



# atlas

UNDERSTANDING DEEP ATLANTIC ECOSYSTEMS



## Genetic Stock Structure of Dublin Bay Prawn, *Nephrops norvegicus*

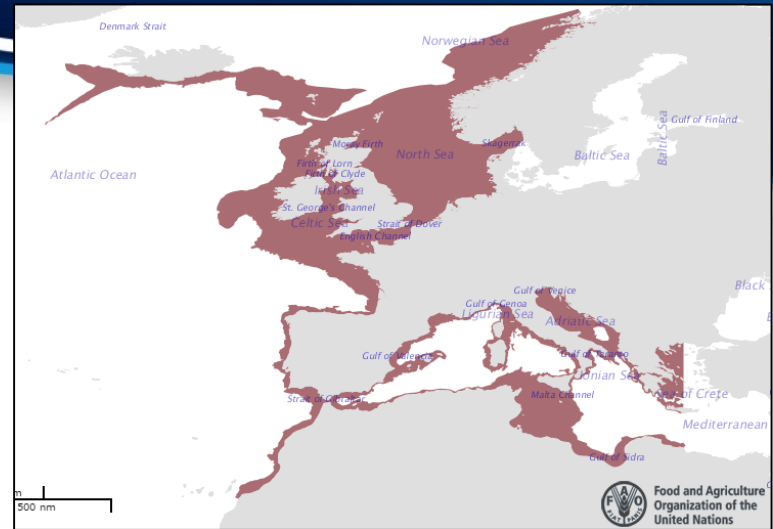
ATLAS 3<sup>rd</sup> General Assembly 2018

Jeanne Gallagher - University College Dublin, Ireland



## *Nephrops norvegicus*

- Norway lobster, Dublin Bay prawn, langoustine, scampi
- EU 2017 *Nephrops* landings are estimated to be worth over €165 million
- *Nephrops* live ~5-10 years, dwelling in burrows on patches of soft muddy sediment on the sea-floor at ~4 - 800m depth
- Adults do not migrate/leave their mud patches at any point in their life





## Project Objectives

- **Identify genetic tools** to assess Nephrops
- **Timescales** Deep and current timescales
- **Deep time-** Phylogeny, evolutionary timescales
- **Current time-** Population genetics across distribution
- Findings contribute to:
  - Biology
  - Management /conservation

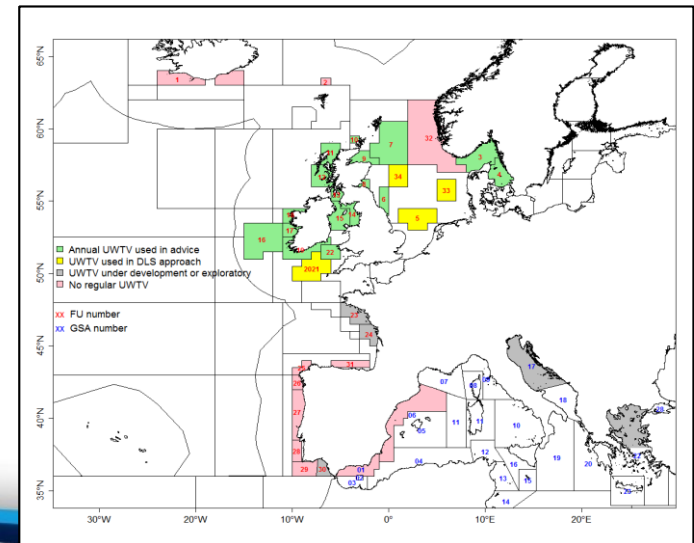
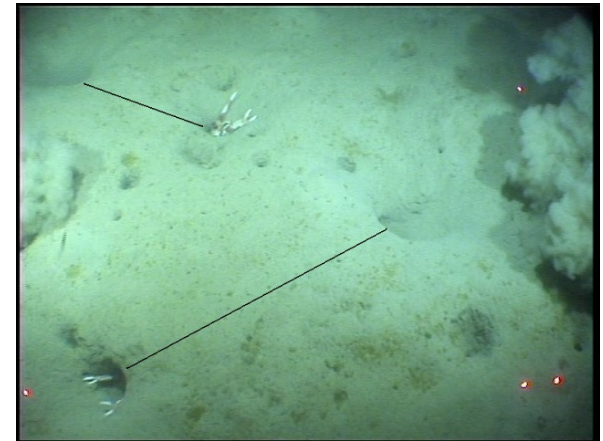






## Current Assessment of Nephrops

- Underwater TV surveys
- Burrow counting
- Fisheries Ecosystems Advisory Services (FEAS), Irish Marine Institute
- International Council for the Exploration of the Sea (ICES)





