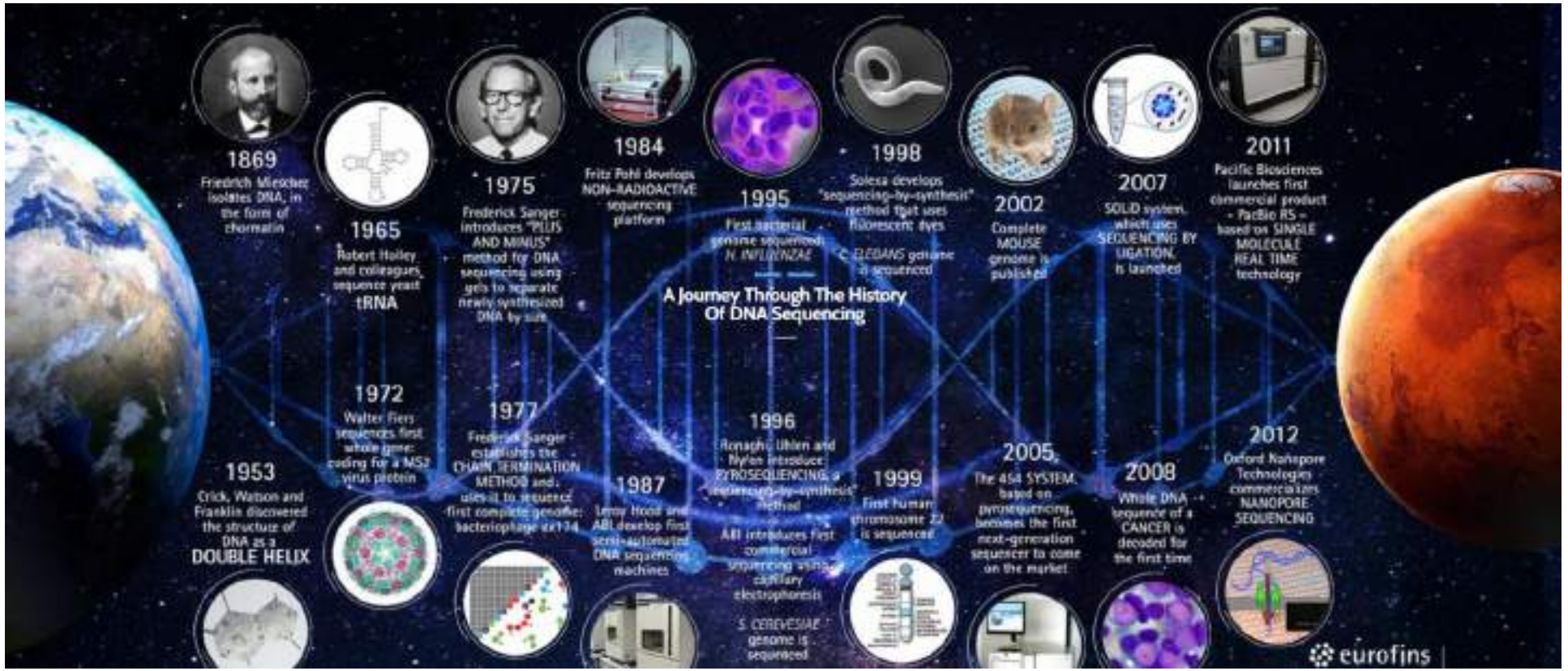
Harnessing the Power of Genomics to Secure the Future of Seafood

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. Withler[6]

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



Sequencing history

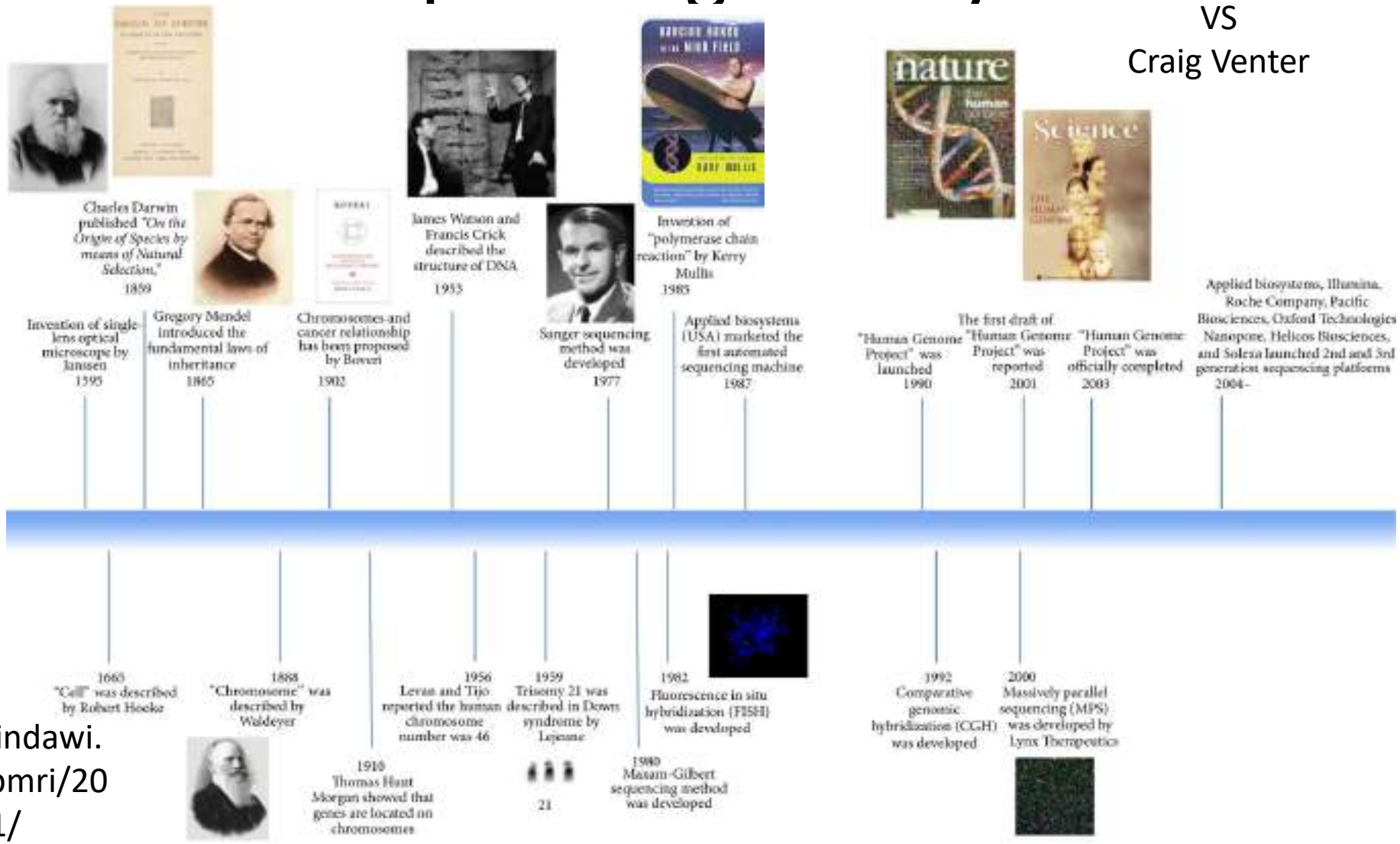


https://the-dna-universe.com/2020/11/02/a-journey-through-the-history-of-dna-sequencing/

QUICK INTRO TO METHODS (QUICK I PROMISE)

Sequencing history

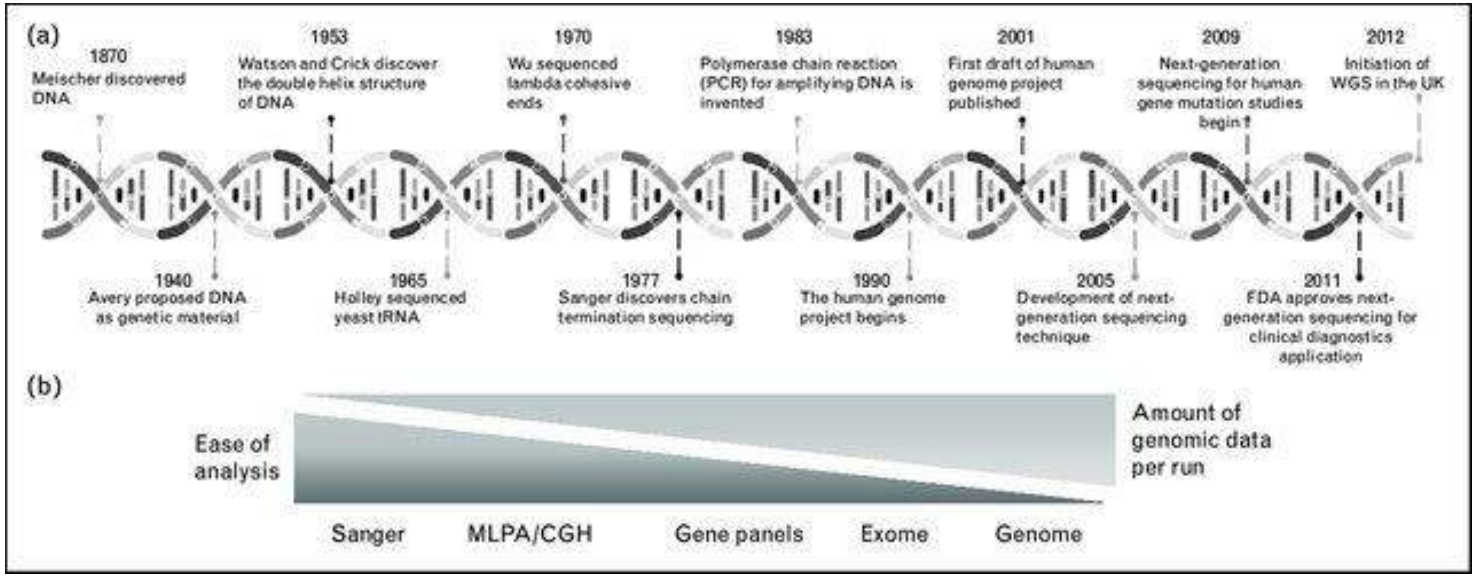
Renato Dulbecco
VS
Craig Venter

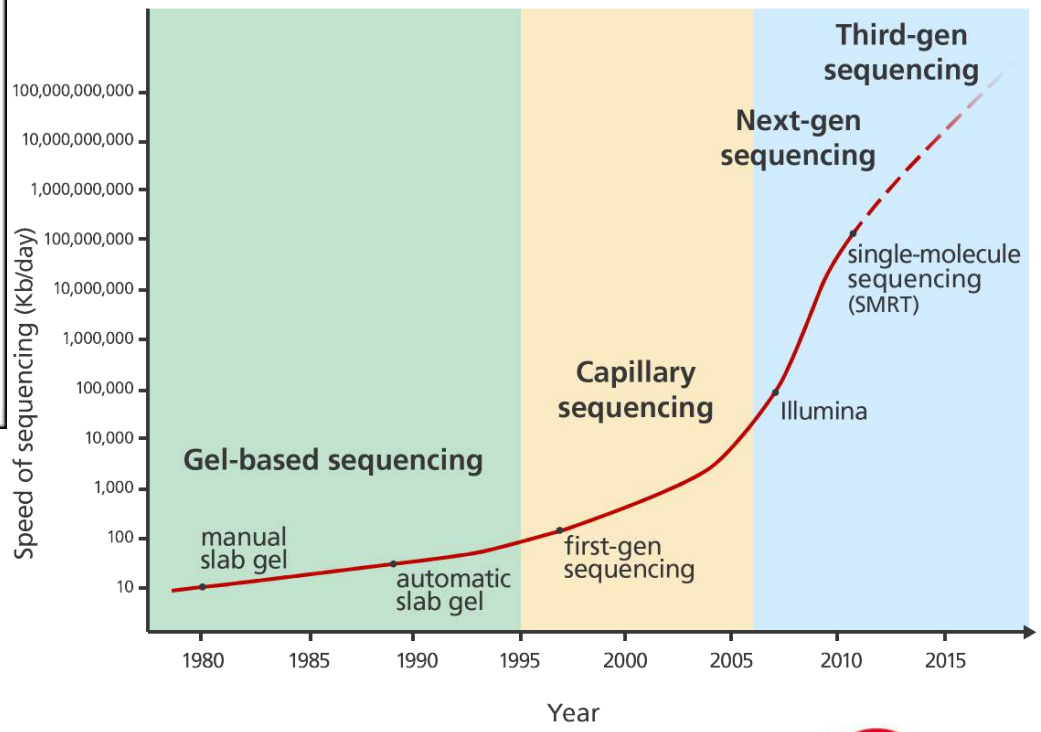


https://www.hindawi.com/journals/bmri/2015/461524/fig1/

QUICK INTRO TO METHODS (QUICK I PROMISE)

Sequencing history





https://www.yourgenome.org/stories/pacbio-and-third-generation-sequencing/

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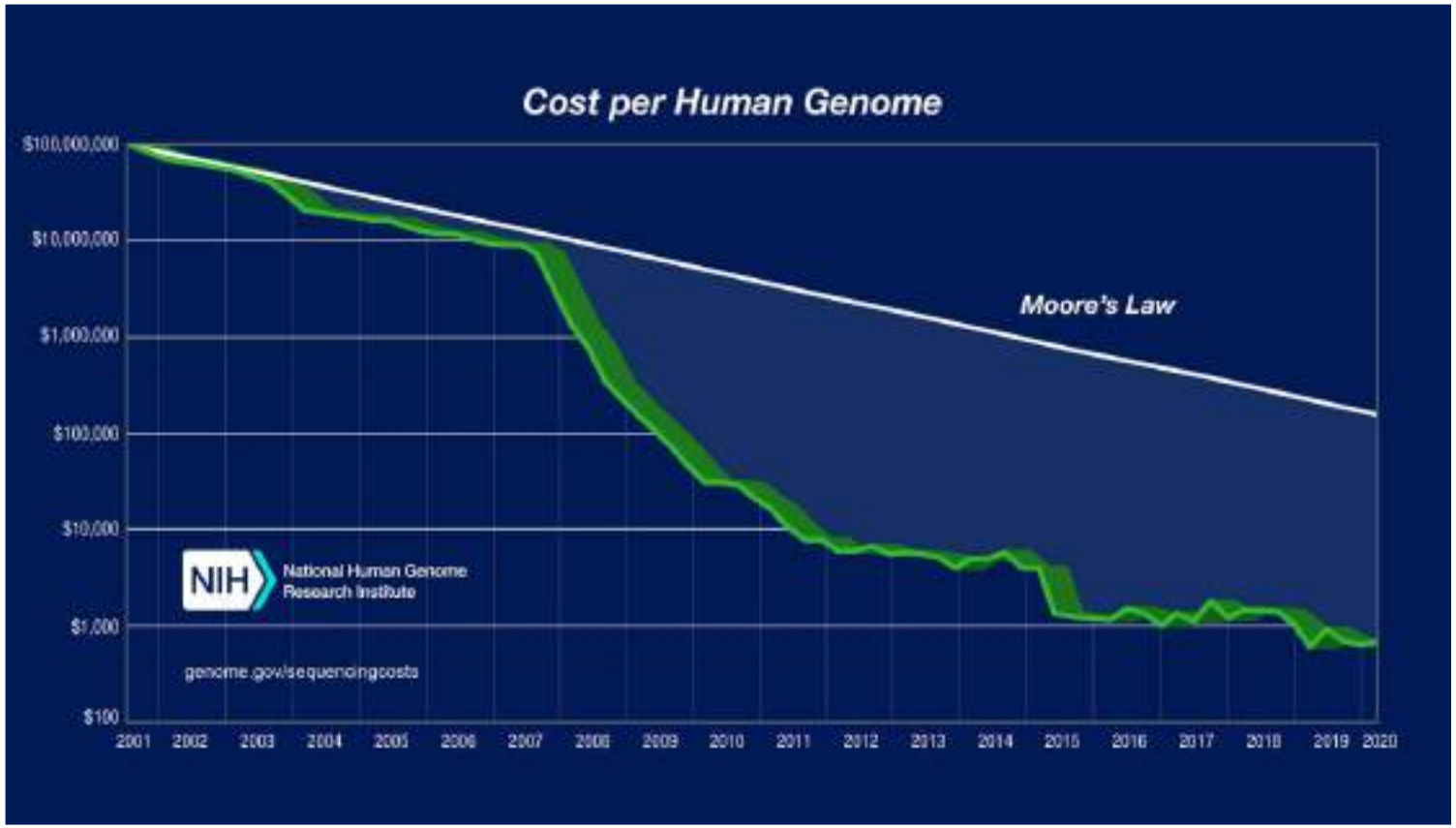
Sequencing history

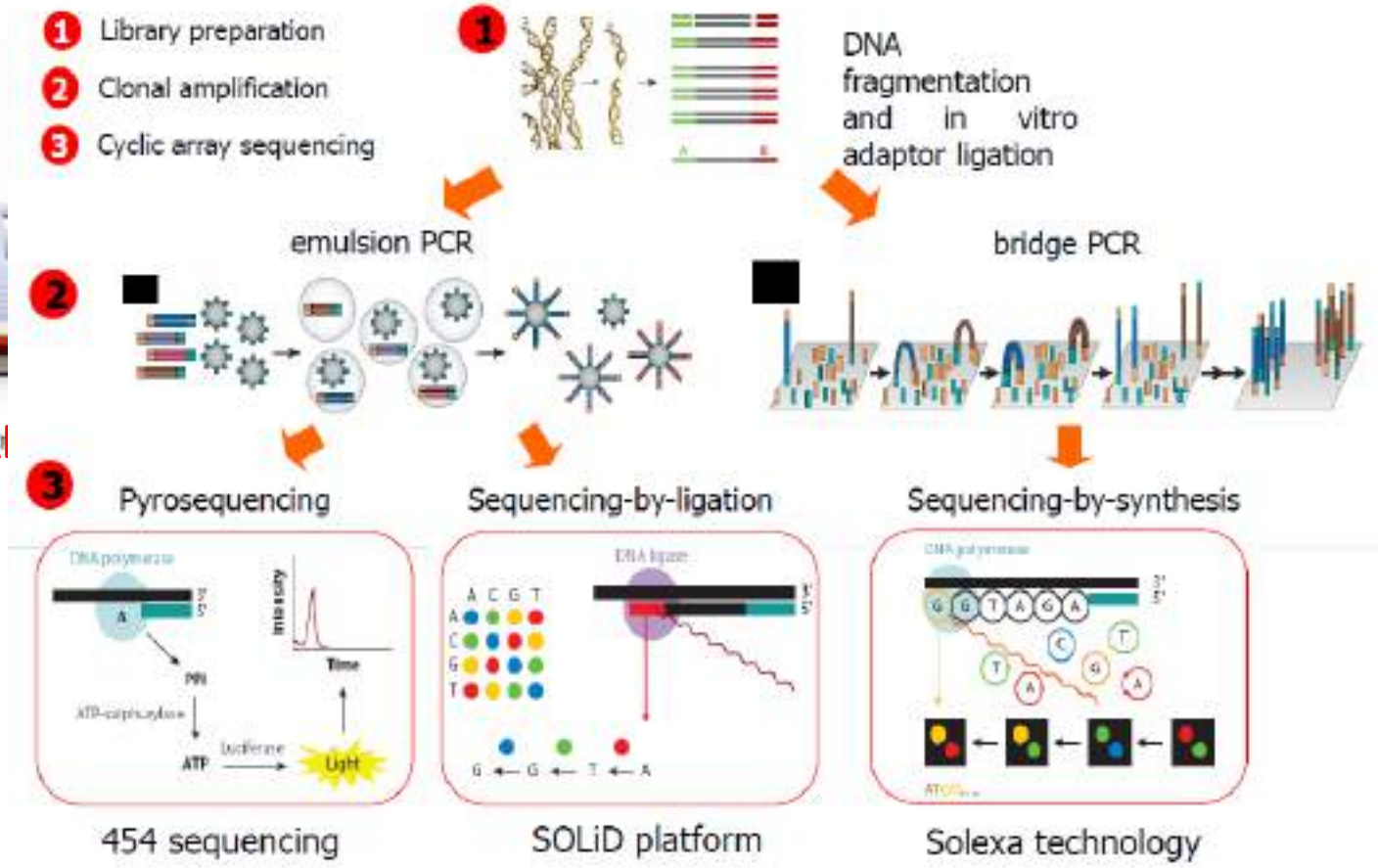


Growth of genomic data, drop of sequencing costs

Sequencing history

«NEXT» GENERATION SEQUENCING (NGS) PLATFORMS

«DEA



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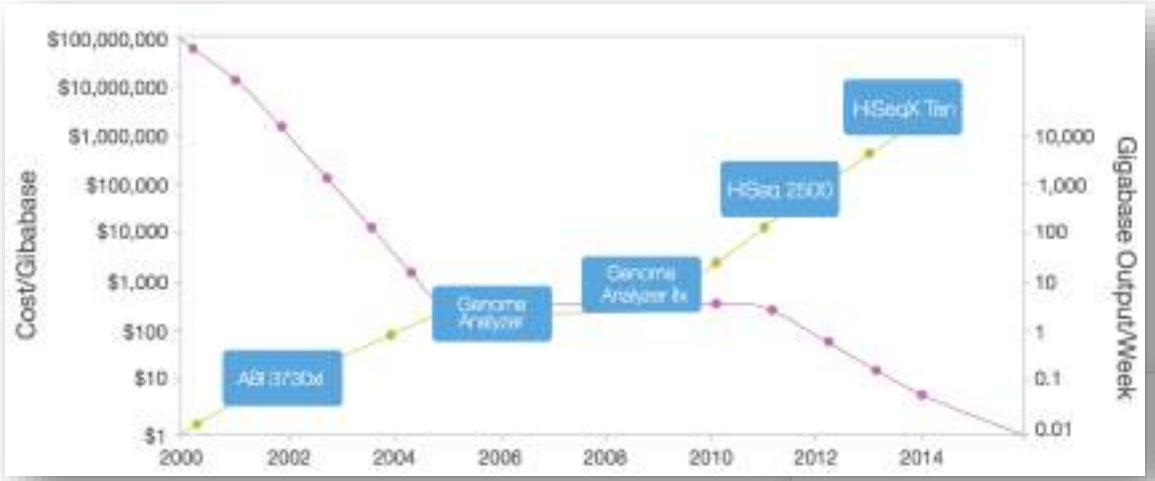
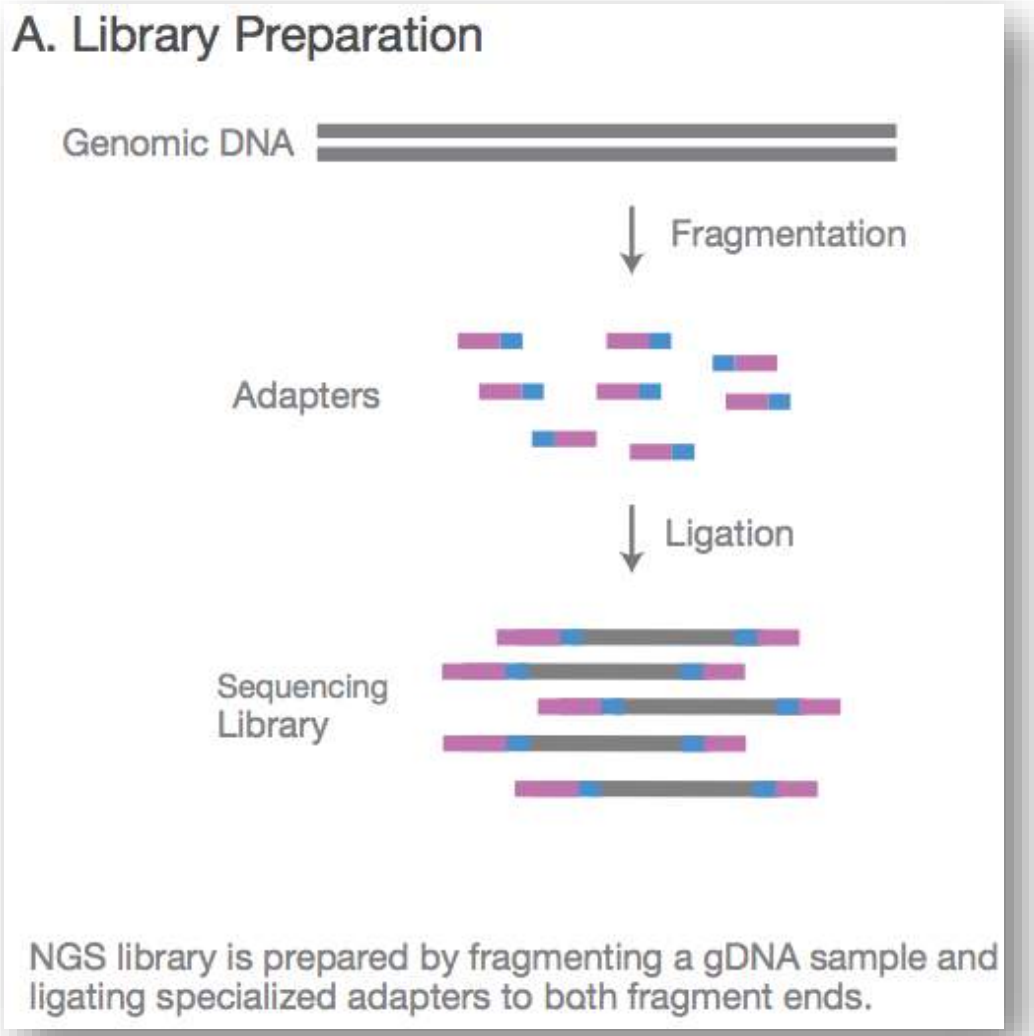
QUICK INTRO TO NGS METHODS

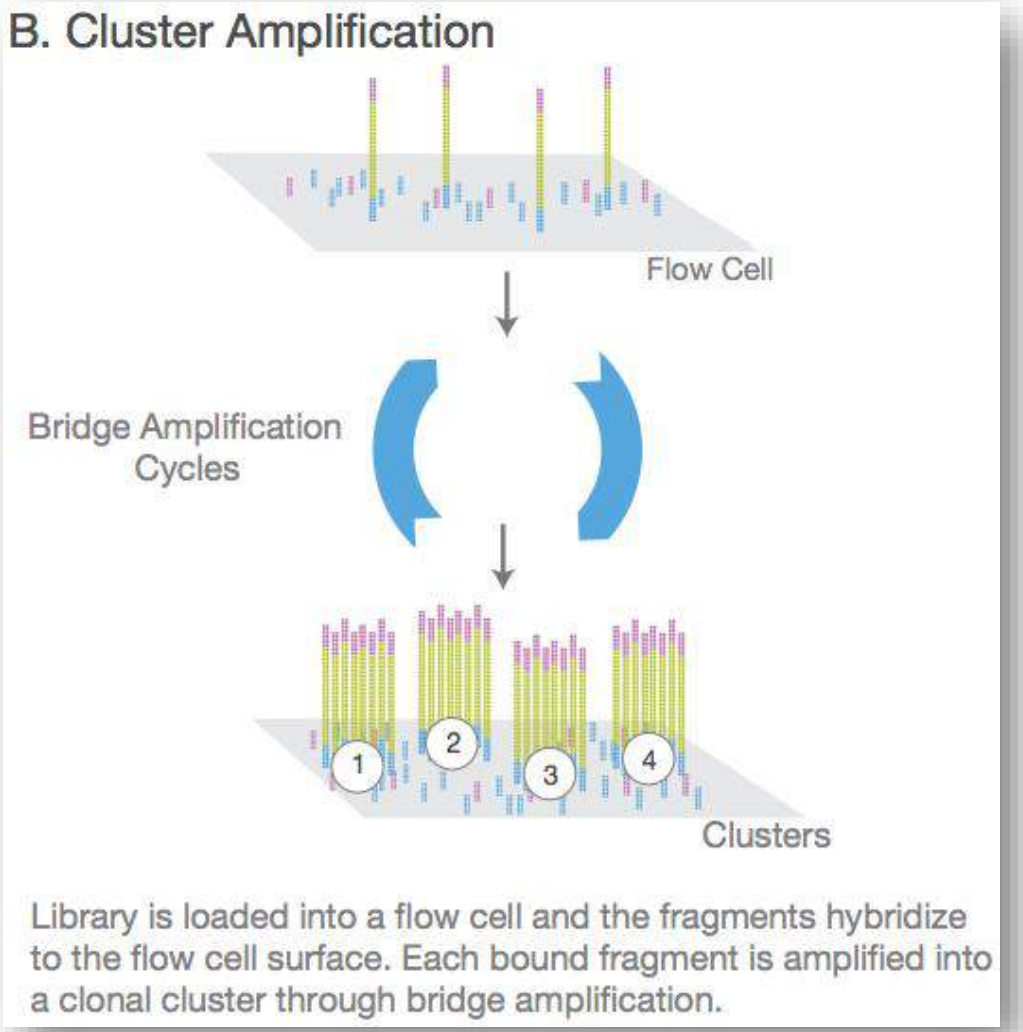
NGS PLATFORMS -> Illumina Sequencing



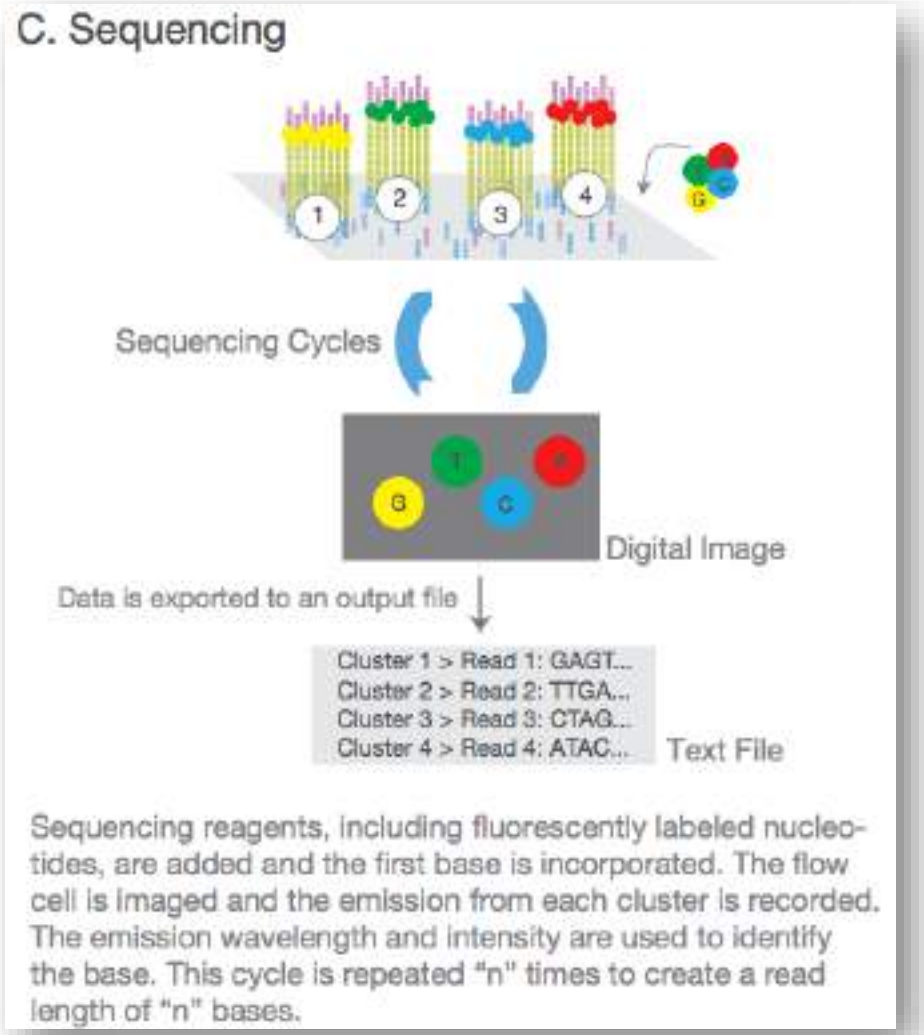
https://www.illumina.com/content/dam/illumina-marketing/documents/products/illumina_sequencing_introduction.pdf

NGS PLATFORMS -> Illumina Sequencing





NGS PLATFORMS -> Illumina Sequencing



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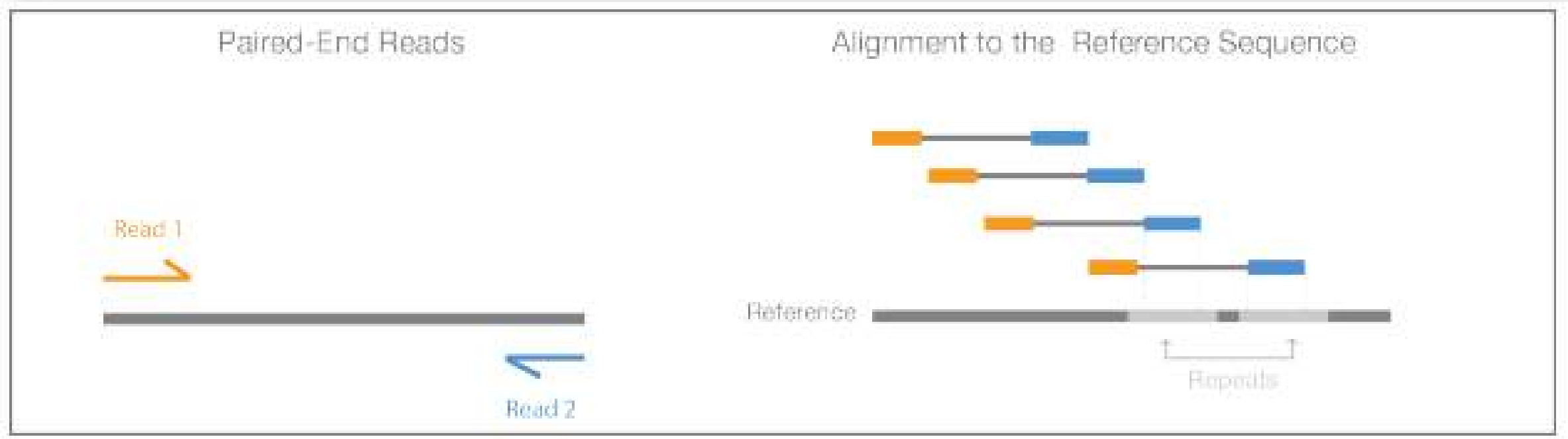
NGS PLATFORMS -> Illumina Sequencing



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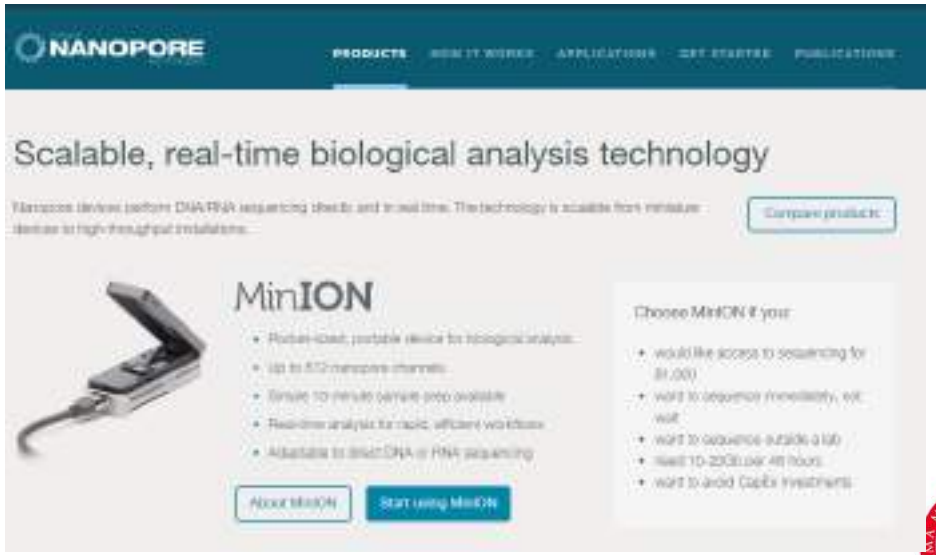
NEW/NOW GENERATION SEQUENCING (NGS) PLATFORMS
AKA
THIRD GENERATION SEQUENGING

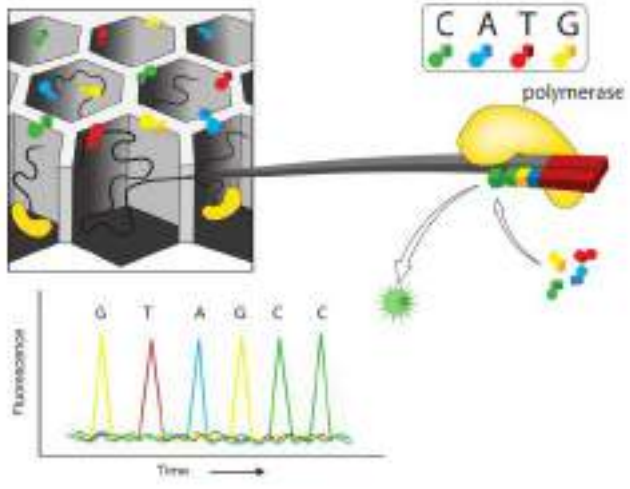
SINGLE MOLECULE REAL-TIME SEQUENCING

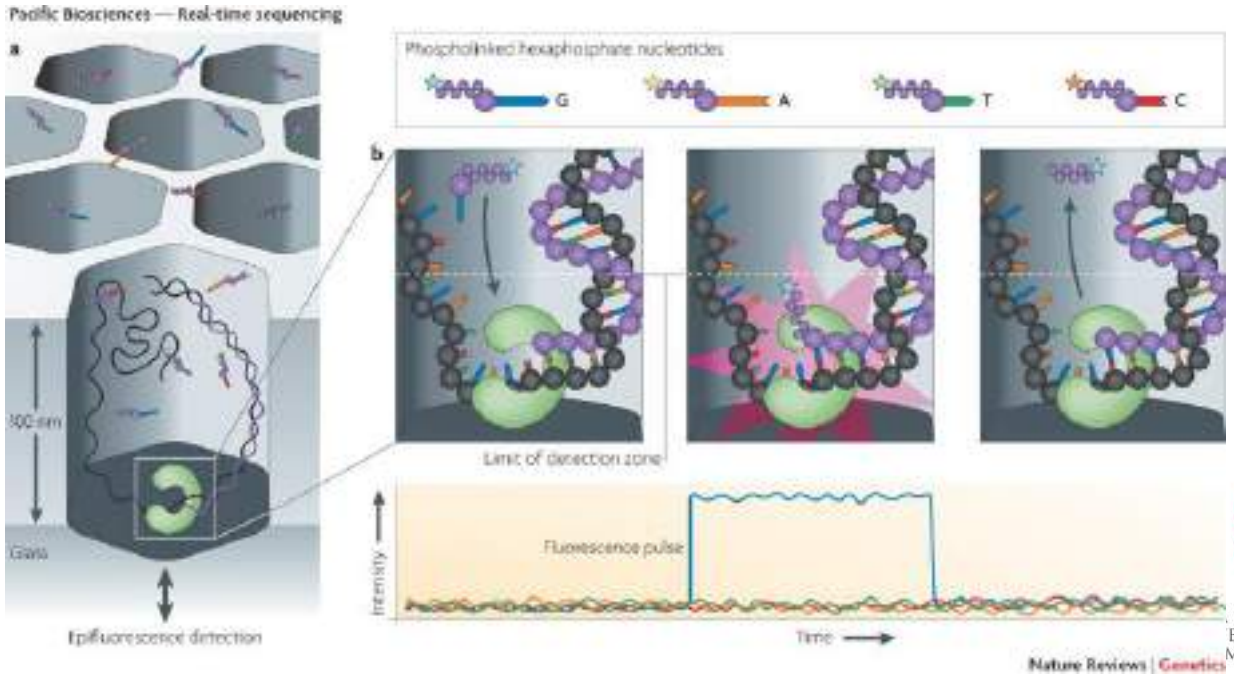
NANOPORE SEQUENCING



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

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





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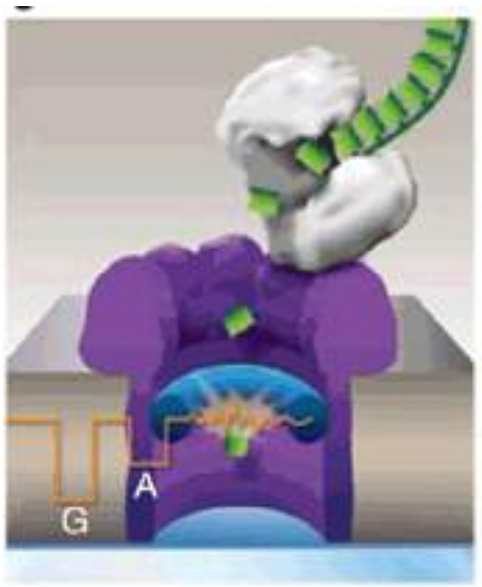
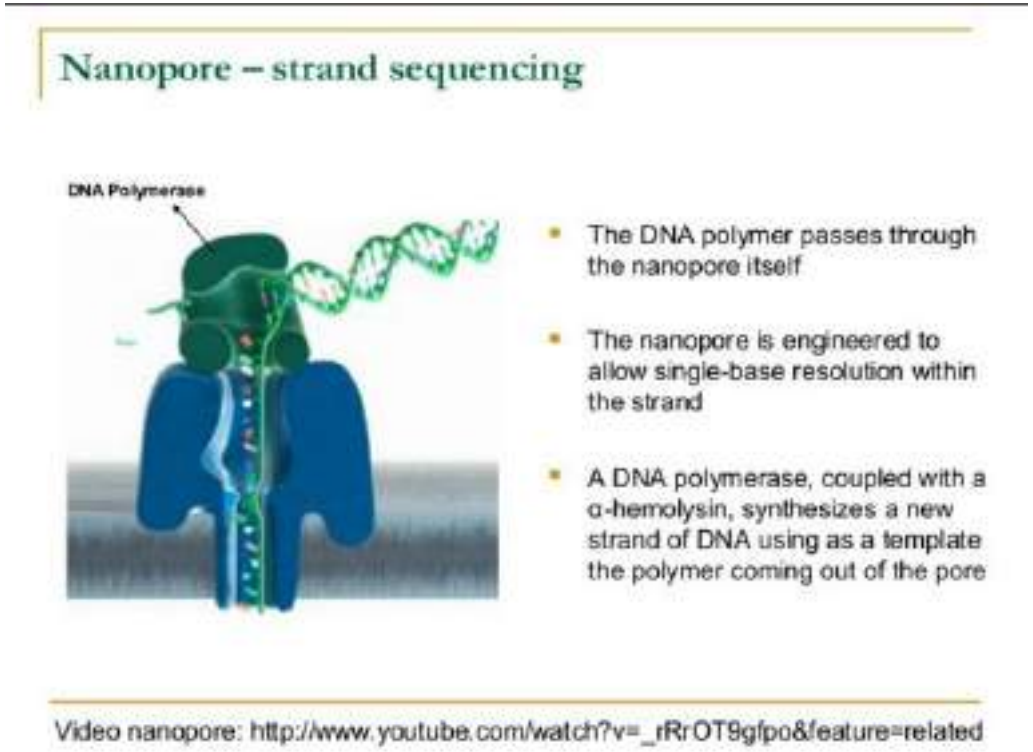
NEW/NOW GENERATION SEQUENCING (NGS) PLATFORMS AKA THIRD GENERATION SEQUENGING

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.