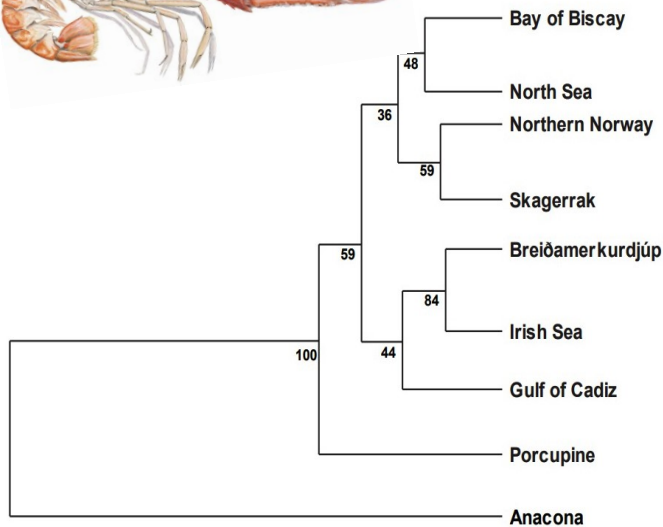
## Genetics for Fisheries Management

- Essential to provide fisheries management with key information:
  - Patterns of historical biogeography
  - Population structure (stock)
  - Demographics (Effective pop size, bottlenecks, gene flow)
- Recent molecular technological advances:
  - Decreased costs
  - Increased sampling output via Next Generation Sequencing
- Limited genetic studies on Nephrops