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

PacBio
Long reads

Oxford Nanopore
Long reads

Illumina sequences: _ _ _ _ _ _ _ _ _   _ _ _ _ _ _ _ _   _ _ _ _   _ _ _ _ _

PacBio sequences: ______________________   ___________________________

MinION sequences: _______________________   ___________________________

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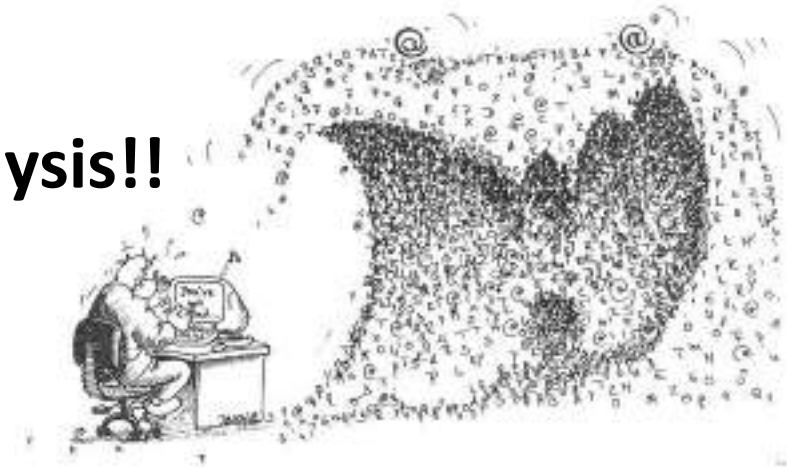
Take home message

- 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!!



Bioinformatic challenges of genomic data

Marine Genomics 30 (2016) 3–13

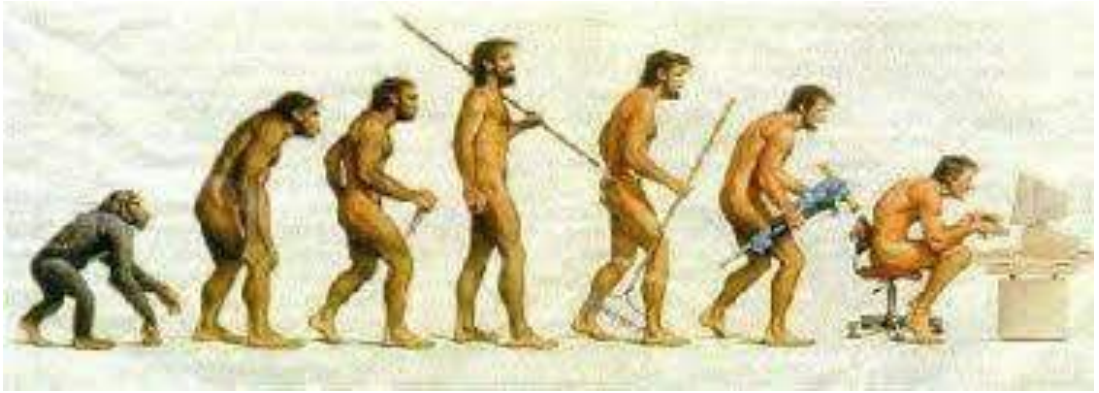
Contents lists available at ScienceDirect

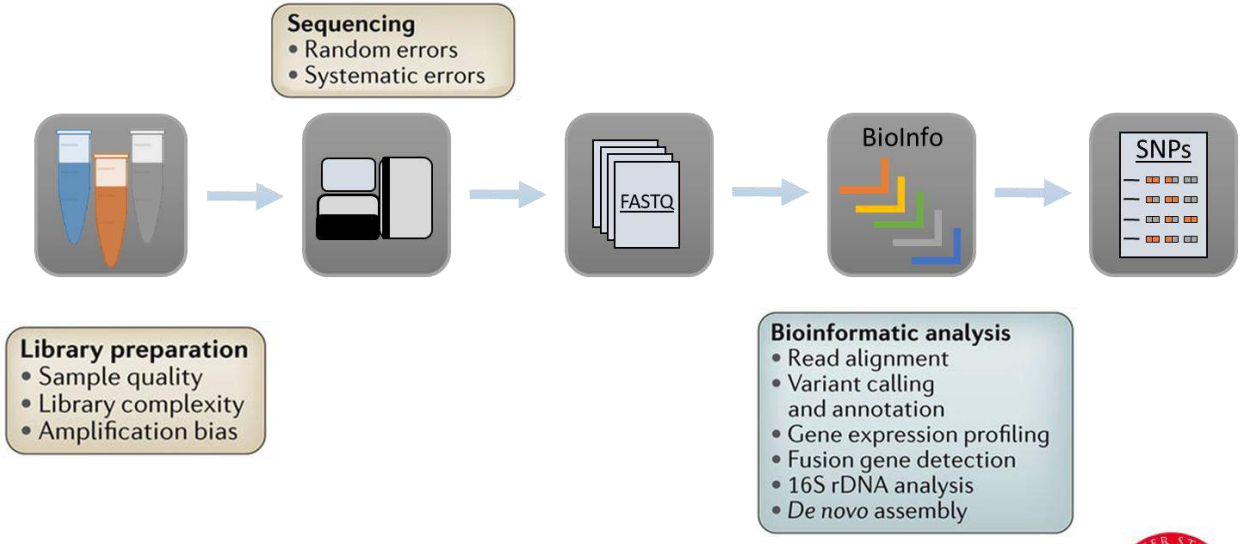
Marine Genomics

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

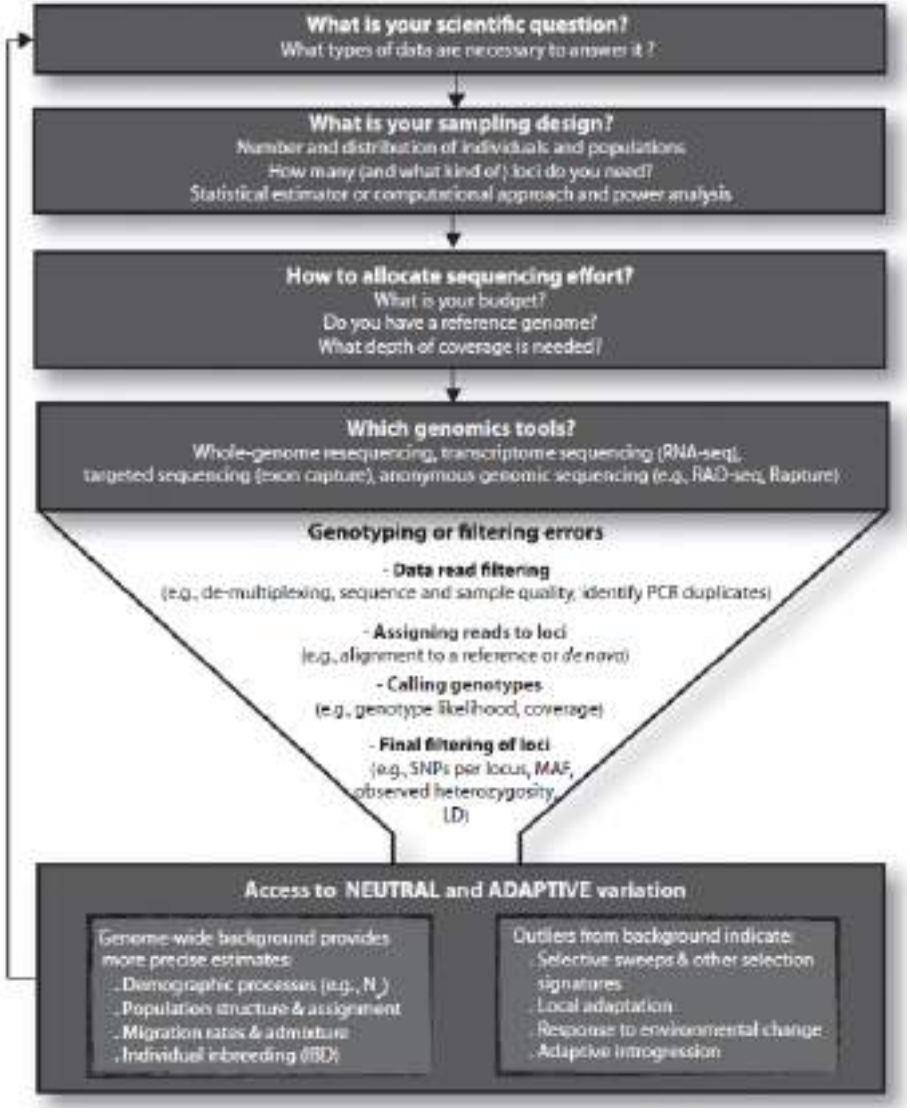
Next-generation biology: Sequencing and data analysis approaches for non-model organisms

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





GENOMIC CONCEPTUAL FRAMEWORK



Benestan *et al.* 2016

GENOMIC CONCEPTUAL FRAMEWORK

GENOMICS FOR NON-MODEL ORGANISMS

Aim of Study	Optimal sequencing method	Minimal Reference Needed
Population subdivision, migration rates, population size changes through time	RAD	None
Genes under selection	Exome Sequencing	De novo transcriptome**
Selection signatures and genomic regions underlying ecological speciation	Low-coverage WGS	Draft genome
Molecular basis of acclimatization, adaptation	RNAseq or TagSeq	None or De novo transcriptome

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

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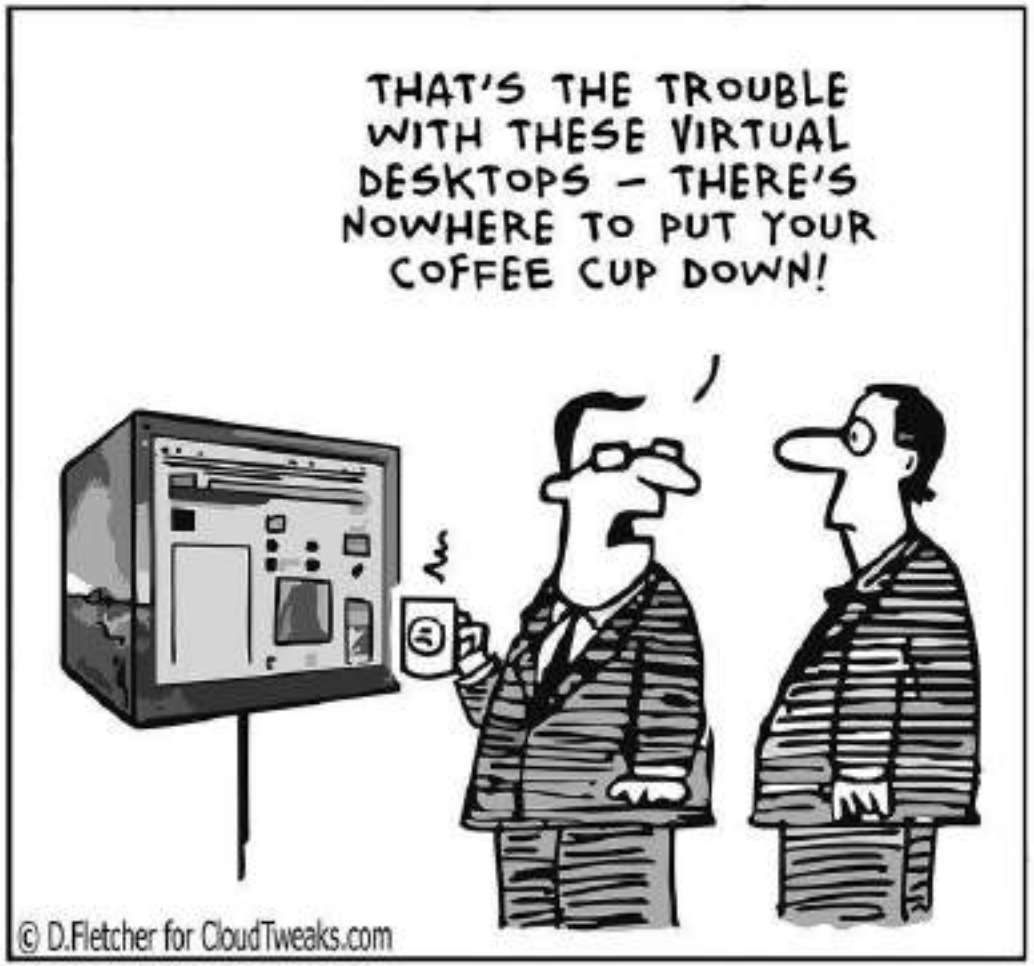
while (sleepy)
fillCup();
drinkCoffee();
}


THAT'S THE TROUBLE WITH THESE VIRTUAL DESKTOPS – THERE'S NOWHERE TO PUT YOUR COFFEE CUP DOWN!
© D.Fletcher for CloudTweaks.com

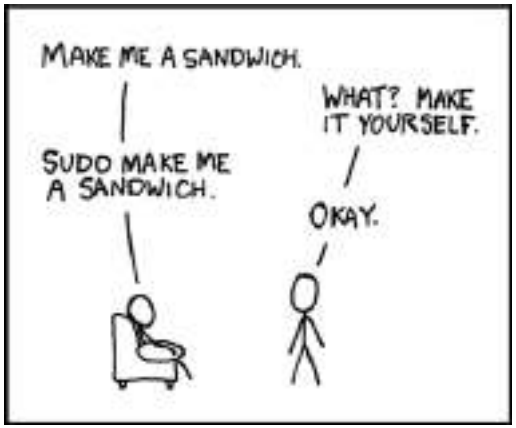
Genomic approaches in marine fisheries research: challenges and opportunities

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.

WHEN/WHO/WHAT/WHY???
Really today??



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WHEN/WHO/WHAT/WHY???
Really today??

Genomic approaches in marine fisheries research: challenges and opportunities

FISH and FISHERIES

FISH and FISHERIES, 2015, 16, 125–159

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 Berry*[2], *David J W*

[1]Molecular Fisheries Laboratory, Queensland Gover
Oceans Flagship, CSIRO Marine and Atmospheric F
Fisheries, Woolgoolga, NSW, Australia; [4]Wealth fr
Queensland Biosciences Precinct, 306 Carmody Ro
Biomedical Sciences, The University of Queensland,

Abstract

Significant changes have occurred in the well-established partnership between fisheries managers and geneticists over the last 50 years. It is therefore timely to review and recalibrate the ways in which genetic technologies can assist the fishing industry to maintain productive and sustainable harvests. Our objective is to 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 non-specialist 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.

Keywords environmental monitoring, genetic effective population size, genetic mark–recapture, product provenance, stock structure, unnatural selection

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

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Accepted 3 Aug 2013

Genomic approaches in marine fisheries research: challenges and opportunities

FISH and FISHERIES

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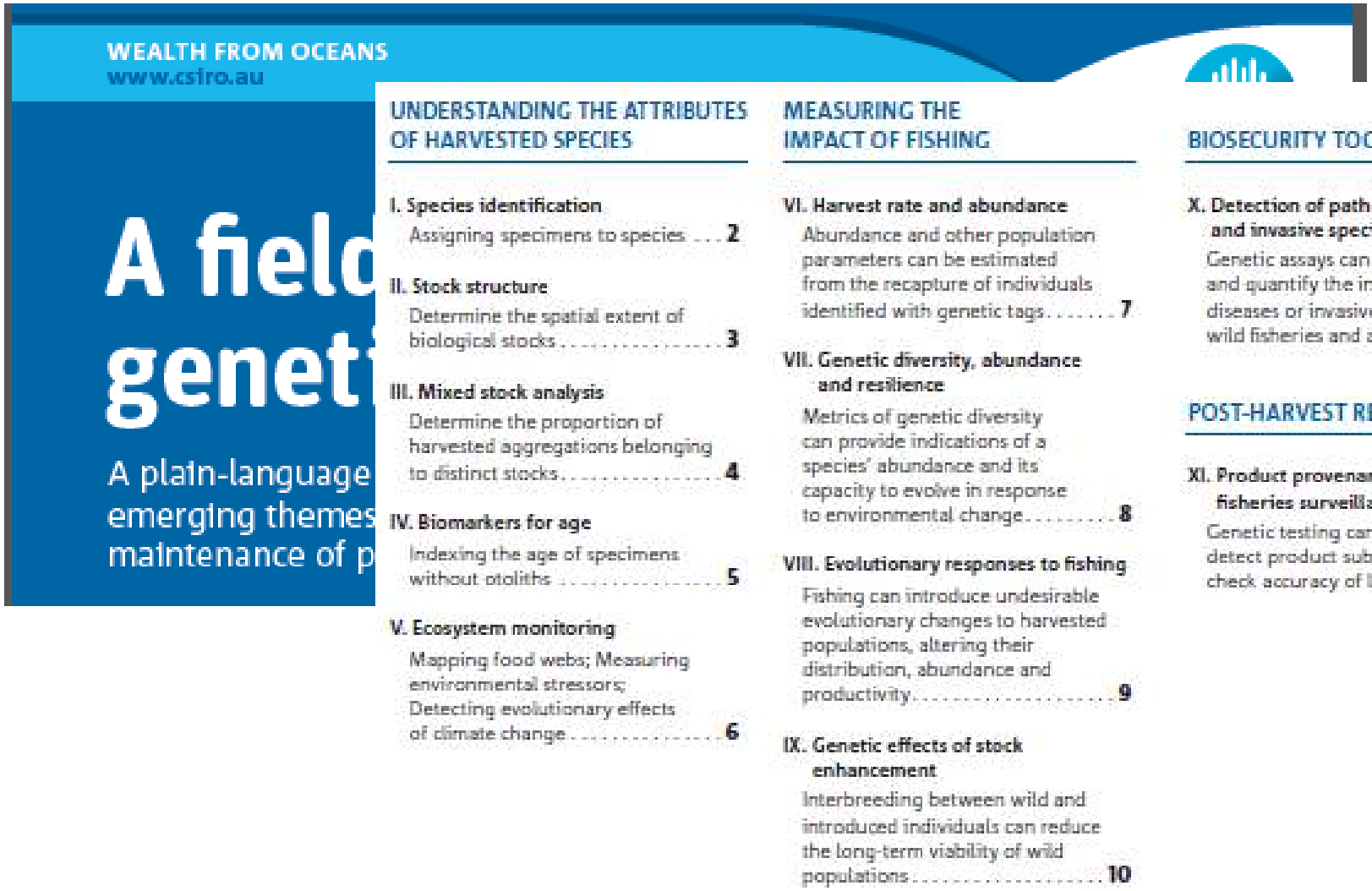
Ocean's eleven: a critical evaluation of the role of population, evolutionary and molecular genetics in the management of wild fisheries

Jennifer R Ovenden[1,5], *Oliver Berry*[2], *David J Welch*[3], *Rik C*

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

Genomic approaches in marine fisheries research: challenges and opportunities



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A plain-language
emerging themes
maintenance of p

UNDERSTANDING THE ATTRIBUTES OF HARVESTED SPECIES

I. Species identification
Assigning specimens to species . . . 2

II. Stock structure
Determine the spatial extent of biological stocks . . . 3

III. Mixed stock analysis
Determine the proportion of harvested aggregations belonging to distinct stocks . . . 4

IV. Biomarkers for age
Indexing the age of specimens without otoliths . . . 5

V. Ecosystem monitoring
Mapping food webs; Measuring environmental stressors; Detecting evolutionary effects of climate change . . . 6

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
Metrics of genetic diversity can provide indications of a species' abundance and its capacity to evolve in response to environmental change . . . 8

VIII. Evolutionary responses to fishing
Fishing can introduce undesirable evolutionary changes to harvested populations, altering their distribution, abundance and productivity . . . 9

IX. Genetic effects of stock enhancement
Interbreeding between wild and introduced individuals can reduce the long-term viability of wild populations . . . 10

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

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.

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.

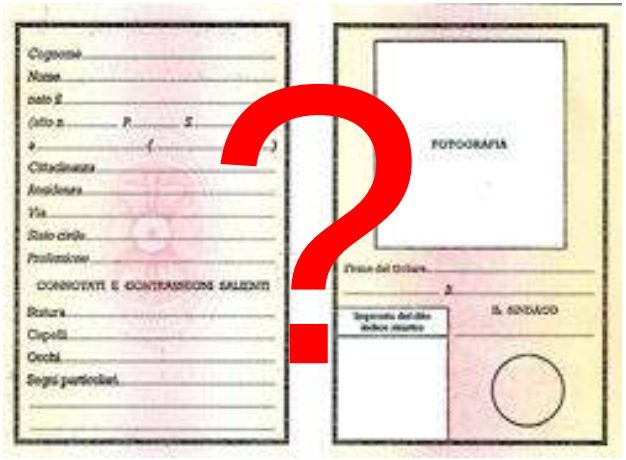
GenoDREAM Experience

- **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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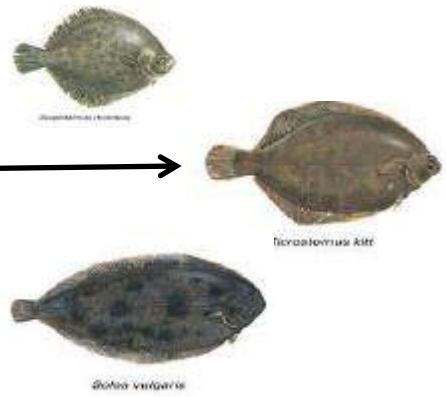
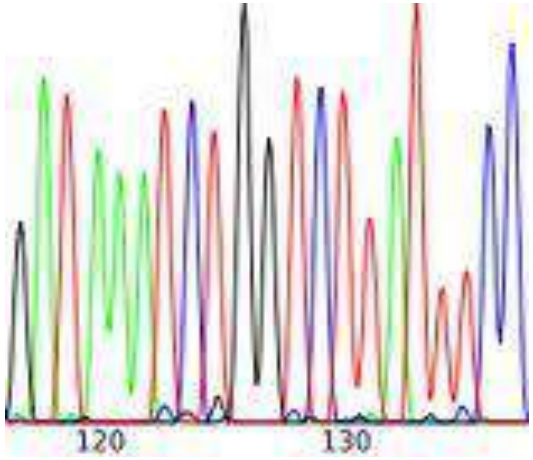
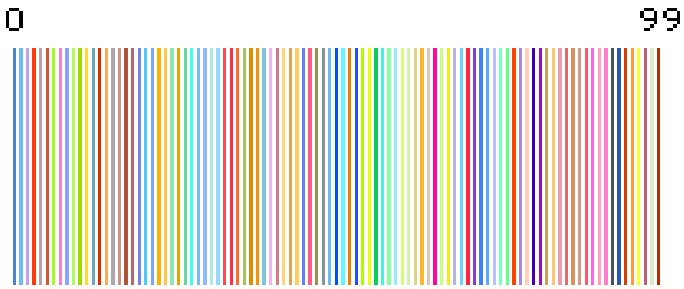
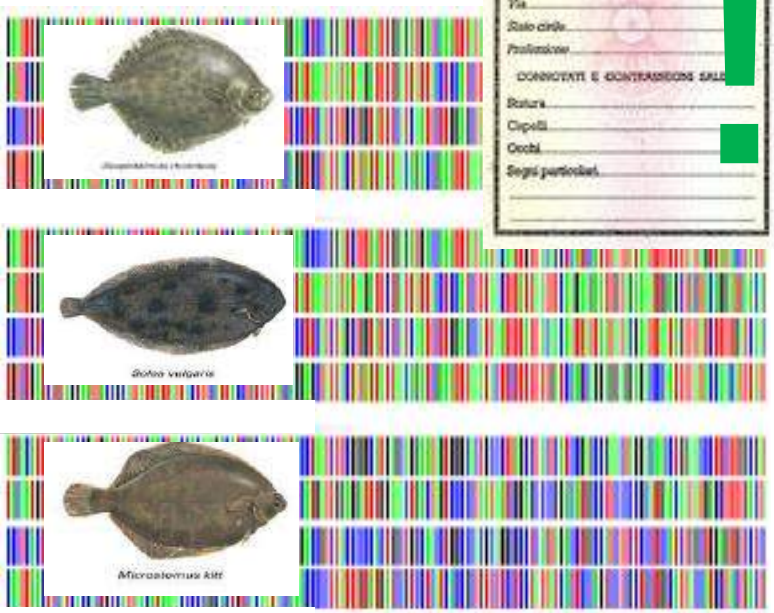


Theme I: Species identification

GenoDREAM Experience







Theme I: Species identification

GenoDREAM Experience

Theme I: Species identification

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 ACCESS Freely available online

PLoS one

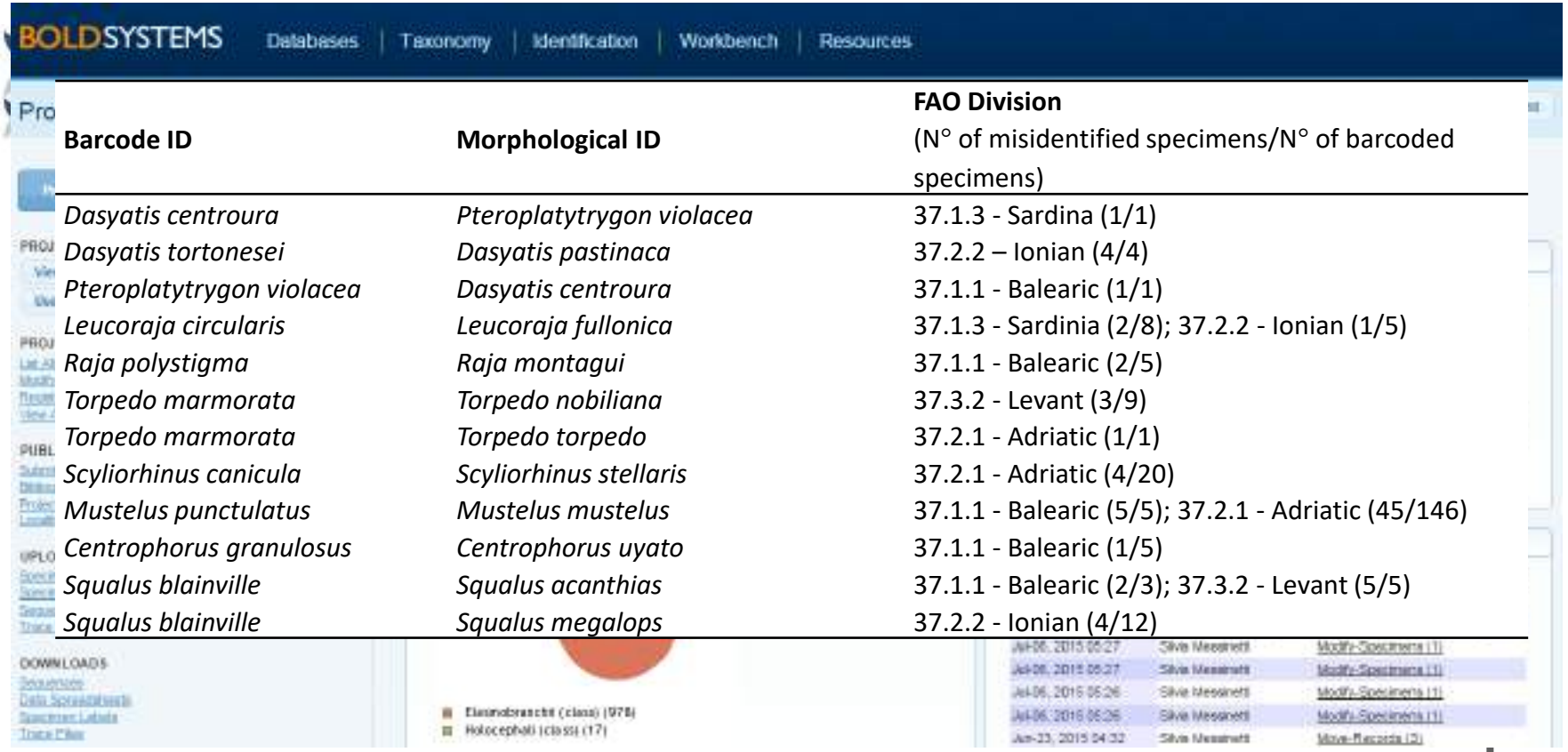
Identifying Fishes through DNA Barcodes and Microarrays

Marc Kochzius[1,2]*, Christian Seidel[1¤a], Aglaia Antoniou[3], Sandeep Kumar Botla[1¤b], Daniel Campo[4¤c], Alessia Cariani[5], Eva Garcia Vazquez[4], Janet Hauschild[1¤d], Caroline Hervet[6¤e], Sigridur Hjörleifsdottir[7], Gudmundur Hreggvidsson[7,8], Kristina Kappel[1], Monica Landi[5¤f], Antonios Magoulas[3], Viggo Marteinsson[7], Manfred Nölte[9], Serge Planes[6¤g], Fausto Tinti[5], Cemal Turan[10], Moleyur N. Venugopal[11], Hannes Weber[1], Dietmar Blohm[1]

September 2010 | Volume 5 | Issue 9 | e12620

Theme I: Species identification

GenoDREAM Experience **ELASMOMED network**



Barcode ID	Morphological ID	FAO Division (N° of misidentified specimens/N° of barcoded specimens)
Dasyatis centroura	*Pteroplatytrygon violacea*	37.1.3 - Sardina (1/1)
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)

Theme I: Species identification

GenoDREAM Experience ABFT larvae and bones ID

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 Puncher[1]*, Haritz Arrizabalaga[2], Francisco Alemany[3], Alessia Cariani[1], Isik K. Oray[4], F. Saadet Karakulak[4], Gualtiero Basilone[5], Angela Cuttitta[5], Salvatore Mazzola[5], Fausto Tinti[1]

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

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

REVIEWS

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

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

Theme I: Species identification

GenoDREAM Experience Egg case identification

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] | 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

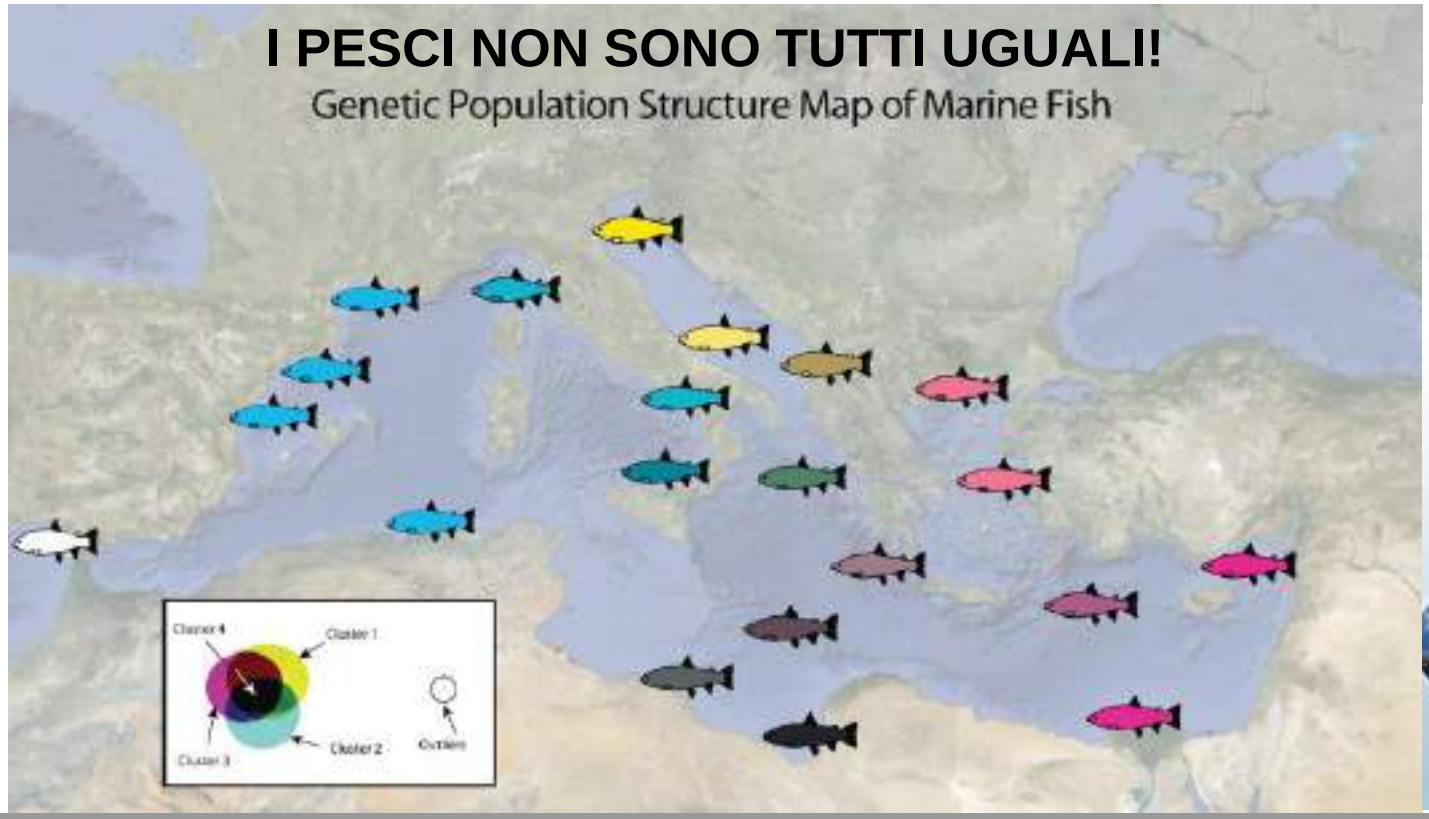
- The power of genetic markers to reveal stocks will increase.
- Analyses will increasingly focus on the behaviour of individual organisms on ecological time frames, rather than on the long-term average behaviours of entire populations.
- The availability of genomic resources for fisheries species will 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



FishPopTrace

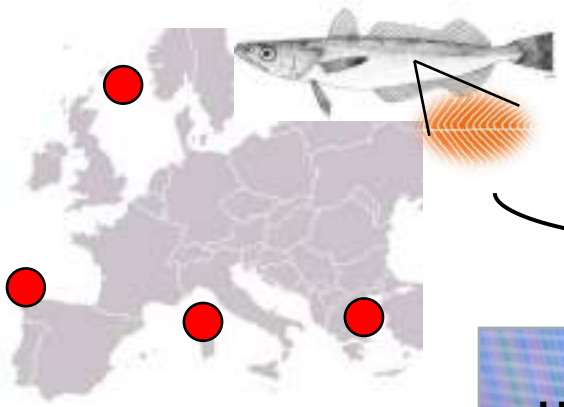
The Structure of Fish Populations and Traceability of Fish and Fish Products

Theme II: Fisheries stock structure

GenoDREAM Experience FishPopTrace EU project

FishPopTrace

TRANSCRIPTOME SEQUENCING



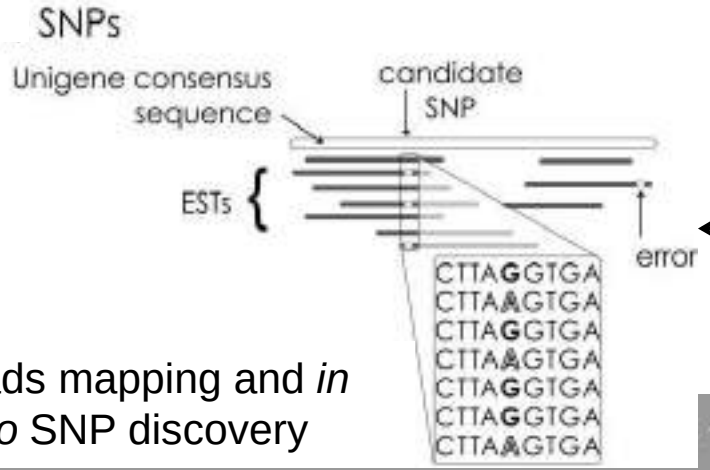
mRNA molecules (expressed genes)

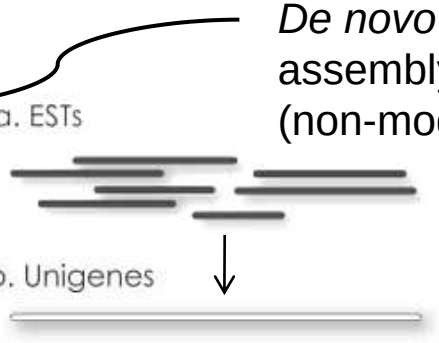
Reverse transcription to double-stranded cDNA

Short fragment (ESTs) massive parallel sequencing

De novo clustering/ assembly in contigs (non-model species)

SNP DISCOVERY





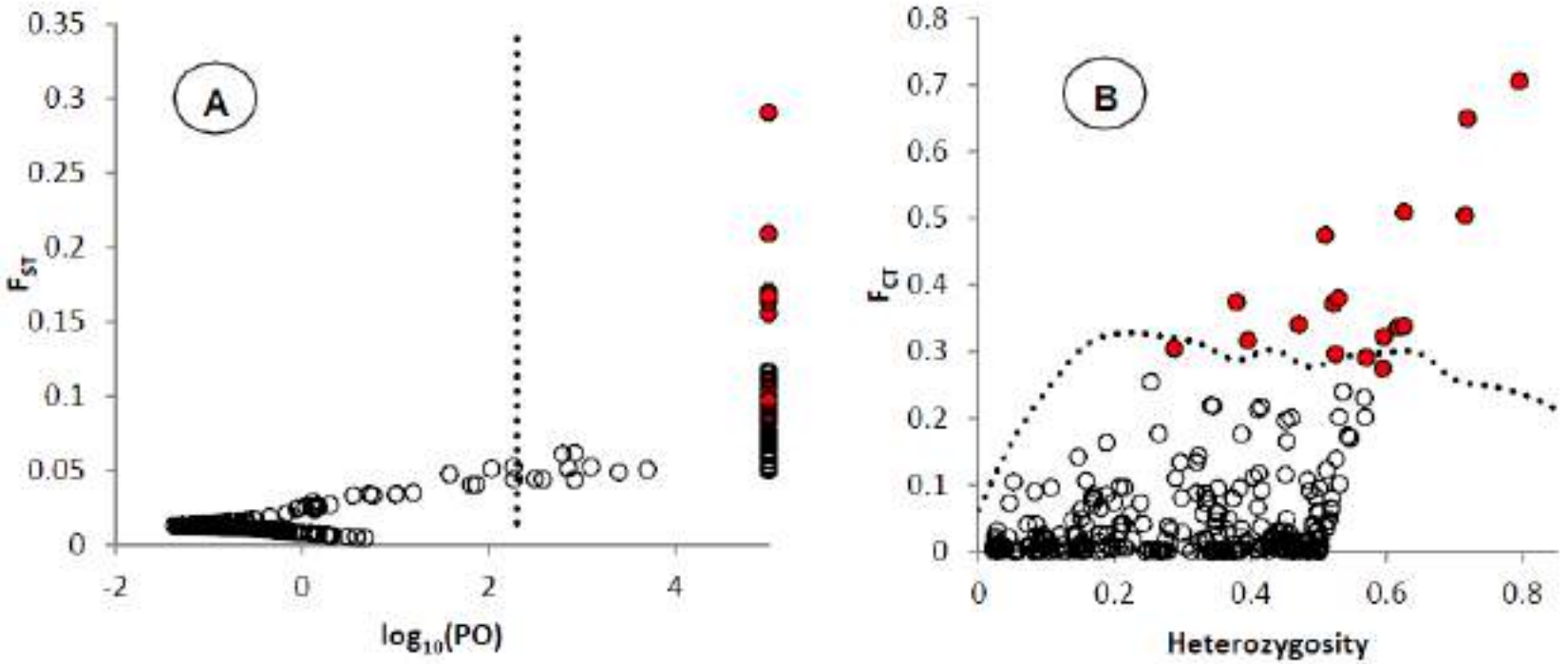
Reads mapping and *in silico* SNP discovery

Theme II: Fisheries stock structure

GenoDREAM Experience FishPopTrace EU project

FishPopTrace

SNP SELECTION STRATEGY



"GENOME SCAN" APPROACHES TO IDENTIFY "OUTLIER" LOCI

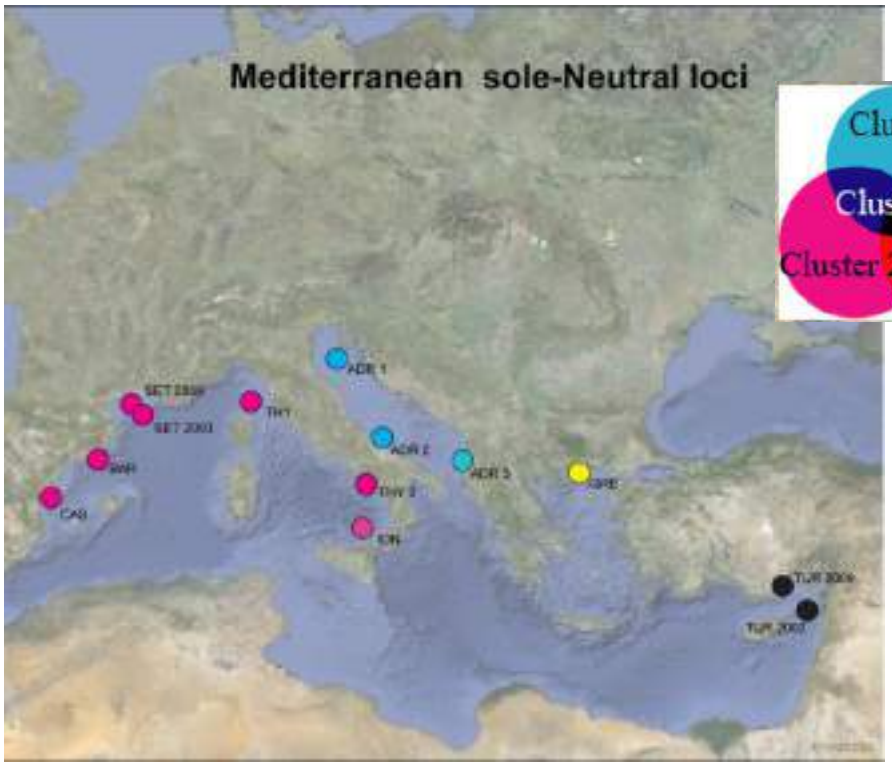
Theme II: Fisheries stock structure

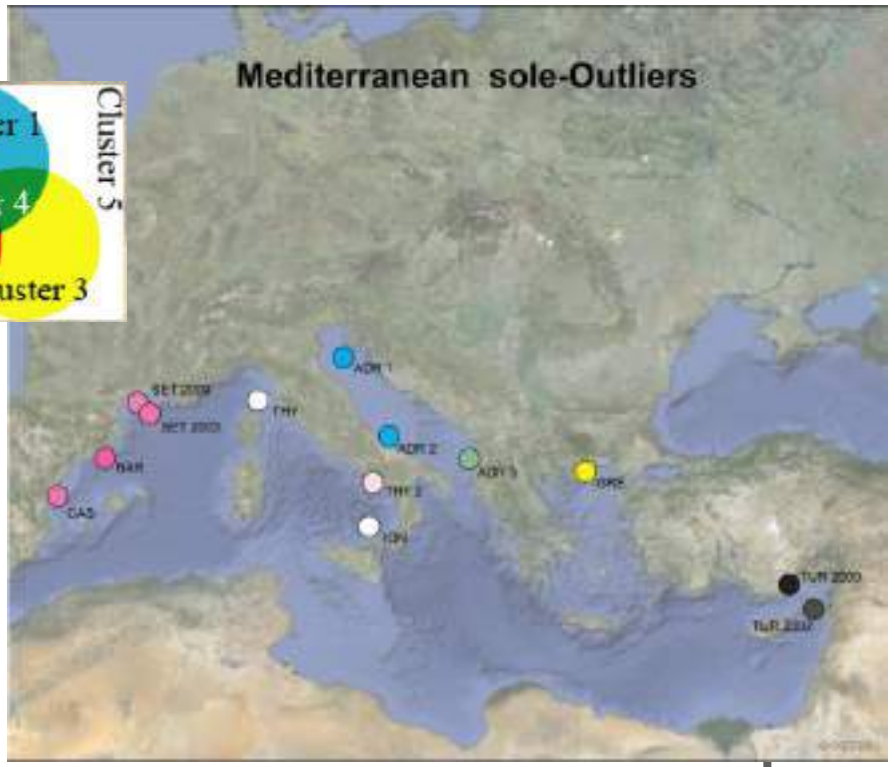
GenoDREAM Experience FishPopTrace EU project