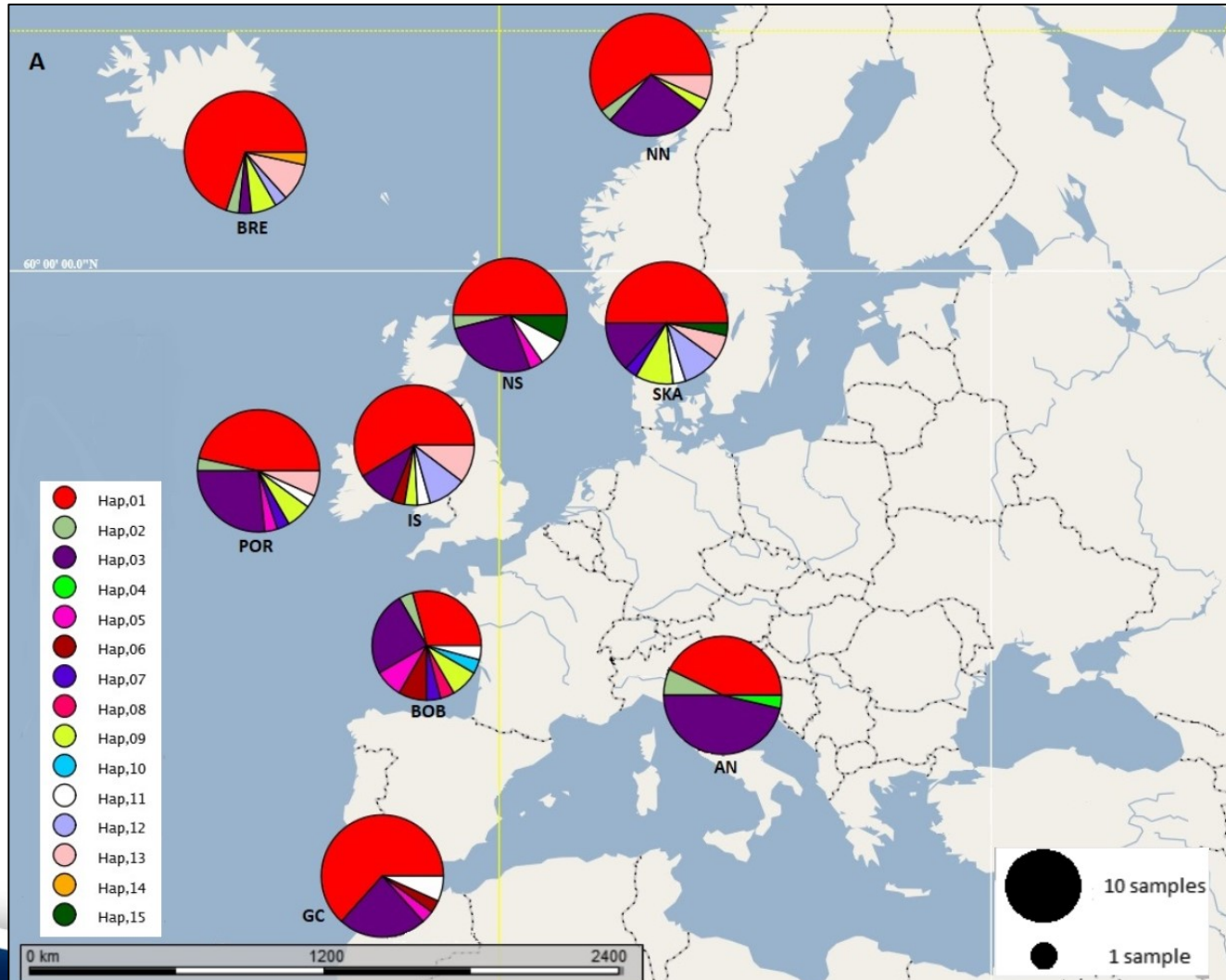




## Mitochondrial D-loop Analyses (Deep Time)



- 30 individuals, 9 areas across distribution
- *De novo* primers - mtDNA D-loop region
- Significant genetic differentiation between northeast Atlantic and the east Mediterranean samples
- Species expansion time between 10,500 to 19,000 ybp
- High haplotype diversity - Bay of Biscay potential glacial refugium for the Atlantic distribution







# atlas Genetics for the masses

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Research



**Cite this article:** Vartia S et al. 2016 A novel method of microsatellite genotyping-by-sequencing using individual combinatorial barcoding. *R. Soc. open sci.* 3: 150565.  
<http://dx.doi.org/10.1098/rsos.150565>

Received: 21 October 2015  
Accepted: 10 December 2015

## A novel method of microsatellite genotyping-by-sequencing using individual combinatorial barcoding

Salla Vartia<sup>1,3,4</sup>, José L. Villanueva-Cañas<sup>5</sup>, John Finarelli<sup>2,3</sup>, Edward D. Farrell<sup>1,3</sup>, Patrick C. Collins<sup>6</sup>, Graham M. Hughes<sup>2,3</sup>, Jeanette E. L. Carlsson<sup>1,3</sup>, David T. Gauthier<sup>7</sup>, Philip McGinnity<sup>8</sup>, Thomas F. Cross<sup>8</sup>, Richard D. Fitzgerald<sup>4</sup>, Luca Mirimin<sup>9</sup>, Fiona Crispie<sup>10,11</sup>, Paul D. Cotter<sup>10,11</sup> and Jens Carlsson<sup>1,3</sup>

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Research



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Received: 30 August 2016

Journal of **FISH**  
BIOLOGY



*Journal of Fish Biology* (2013) **82**, 944–958  
doi:10.1111/jfb.12034, available online at [wileyonlinelibrary.com](http://wileyonlinelibrary.com)

## Rapid, economical single-nucleotide polymorphism and microsatellite discovery based on *de novo* assembly of a reduced representation genome in a non-model organism: a case study of Atlantic cod *Gadus morhua*

J. CARLSSON\*†‡, D. T. GAUTHIER§, J. E. L. CARLSSON\*, J. P. COUGHLAN\*, E. DILLANE\*, R. D. FITZGERALD||, U. KEATING\*, P. MCGINNITY\*, L. MIRIMIN|| AND T. F. CROSS\*

ARTICLE IN PRESS

## Next Gen Pop Gen: implementing a high-throughput approach to population genetics in boarfish (*Capros aper*)

Edward D. Farrell, Jeanette E. L. Carlsson and Jens Carlsson

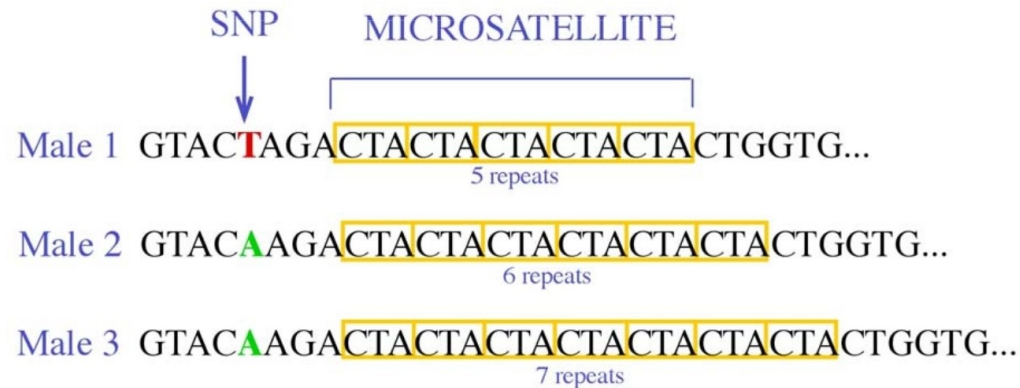
Area 52 Research Group, School of Biology and Environmental Science/Earth Institute, University College Dublin, Belfield, Dublin 4, Republic of Ireland