FishPopTrace

NEUTRAL LOCI *VS* OUTLIER LOCI

Solea solea





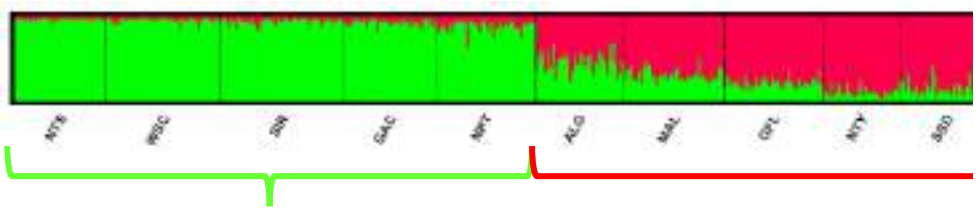
Theme II: Fisheries stock structure

GenoDREAM Experience FishPopTrace EU project

FishPopTrace

Merluccius merluccius

299 SNPs NEUTRAL



ATLANTIC

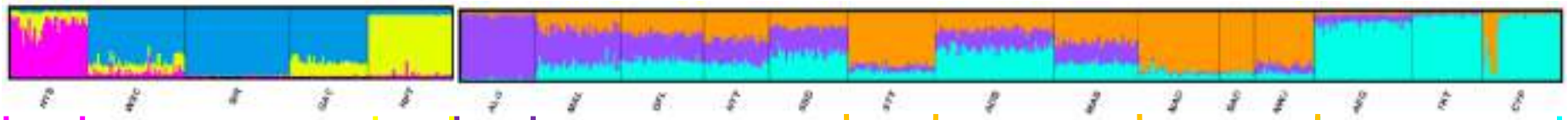
MOLECULAR ECOLOGY
Molecular Ecology (2014) 23, 118–135 doi: 10.1111/mec.12568

Outlier SNP markers reveal fine-scale genetic structuring across European hake populations (*Merluccius merluccius*)

ILARIA MILANO,*[1] MASSIMILIANO BABBUCCI,†[1] ALESSIA CARIANI,* MIROSLAVA ATANASSOVA,‡ DORTE BEKKEVOLD,§ GARY R. CARVALHO,¶ MONTSERRAT ESPIÑEIRA,‡ FABIO FIORENTINO,** GERMANA GAROFALO,** AUDREY J. GEFFEN,†† JAKOB. H. HANSEN,‡ SARAH J. HELYAR,‡‡ EINAR E. NIELSEN,§ ROB OGDEN,§§ TOMASO PATARNELLO,† MARCO STAGIONI,* FISHPOPTRACE CONSORTIUM,¶¶ FAUSTO TINTI* and LUCA BARGELLONI†

7 SNPs OUTLIER

19 SNPs OUTLIER



NORTH SEA | **PORTUGAL** | **ALGERIA** | **CENTRAL MED** | **CENTRAL MED** | **EASTERN MED**

Theme II: Fisheries stock structure

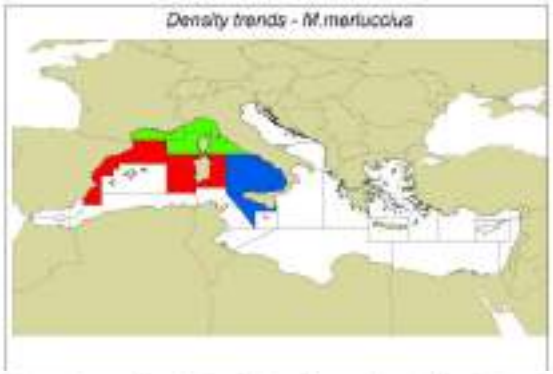
GenoDREAM Experience **STOCKMED EU project**

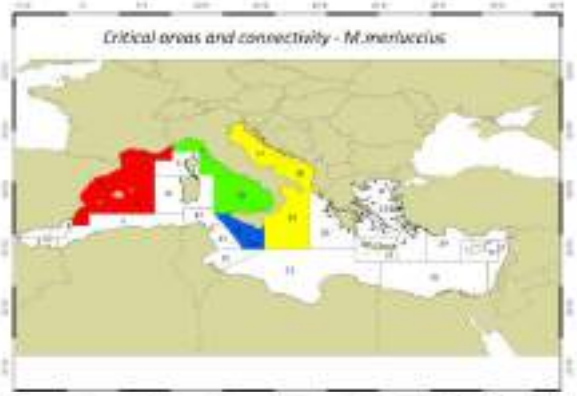
MAREA

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"*

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

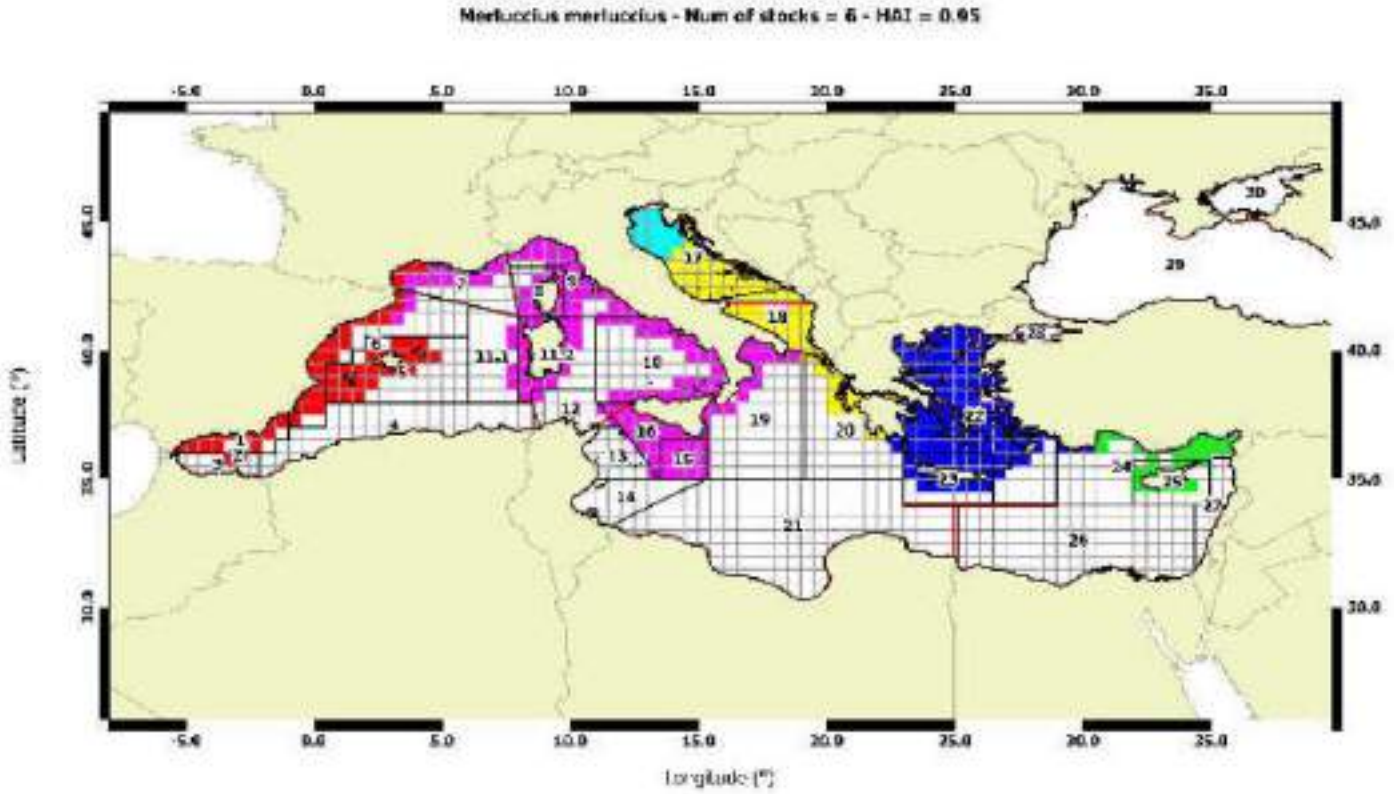




Theme II: Fisheries stock structure

GenoDREAM Experience **STOCKMED EU project**

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



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

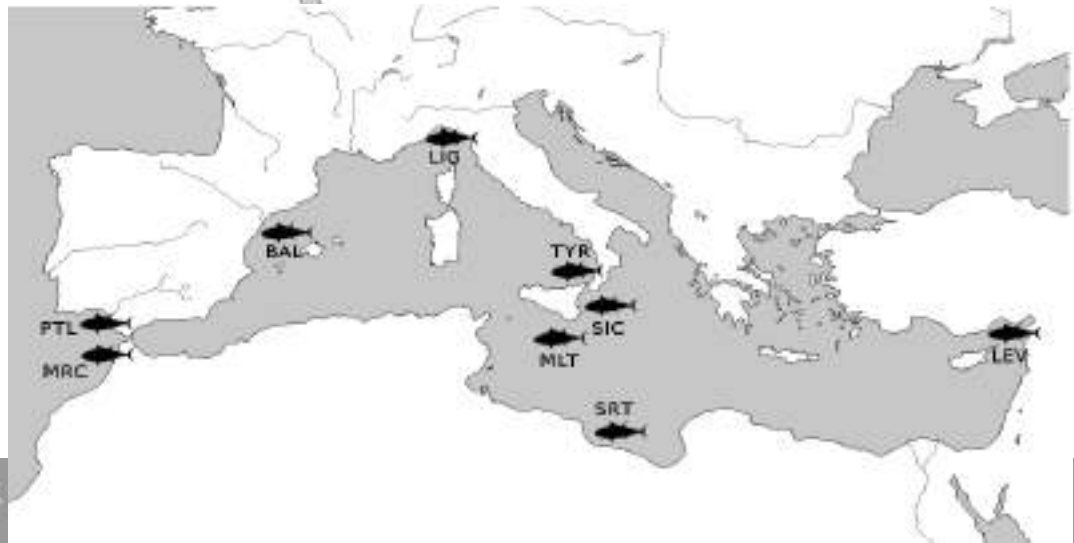
Subcontractors:

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

Theme III: Resolving mixed-stock fisheries

GenoDREAM Experience ICCAT GBYP consortium 2011-2019

Extensive sampling with several temporal replicates

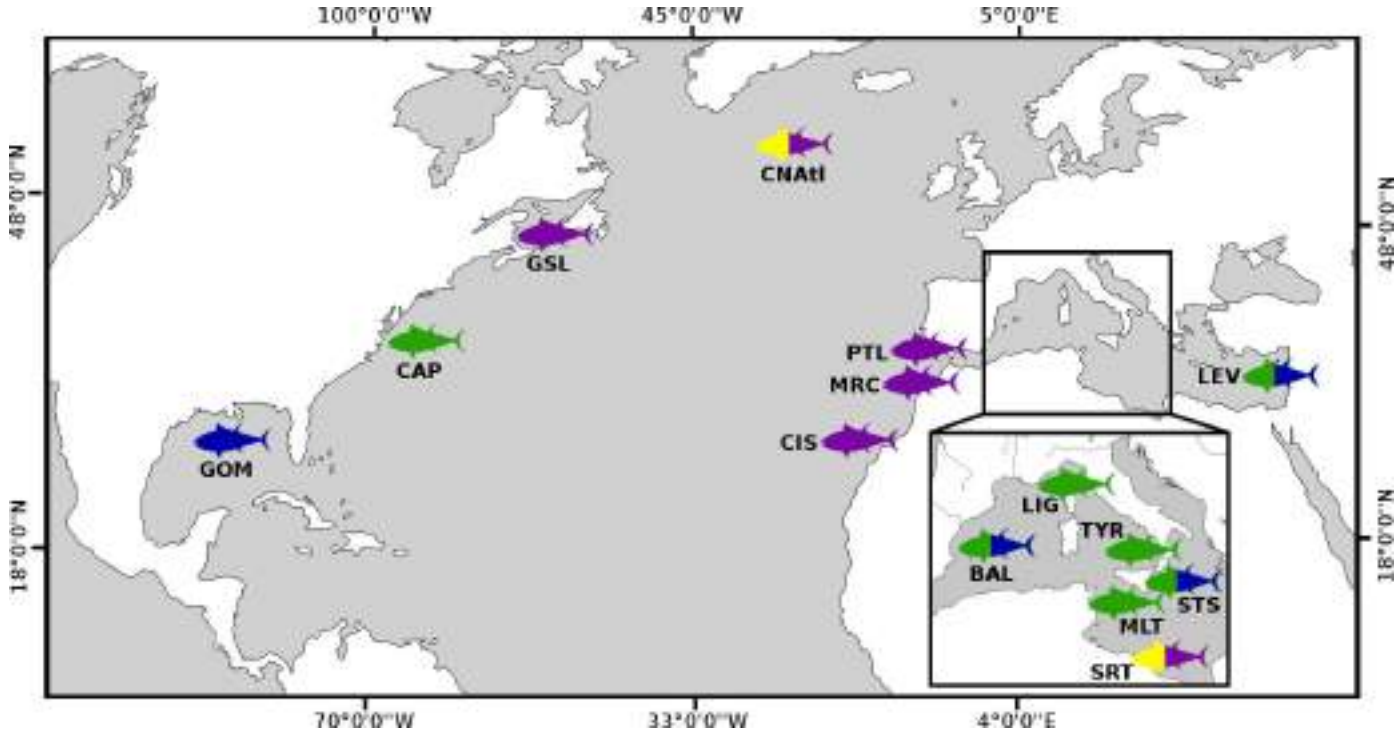


https://doi.org/10.1111/1755-0998.12764

Theme III: Resolving mixed-stock fisheries

GenoDREAM Experience ICCAT GBYP consortium 2011-2019

Extensive sampling with several temporal replicates

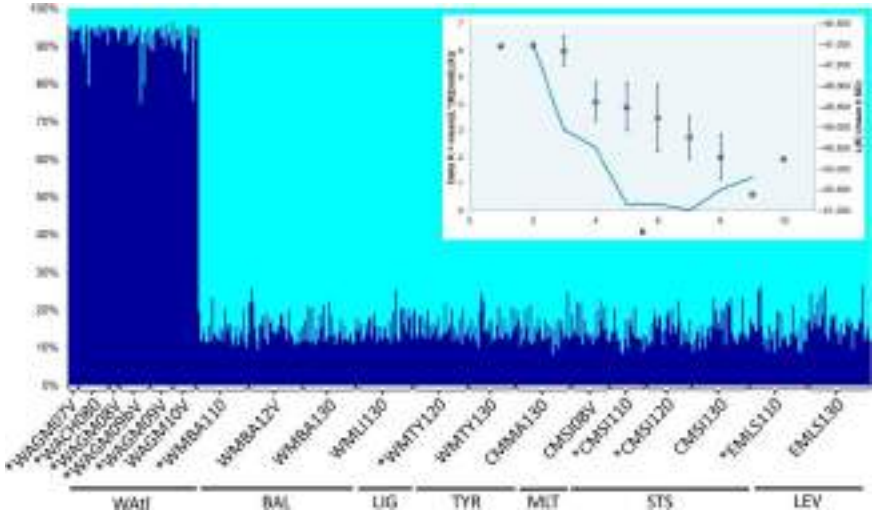


Larvae Blue
Young-of-the-year Green
Medium adult Yellow
Large adult Purple

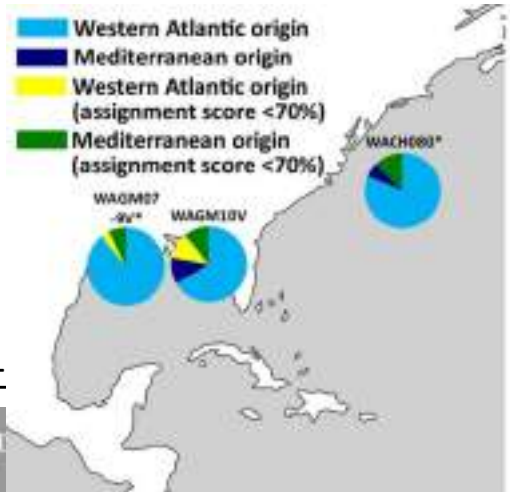
https://doi.org/10.1111/1755-0998.12764

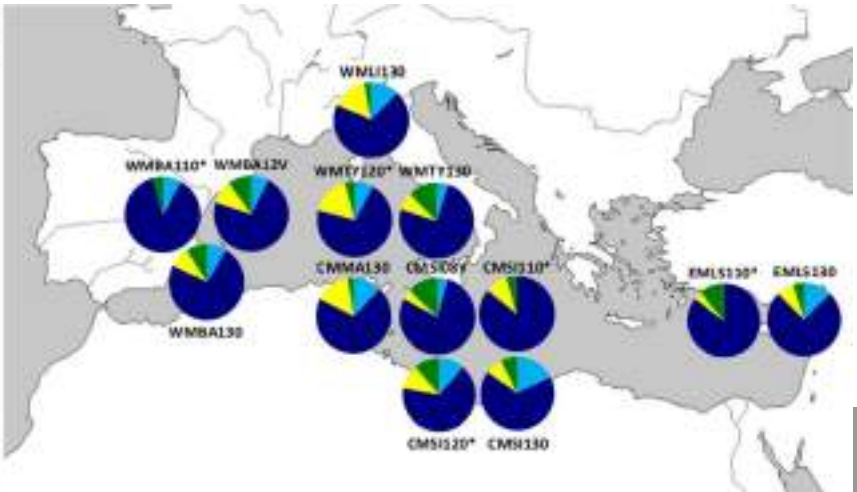
Theme III: Resolving mixed-stock fisheries

GenoDREAM Experience ICCAT GBYP consortium 2011-2019



Genome wide SNP profiling with cutting-edge NGS Genotyping-By-Sequencing techniques

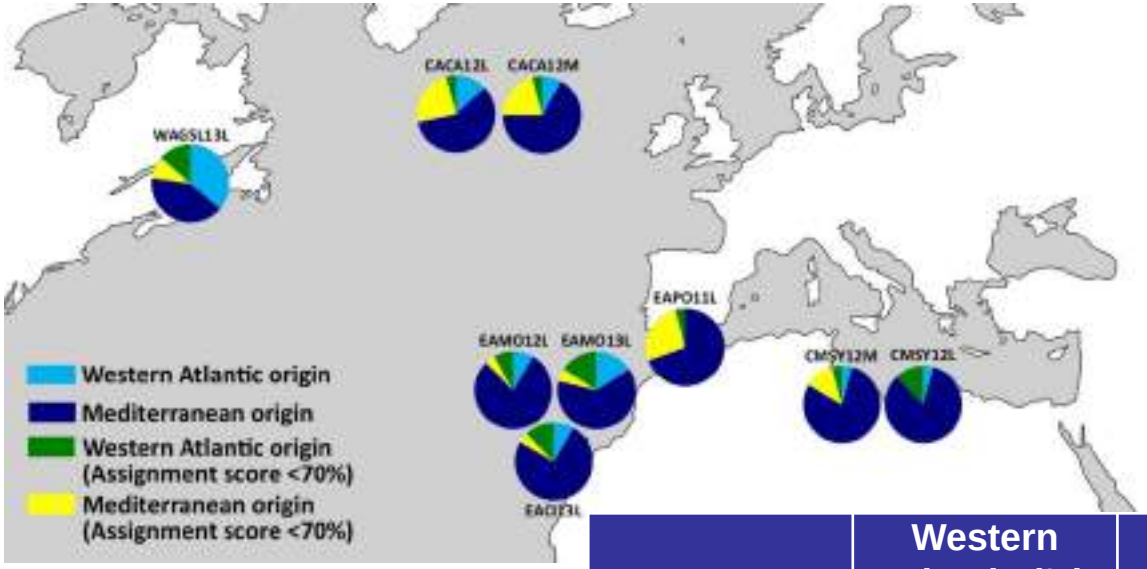




https://doi.org/10.1111/1755-

Theme III: Resolving mixed-stock fisheries

GenoDREAM Experience ICCAT GBYP consortium 2011-2019



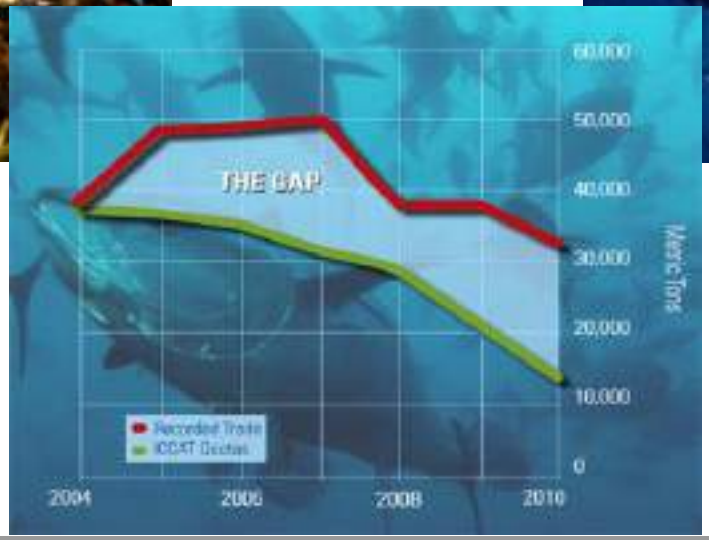
	Western Atlantic (%)	95% CI	Mediterranean (%)	95% CI
WAGSL13L	31.3	(6.4, 74.1)	68.7	(25.9, 93.6)
CACA12L	20.9	(6.4, 53.4)	79.2	(46.6, 93.6)
CACA12M	0.1	(0.0, 58.5)	99.9	(41.5, 100.0)
EACI13L	7.0	(0.1, 55.2)	93.0	(44.8, 99.9)
EAMO12L	0.0	(0.0, 48.0)	100	(52.0, 100.0)
EAMO13L	0.7	(0.0, 54.2)	99.3	(45.8, 100.0)
EAPO11L	0.0	(0.0, 61.7)	100.0	(38.3, 100.0)
CMSY12L	6.4	(0.0, 43.5)	93.6	(56.5, 100.0)
CMSY12M	3.1	(0.0, 41.4)	97.0	(58.6, 100.0)

https://doi.org/10.1111/1755-09

Theme III: Resolving mixed-stock fisheries

GenoDREAM Experience ICCAT GBYP project still active…

… and TO BE CONTINUED

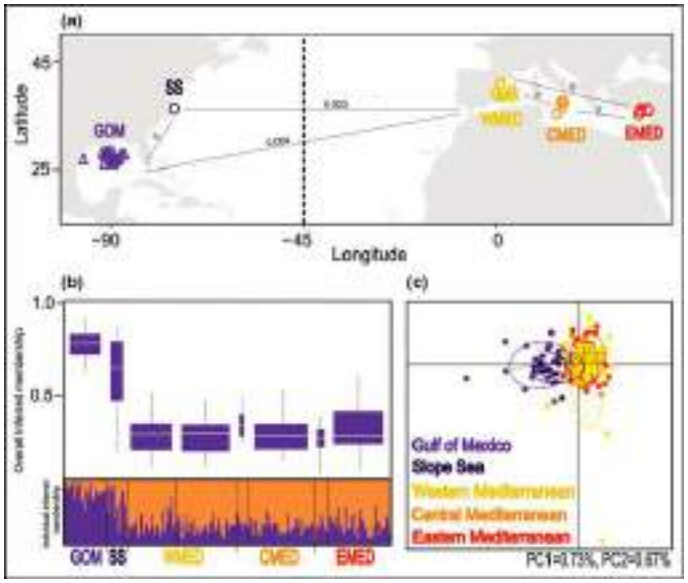


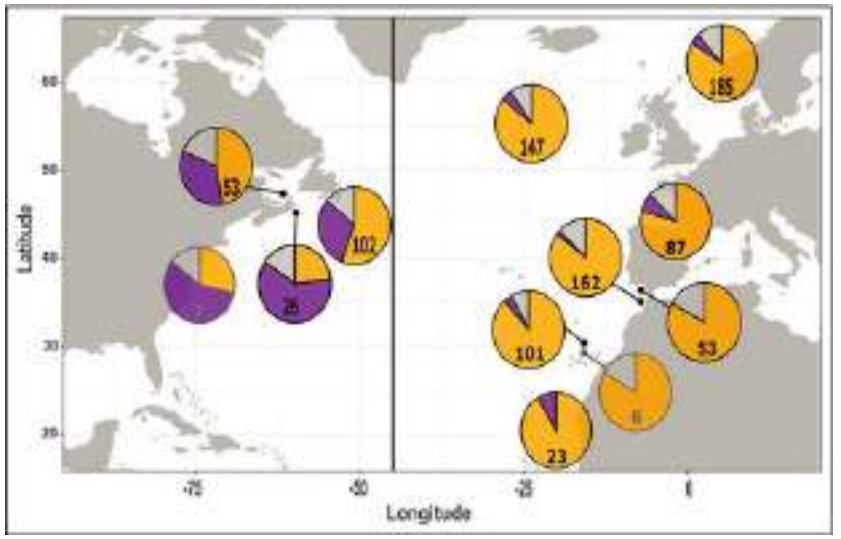
Theme III: Resolving mixed-stock fisheries

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

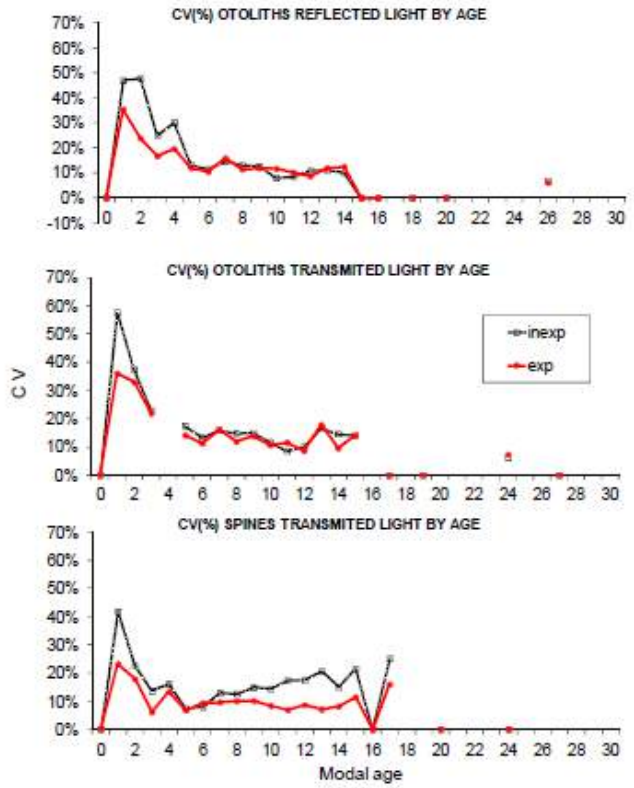


Figure 7.1- CV (%) trend by age and by calcified structure/type of light and reader experience (exp= experienced, inexp= inexperienced).

Theme IV: DNA as a biomarker for age

GenoDREAM *indirect* Experience

Friday morning DONATA LUISELLI
Human population dynamics in traditional fishing communities: genetics, nutrition, and health.

American Journal of PHYSICAL ANTHROPOLOGY
The Official Journal of the American Association of Physical Anthropologists

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

Open Acces

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 Gori[3], Cristina Giuliani[4], Daniela Mari[5,6], Anna M. Di Blasio[7], Davide Gentilini[7], Giovanni Vitale[5,7], Sebastiano Collino[8], Serge Rezzi[8], Gastone Castellani[9], 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

Theme IV: DNA as a biomarker for age

GenoDREAM *indirect* Experience

Epigenetic clock in humans applied to wild animals (mammals)

frontiers in Genetics

MINI REVIEW
published: 17 August 2017
doi: 10.3389/fgene.2017.00106

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

Ricardo De Paoli-Iseppi[1,2], Bruce E. Deagle[2], Clive R. McMahon[3], Mark A. Hindell[1], Joanne L. Dickinson[4] and Simon N. Jarman[5,6]*

[1] Institute for Marine and Antarctic Studies, University of Tasmania, Hobart, TAS, Australia, [2] Australian Antarctic Division, Hobart, TAS, Australia, [3] Sydney Institute of Marine Science, Sydney, NSW, Australia, [4] Cancer, Genetics and Immunology Group, Menzies Institute for Medical Research, Hobart, TAS, Australia, [5] Trace and Environmental DNA Laboratory, Department of Environment and Agriculture, Curtin University, Perth, WA, Australia, [6] CSIRO Indian Ocean Marine Research Centre, University of Western Australia, Perth, WA, Australia

MOLECULAR ECOLOGY

Molecular Ecology (2015) 24, 4826–4847 doi: 10.1111/mec.13357

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, ‡Institute 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 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.

Theme IV: DNA as a biomarker for age

GenoDREAM *indirect* Experience

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

Received: 31 May 2019 | Accepted: 22 October 2019
DOI: 10.1111/1755-0998.13111

RESOURCE ARTICLE

MOLECULAR ECOLOGY RESOURCES WILEY

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

Dafni Anastasiadi | Francesc Piferrer

Received: 18 August 2020 | Revised: 17 November 2020 | Accepted: 26 November 2020
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 Anastasiadi[1] | Changwei Shao[2,3] | Songlin Chen[2,3] | Francesc Piferrer[1]

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 ecosystem-based 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 next-generation 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)**
- **ELASMODROP (aka Martina Spiga's PhD)**

Theme V: Ecosystem monitoring

GenoDREAM Experience Hake diet by NGS metabarcoding

Received: 7 May 2018 | Revised: 25 July 2018 | Accepted: 8 August 2018

DOI: 10.1002/ece3.4500

ORIGINAL RESEARCH

WILEY Ecology and Evolution

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

Giulia Riccioni[1] | Marco Stagioni[1] | Corrado Piccinetti[1] | Simone Libralato[2]

[1]Department of Biological, Geological and Environmental Sciences, University of Bologna, Bologna, Italy

[2]Chapter of Oceanography, Echo Group, National Institute of Oceanography and Experimental Geophysics – OGS, Trieste, Italy

Correspondence
Giulia Riccioni, Department of Biological, Geological and Environmental Sciences, University of Bologna, Bologna, Italy.
Email: giulia.riccioni@unibo.it

Funding information
Italian RITMARE Flagship Project: MEDITS (International Bottom Trawl Survey in the Mediterranean) 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 Miseq 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[1,3], Marco Stagioni[1,2], Chiara Manfredi[1,2], Fausto Tinti[1], Corrado Piccinetti[1] & Simone Libralato[4]

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 presence of a specific niche partitioning and food preferences between hakes living inside and outside 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 Thomsen[1]*, Peter Rask Møller[2], Eva Egelyng Sigsgaard[2], Steen Wilhelm Knudsen[2], Ole Ankjær Jørgensen[3,4], Eske Willerslev[1,5,6]*

nature 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 Sønvig 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

Theme V: Ecosystem monitoring

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

ORIGINAL ARTICLE

WILEY

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

Brian Kilgaard Hansen[1] | Dorte Bekkevold[1] | Lotte Worsøe Clausen[1,2] | Einar Eg Nielsen[1]

[1]Section for Marine Living Resources, National Institute of Aquatic Resources, Technical University of Denmark, Silkeborg, Denmark
[2]International Council for the Exploration of the Sea (ICES), Copenhagen V, Denmark

Correspondence
Brian Kilgaard Hansen, Section for Marine Living Resources, National Institute of Aquatic Resources, Technical University of Denmark, Silkeborg, Denmark.
Email: bkhan@aqua.dtu.dk

Funding information
Danish AgriFish Agency's Green Development and Demonstration Programme (GUDP-VND); European Union Atlantic2O, Grant/Award Number: 607825; Danish Ecos, Grant/Award Number: 4331601

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, supporting 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 potentials for marine fisheries application. We describe fundamental processes governing eDNA generation, breakdown and transport and summarize current understanding 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 monitoring

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,[11] David Mouillot[2,11]†

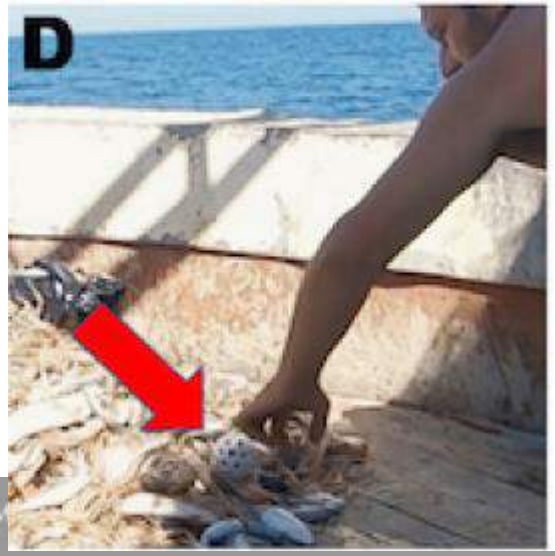
In the era of "Anthropocene defaunation," large species are often no longer detected in habitats where they formerly occurred. However, it is unclear whether this apparent missing, or "dark," diversity of megafauna results from local species extirpations or from failure to detect elusive remaining individuals. 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)



Theme V: Ecosystem monitoring

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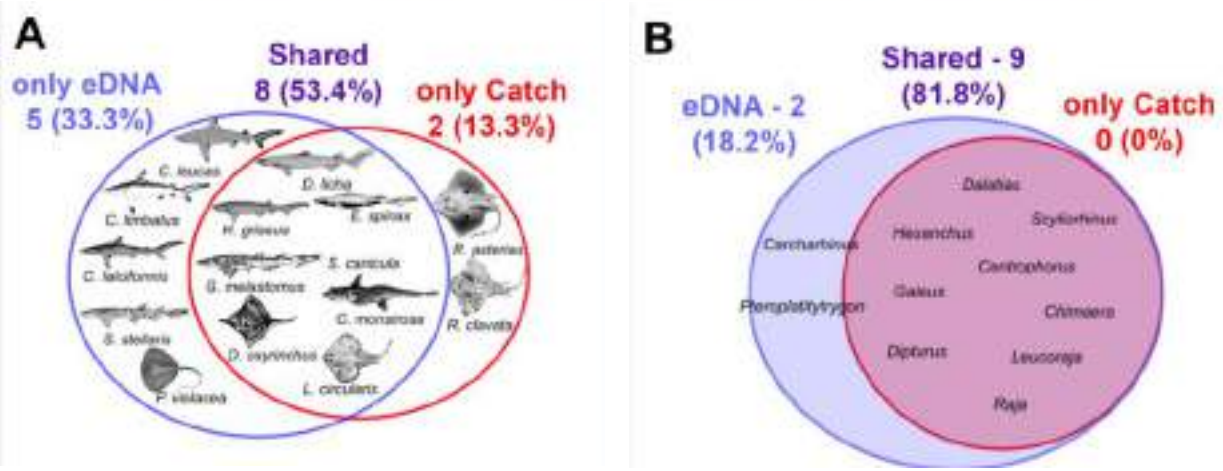
SUBSTRATE Sea water collected directly during fishing activities by METAPROBE (Maiello, et al. 2022)

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

ICES CIEM

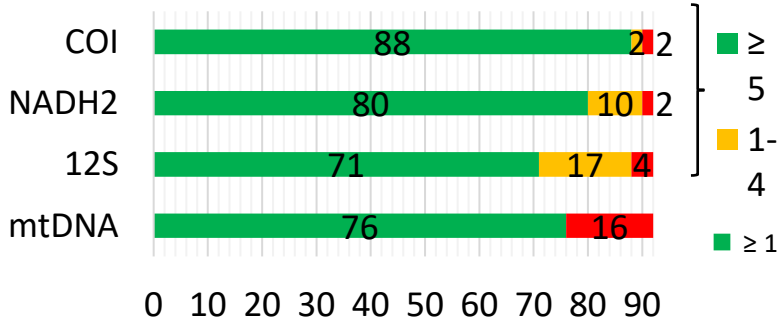
DNA metabarcoding of trawling bycatch reveals diversity and distribution patterns of sharks and rays in the central Tyrrhenian Sea

Linda Albonetti[1,2,3], Giulia Maiello[2,4,*,§], Alessia Cariani[1], Paolo Carpentieri[5], Alice Ferrari[1], Alice Sbrana[2,4], Peter Shum[6], Lorenzo Talarico[2,7], Tommaso Russo[2,†] and Stefano Mariani[6,†]

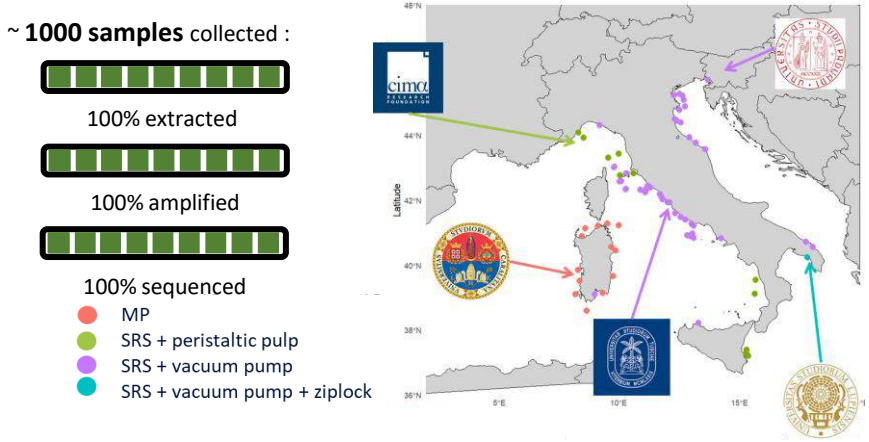


ELASMODROP: eDNA Monitoring of Mediterranean elasmobranchs

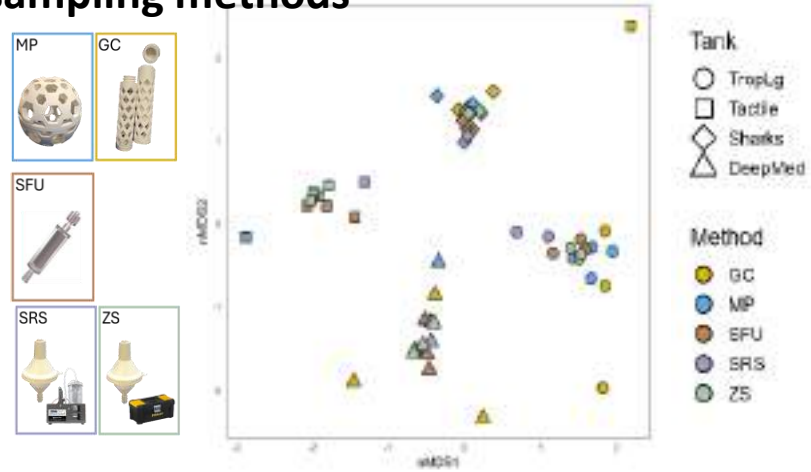
Task 5.3 & 5.4 Mediterranean elasmobranchs Reference Database

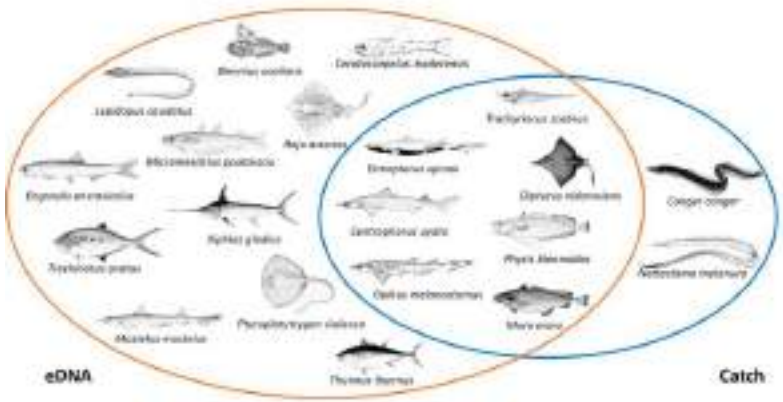


Task 5.1 & 5.5 eDNA field application studies



Task 5.1 & 5.2- Benchmarking eDNA sampling methods





ELASMODROP: eDNA Monitoring of Mediterranean elasmobranchs

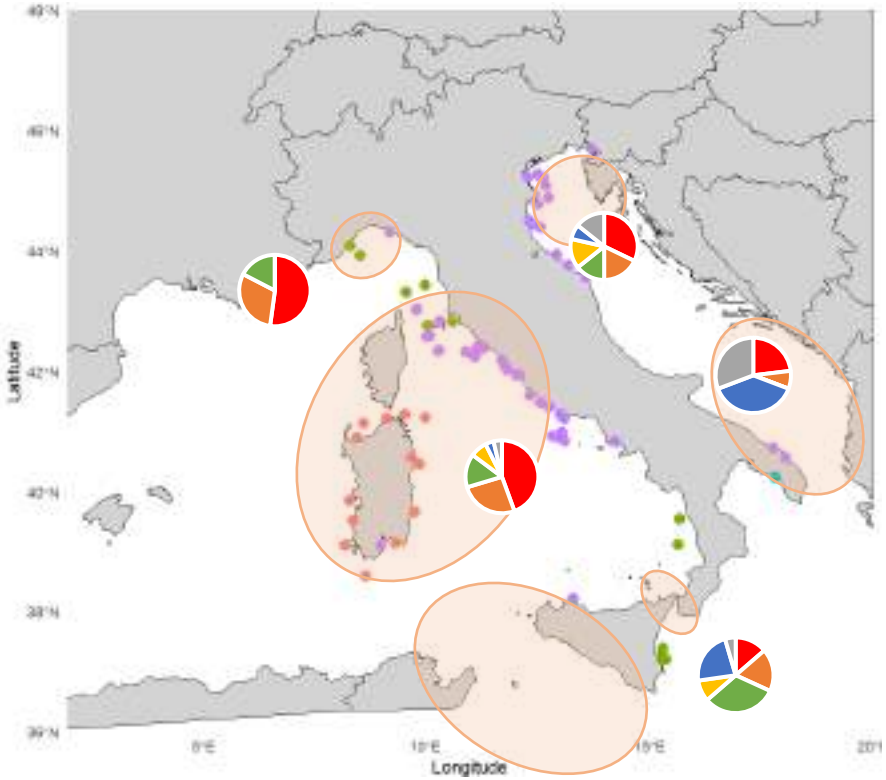
Task 5.1 & 5.5 eDNA field application studies

~ **1000 samples** collected: Ongoing analysis – Preliminary results

elasmo species assessed in Med

- Critically Endangered (CE)
- Endangered (E)
- Vulnerable (VU)

Important Shark and Ray Areas (ISRA)



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 capture-recapture, 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)

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.

Theme VI: Estimating harvest rates and abundance

GenoDREAM *indirect* Experience

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

But…

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.

Theme VI: Estimating harvest rates and abundance

GenoDREAM *indirect* Experience

ARTICLE

Received 17 Nov 2015 | Accepted 8 Sep 2016 | Published 14 Nov 2016

DOI: 10.1038/ncomms13162 OPEN

Absolute abundance of southern bluefin tuna estimated by close-kin mark-recapture

Mark V. Bravington[1], Peter M. Grewe[1] & Campbell R. Davies[1]

Southern bluefin tuna is a highly valuable, severely depleted species, whose abundance and productivity have been difficult to assess with conventional fishery data. Here we use large-scale genotyping to look for parent–offspring pairs among 14,000 tissue samples of juvenile and adult tuna collected from the fisheries, finding 45 pairs in total. Using a modified mark-recapture framework where 'recaptures' are kin rather than individuals, we can estimate adult abundance and other demographic parameters such as survival, without needing to use contentious fishery catch or effort data. Our abundance estimates are substantially higher and more precise than previously thought, indicating a somewhat less-depleted and more productive stock. More broadly, this technique of 'close-kin mark-recapture' has widespread utility in fisheries and wildlife conservation. It estimates a key parameter for management—the absolute abundance of adults—while avoiding the expense of independent surveys or tag-release programmes, and the interpretational problems of fishery catch rates.

Theme VI: Estimating harvest rates and abundance

GenoDREAM *indirect* Experience

www.nature.com/scientificreports

SCIENTIFIC REPORTS

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

R. M. Hillary[1], M.V. Bravington[2], T. A. Patterson[1], P. Grewe[1], R. Bradford[1], P. Feutry[1], R. Gunasekera[1], V. Peddemors[3], J. Werry[4], M. P. Francis[5], C. A. J. Duffy[6] & B. D. Bruce[1]

Conservation concerns exist for many sharks but robust estimates of abundance 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 close-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

ORIGINAL ARTICLE

FISH and FISHERIES WILEY

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

Robin S. Waples[1] | Pierre Feutry[2]

[1]Northwest Fisheries Science Center, National Marine Fisheries Service, National Oceanic and Atmospheric Administration, Seattle, Washington, USA

[2]Commonwealth Scientific and Industrial Research Organisation, Oceans and Atmosphere, Hobart, Tasmania, Australia

Correspondence
Robin Waples, Northwest Fisheries Science Center, 2725 Montlake Blvd. East, Seattle, WA, 98112 USA.
Email: robin.waples@noaa.gov

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_e) and (2) close-kin mark–recapture (CKMR) methods to estimate abundance based on the incidence of close relatives. Whereas N_e 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 N_e/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_e estimation methods depend upon. Coordinating N_e 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

Theme VI: Estimating harvest rates and abundance

GenoDREAM *indirect* Experience

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

Jan R. McDowell[1]✉, Mark Bravington[2]✉, Peter M. Grewe[2]✉, Matthew Lauretta[3]✉, John F. Walter III[3], Shane M. Baylis[2], Thierry Gosselin[4], Estrella Malca[3,5], Trika Gerard[3], Akihiro Shiroza[3,5], John T. Lamkin[3], Ellen E. Biesack[1], Glenn Zapfe[3], Walter Ingram[3], Campbell Davies[2] & Clay Porch[3]

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

COMMISSION INTERNATIONALE POUR LA CONSERVATION DES THONIDES DE L'ATLANTIQUE

COMISIÓN INTERNACIONAL PARA LA CONSERVACIÓN DEL ATUN ATLÁNTICO

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.

Theme VII: Monitoring genetic diversity

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 re-stocking (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.

Theme VII: Monitoring genetic diversity

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**

Theme VII: Monitoring genetic diversity

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

Theme VII: Monitoring genetic diversity

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*

Theme VII: Monitoring genetic diversity

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

Ancient DNA SNP-panel data
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Genomic stability through time despite decades of exploitation in cod on both sides of the Atlantic

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], Sissel Jentoft[b], and Bastiaan Star[b,1]

Adam J. Andrews[1,2,11], Gregory N. Puncher[1,3,11], Darío Bernal-Casasola[4], Antonio Di Natale[5], Francesco Massari[1], Vedat Onar[6], Nezir Yaşar Toker[6], Alex Hanke[7], Scott A. Pavey[3], Castrense Savojardo[8], Pier Luigi Martelli[8], Rita Casadio[8], Elisabetta Cilli[2], Arturo Morales-Muñiz[9], Barbara Mantovani[10], Fausto Tinti[1] & Alessia Cariani[1]

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

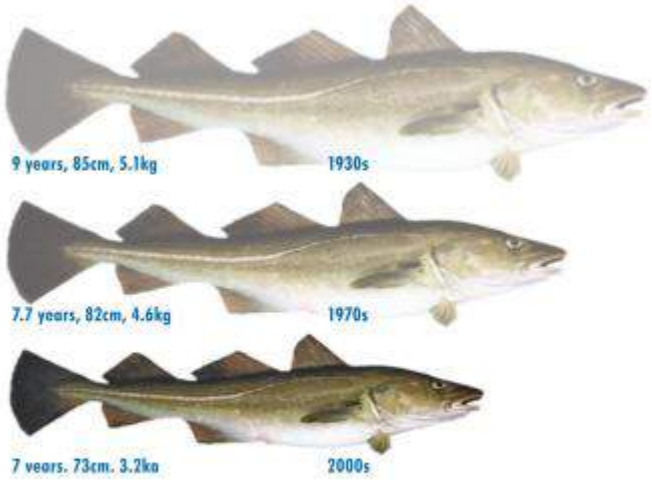
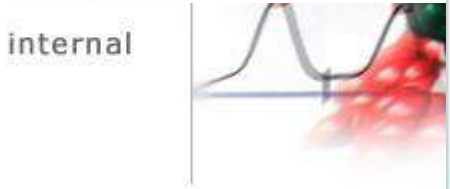
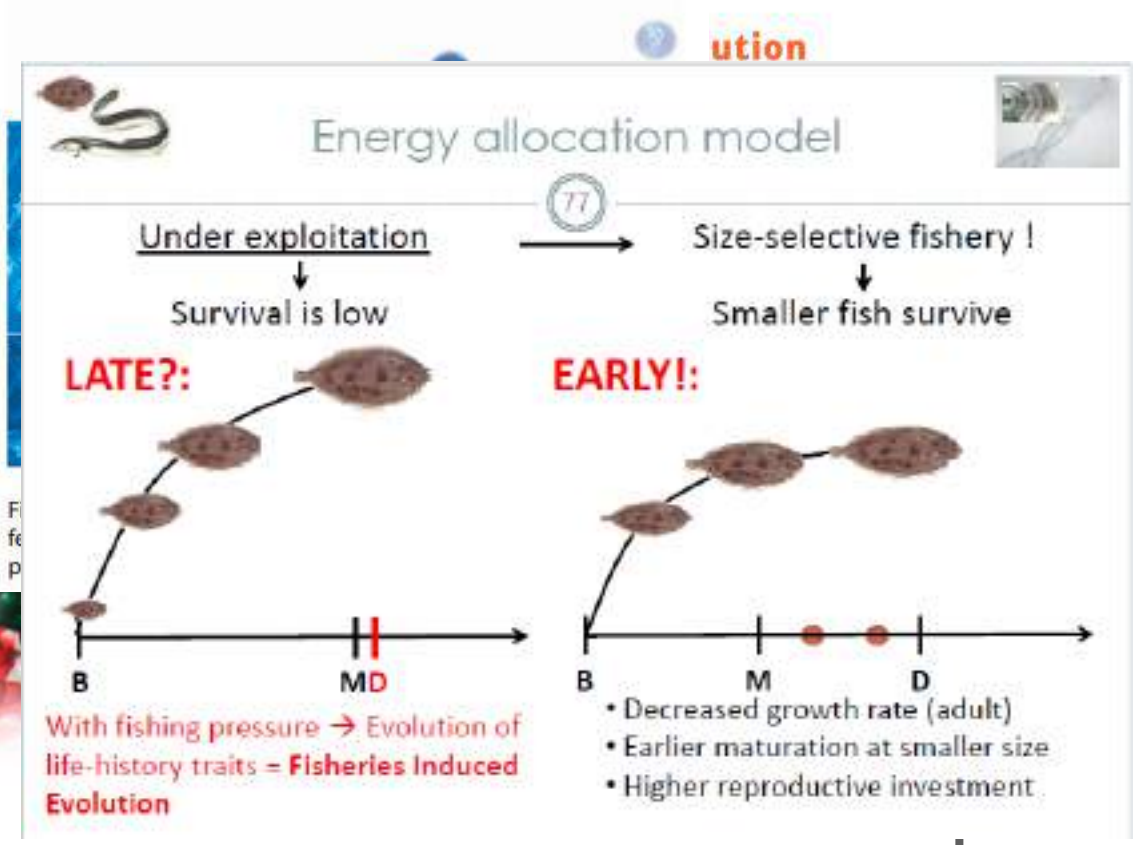


Figure 1: Illustrating the effects of fisheries-induced evolution, the age, size, and weight of first-time spawners have fallen dramatically in Northeast Arctic cod.





Theme VIII: Evolutionary responses to fishing

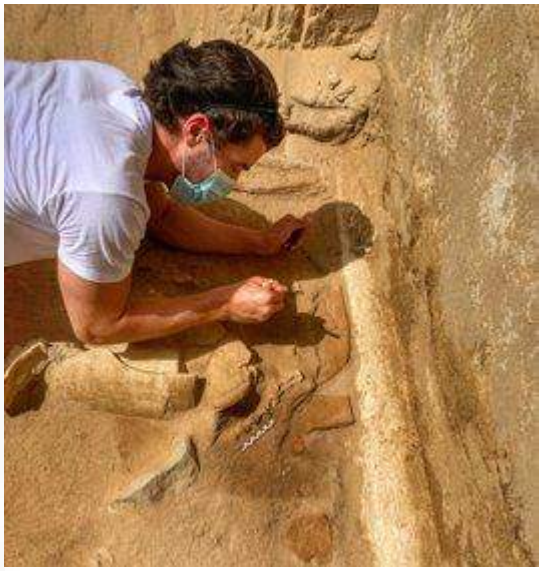
GenoDREAM Experience it all started in this building…

Massimo Sella Archive

Theme VIII: Evolutionary responses to fishing

GenoDREAM Experience ATGC-TUNA UNIBO FARB Project, ICCAT

GBYP Data Recovery Project, MSCA ITN SeaChanges



Theme VIII: Evolutionary responses to fishing

GenoDREAM Experience ATGC-TUNA UNIBO FARB Project, ICCAT

GBYP Data Recovery Project, MSCA ITN SeaChanges

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

Theme VIII: Evolutionary responses to fishing

GenoDREAM Experience ATGC-TUNA UNIBO FARB Project, ICCAT

GBYP Data Recovery Project, MSCA ITN SeaChanges

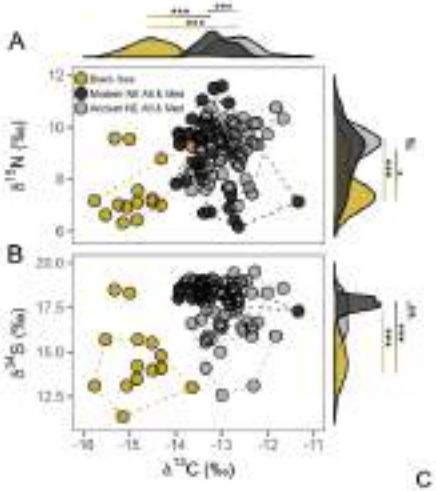
SeaChanges

UNIVERSITY of York

UiO : Centre for Ecological and Evolutionary Synthesis
University of Oslo

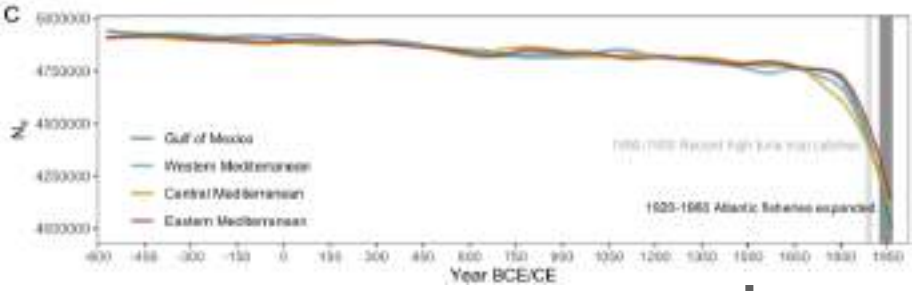
Adam Andrews, MSCA PhD Fellow / PostDoc
adam@palaeome.org

Morphology:
Size reconstructions
Inferring growth using annul



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

WG sequencing:
Demography
Structure
Adaptive responses

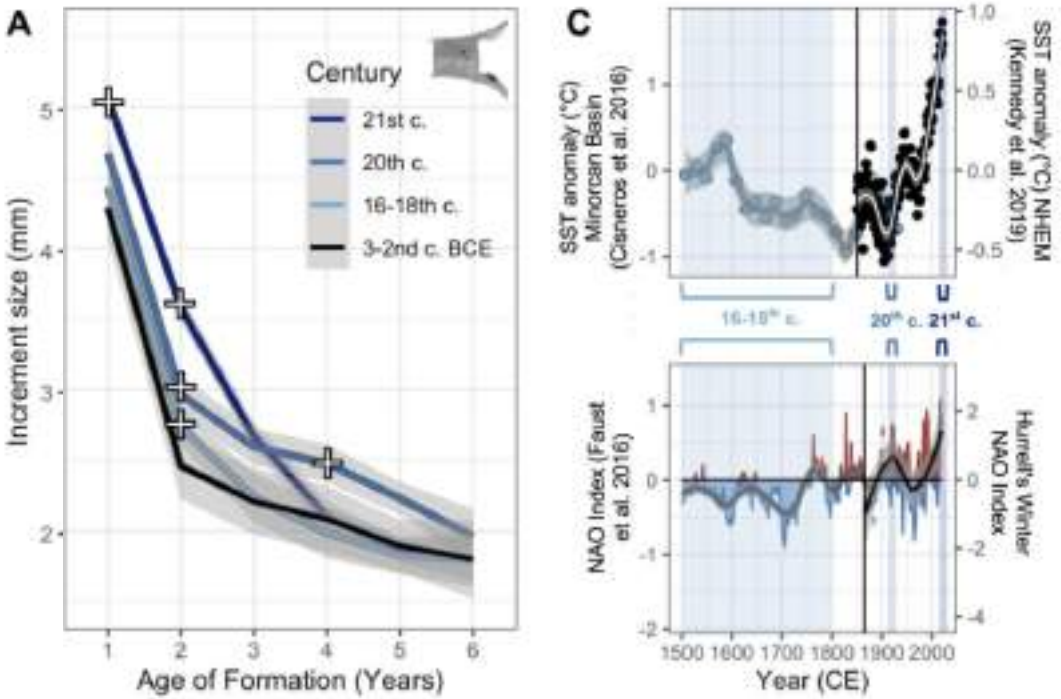


Unlocking ecological history using fish remains

Eco-evolutionary consequences of exploitation in the Atlantic bluefin tuna

measurements over **two millennia** showed that

1. 21st c. ABFT age 1-2 **grew significantly faster** than in the 20th c. and 16-18th c.,
2. 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**

Theme IX: Genetic consequences of stock enhancement

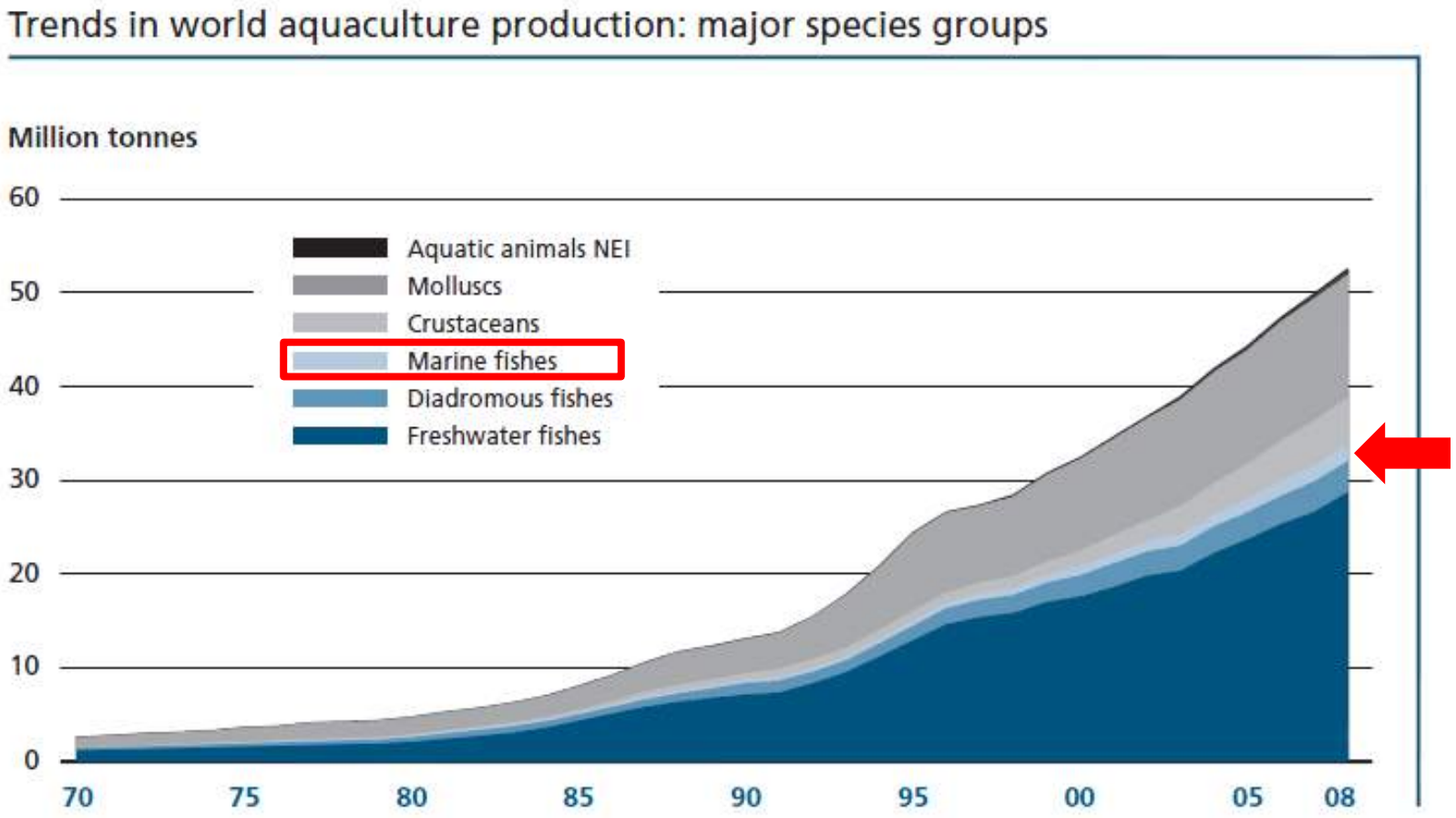
GenoDREAM Experience

AQUAGEN EU Tender & AQUATRACE EU Project

Theme IX: Genetic consequences of stock enhancement

GenoDREAM Experience

AQUAGEN EU Tender & AQUATRACE EU Project

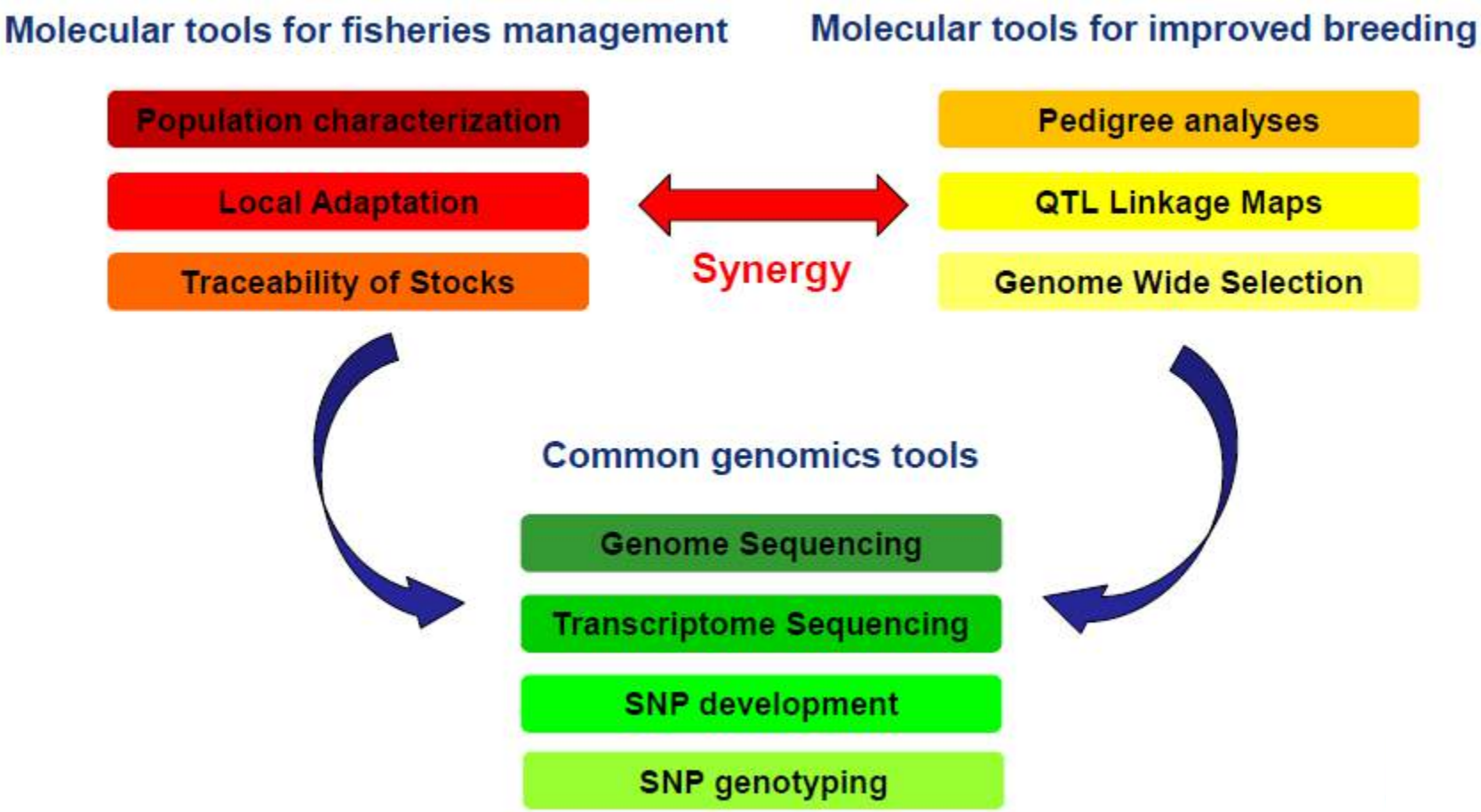


Note: NEI = not elsewhere included. FAO 'State of World Fisheries and Aquaculture-2010' report

Theme IX: Genetic consequences of stock enhancement

GenoDREAM Experience

AQUAGEN EU Tender & AQUATRACE EU Project



Theme IX: Genetic consequences of stock enhancement

GenoDREAM Experience

AQUAGEN EU Tender & AQUATRACE EU Project

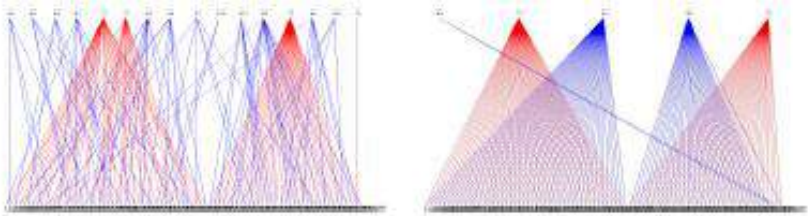
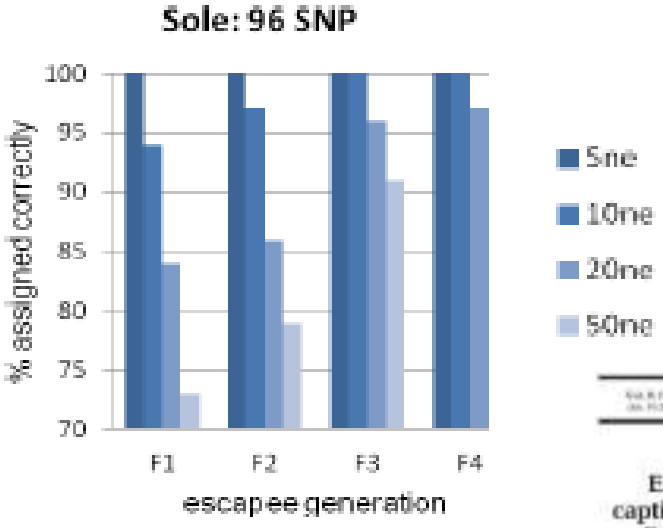
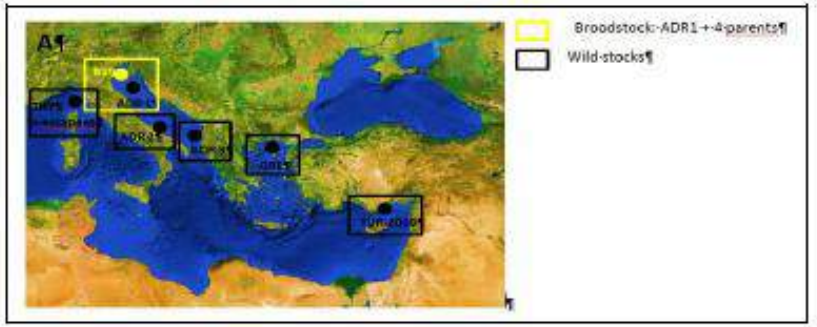
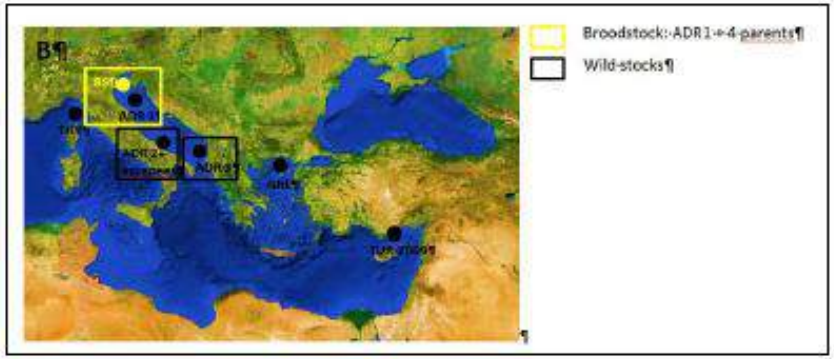


Figure 4: *Pedigree reconstruction of the two aquaculture families drawn by Pedigree viewer (Kinghorn, 1990-2010). Left: based on 21SNPs. Right: based on 50 SNPs. Blue: candidate mothers, red: candidate fathers. Notice the two misassigned individuals, caused by bad DNA quality (leading to genotyping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







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

Jonas Bylemans, Gregory E. Maes, Eveline Diopere, Alessia Cariani, Helen Senn, Martin I. Taylor, Sarah Helyar, Luca Bargelloni, Alessio Benaldo, Gary Carvalho, Ilaria Guarniero, Hans Komen, Jann Th. Martinsohn, Einar E. Nielsen, Fausto Tinti, Filip A. M. Volckaert, Rob Ogden

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BIOSECURITY

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.

BIOSECURITY

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 Morning MARCO BASILI
Molecular Approaches in Microbial Ecology: Processes, Challenges, and Insights into Fish Microbiomes
Friday afternoon GRAZIA QUERO
The hidden actors of the coastal sea: current knowledge on the occurrence, diversity and threats posed by microbial pollutants in the marine environment

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.

Theme XI: Product provenance and fisheries surveillance

Barriers to uptake

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

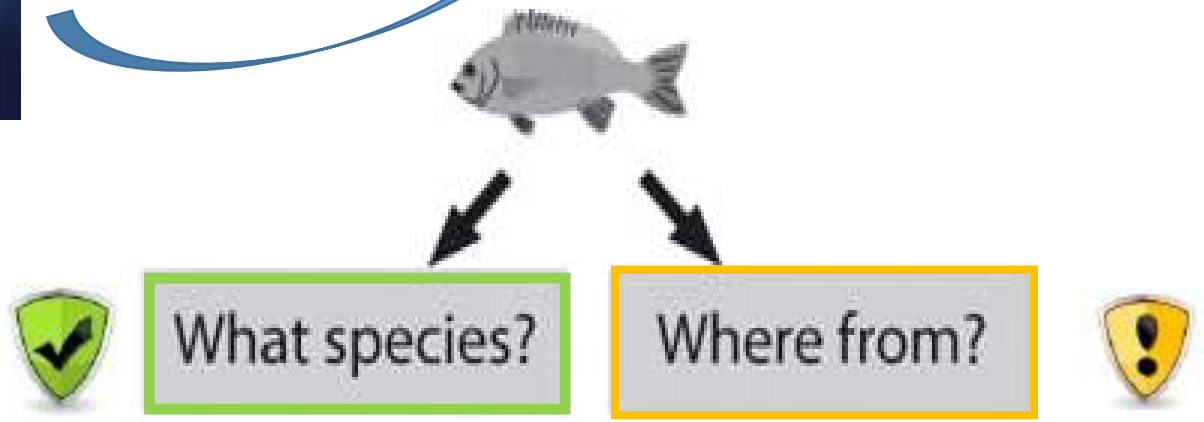
Future

- 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 cross-examination within the legal system.

GenoDREAM Experience

- **FISHPOPTRACE EU Project**

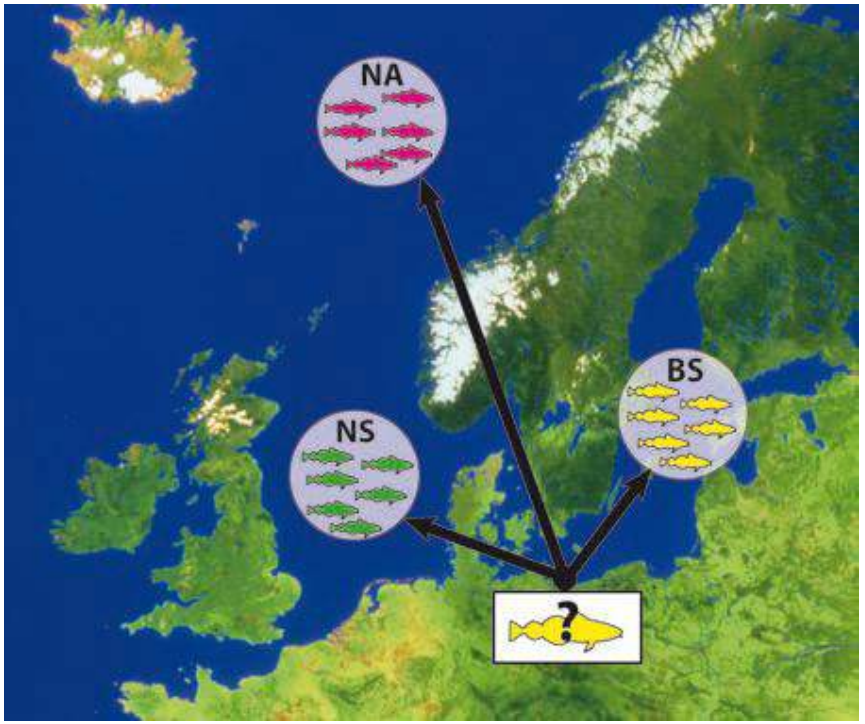
From where??



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

FRAUDS RELATED TO:

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



Theme XI: Product provenance and fisheries surveillance

GenoDREAM Experience FishPopTrace EU project

GENOMIC APPROACHES IN MARINE FISHERIES RESEARCH: NEW OPPORTUNITIES AND CHALLENGES

Journal of FISH BIOLOGY fsbi

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 Enrico Fermi 2749, 21027, Ispra, VA, Italy

Journal of FISH BIOLOGY fsbi

Journal of Fish Biology (2016) **89**, 2505–2518
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***

GENOMIC APPROACHES IN MARINE FISHERIES RESEARCH: NEW OPPORTUNITIES AND CHALLENGES

OXFORD

Briefings in Functional Genomics, 2016, 1–6

doi: 10.1093/bfgp/elw006
Review paper

How fisheries management can benefit from genomics?

Fausto Valenzuela-Quiñonez

Correspondence author. Fausto Valenzuela-Quiñonez, CONACYT-Research Fellow, Centro de Investigaciones Bio
Instituto Politécnico Nacional # 195, Colonia Playa Palo de Santa Rita Sur. La Paz, B.C.S. 23096, Mexico. Tel.: (52) 6
3625; E-mail: fvalenzuela@cibnor.mx

Abstract

Fisheries genomics is an emerging field that advocates the application of genomic tools to s
management. Genomic approaches bring a new paradigm for fisheries management by mak
adaptive diversity to understand fundamental aspects of fisheries resources. Hence, this rev
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 the genetic basis of micro-evolutionary effects
and climate change. The understanding of adaptive diversity 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 i
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

GENOMIC APPROACHES IN MARINE FISHERIES RESEARCH: NEW OPPORTUNITIES AND CHALLENGES

Frontiers in Marine Science > Marine Fisheries, Aquaculture and Living Resources > Research Topics

Prospects and Challenges for the Implementation of HTS Genetic Methods in Fisheries Research Surveys and Stock Assessments.

Annual Review of Animal Biosciences

How Fish Population Genomics Can Promote Sustainable Fisheries: A Road Map

Leif Andersson,[1,2] Dorte Bekkevold,[3] Florian Berg,[4] Edward D. Farrell,[5] Sabine Felkel,[1] Mafalda S. Ferreira,[1] Angela P. Fuentes-Pardo,[1] Jake Goodall,[1] and Mats Pettersson[1]

[1]Department of Medical Biochemistry and Microbiology, Uppsala University, Uppsala, Sweden; email: Leif.Andersson@imbim.uu.se

[2]Department of Veterinary Integrative Biosciences, Texas A&M University, College Station, Texas, USA

[3]National Institute of Aquatic Resources, Technical University of Denmark, Silkeborg, Denmark

[4]Institute of Marine Research, Bergen, Norway

[5]Killybegs Fishermen's Organisation, Killybegs, County Donegal, Ireland

Keywords

fish, genomics, fishery, stock management, sustainability

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REVIEW ARTICLE

JOURNAL OF FISH BIOLOGY

Genes, fish and fisheries: translating science into policy

Gary R. Carvalho[1,2]

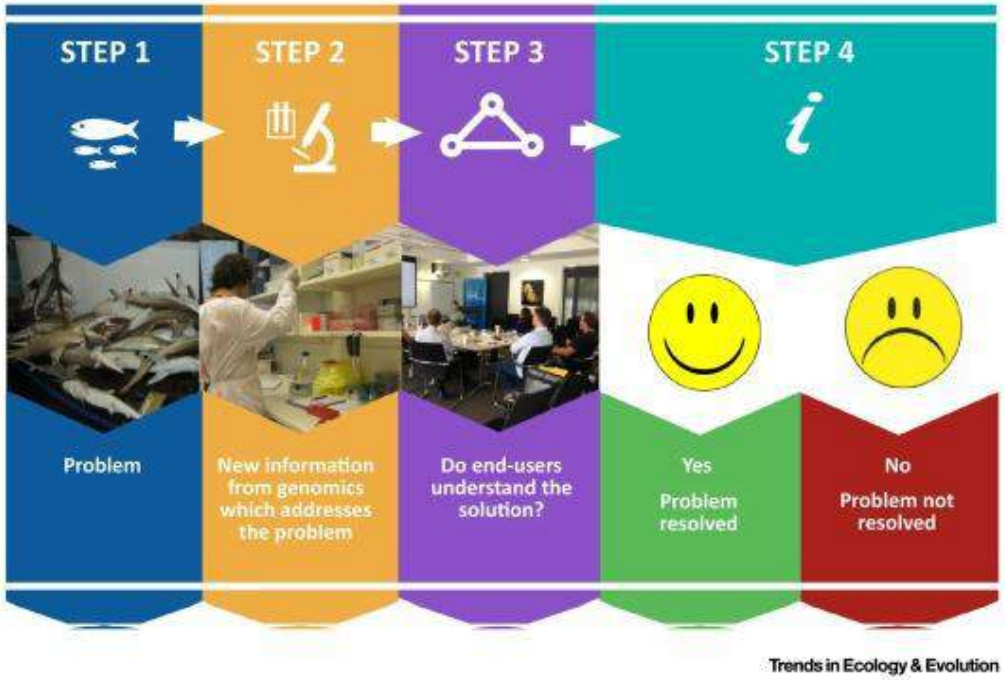
GENOMIC APPROACHES IN MARINE FISHERIES RESEARCH: NEW OPPORTUNITIES AND CHALLENGES

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. Withler[6]

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



GENOMIC APPROACHES IN MARINE FISHERIES RESEARCH: NEW OPPORTUNITIES AND CHALLENGES

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GHOTI

WILEY FISH and FISHERIES

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

Jann Th. Martinsohn[1] | Paul Raymond[2] | Trey Knott[3] | Kevin A. Glover[4,5] | Einar Eg Nielsen[6] | Lars Bonde Eriksen[7] | Rob Ogden[8] | John Casey[1] | Jordi Guillen[1]

[1]European Commission, Joint Research Centre (JRC), Ispra, Italy

[2]Office of Law Enforcement (Retired), National Marine Fisheries Service, National Oceanic and Atmospheric Administration, Washington, District of Columbia

[3]Forensic Laboratory, Northwest Fisheries Science Center, National Marine Fisheries Service, National Oceanic and Atmospheric Administration, Charleston, South Carolina

[4]Institute of Marine Research, Bergen, Norway

[5]Institute of Biology, University of Bergen, Bergen, Norway

[6]Section for Population Ecology and Genetics, National Institute of Aquatic Resources, Technical University of Denmark, Silkeborg, Denmark

[7]Ministry of Foreign Affairs of Denmark, Danish Fisheries Agency, HR, kommunikation og jura, Copenhagen, Denmark

[8]Edinburgh Royal (Dick) School of Veterinary Studies and the Roslin Institute, University of Edinburgh, Easter Bush Campus, Edinburgh, UK

Correspondence
Jann Th. Martinsohn, European Commission, Joint Research Centre (JRC), Directorate D – Sustainable Resources, Unit D2 – Water and Marine Resources, Ispra, Italy
Email: jann.martinsohn@ec.europa.eu

Funding information
European Community Framework Programme FP7, Grant/Award Number: KBBE-212399

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, DNA-analysis 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!!

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

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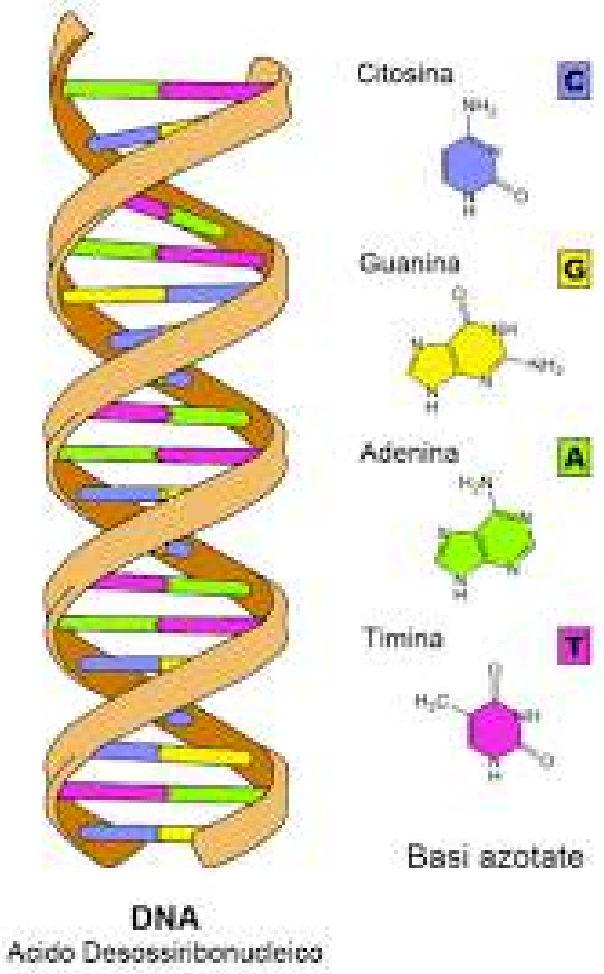
SPECIES/COMMUNITIES

BARCODING/
METABARCONDING

POPULATION/STOCKS

POPGEN IN SPACE AND TIME



AGE

EPIGENETIC

ABUNDANCE

POPGEN IN SPACE AND TIME

CKMR

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Genomic approaches in marine fisheries research: challenges and opportunities

What can **Genetics/Genomics** do more for **your PhD project**??

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Genomic approaches in marine fisheries research: challenges and opportunities

There is no DNA in my PhD, and there never will be

There is already DNA in my PhD, but I could have more/better

There is no DNA in my PhD, but there could be some

There is already DNA in my PhD, but I could get rid of it

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