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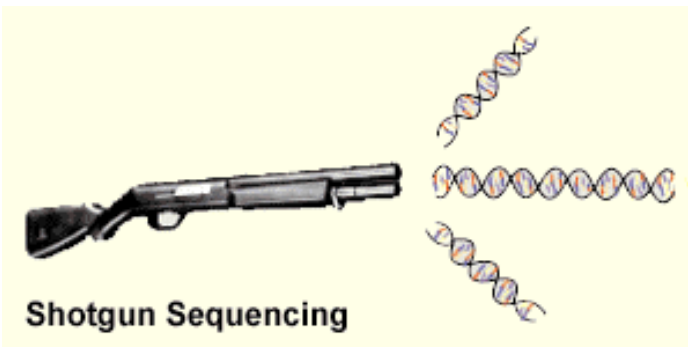
# Microsatellites

- Relatively high mutation rate
- Less abundant
- Relatively inexpensive
- Platform dependent genotyping scoring

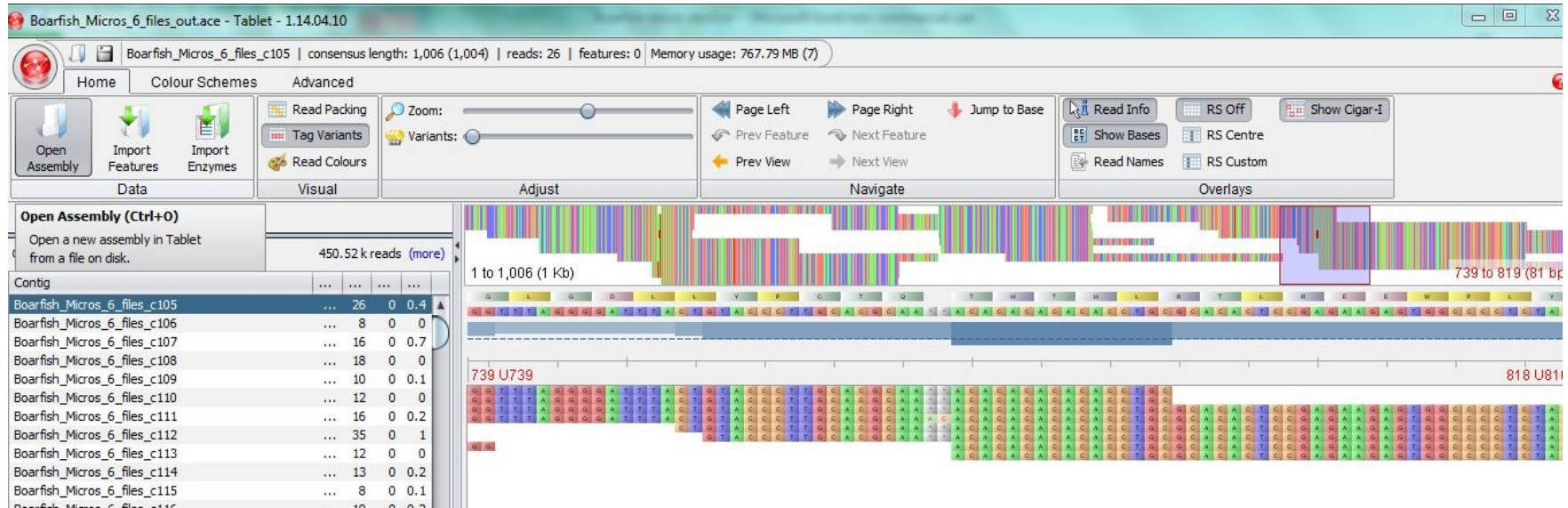




## Population genetics – Current timescale



- Nephrops large genome (C-value 4.9/*H. sapiens* C-value 3.5)
- Reduced representation library
- Shotgun sequencing (+8 million reads)



- Shotgun sequencing – long strands
- Microsatellite discovery- QDD software
- Primer design
- 106 *de novo* pairs of primers



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## OligoAnalyzer 3.1

Instructions | Definitions | Feedback

Sequence

5' GGAAACAGCTATGACCATATACAGCCTATGCCGTAGC 37 Bases

3'

Parameter sets

SpecSheet (Default)

Target type DNA

Oligo Conc 0.25  $\mu$ M

Na<sup>+</sup> Conc 50 mM

Mg<sup>2+</sup> Conc 0 mM

dNTPs Conc 0 mM

CLEAR SEQUENCE

ADD TO ORDER

ANALYZE

HAIRPIN

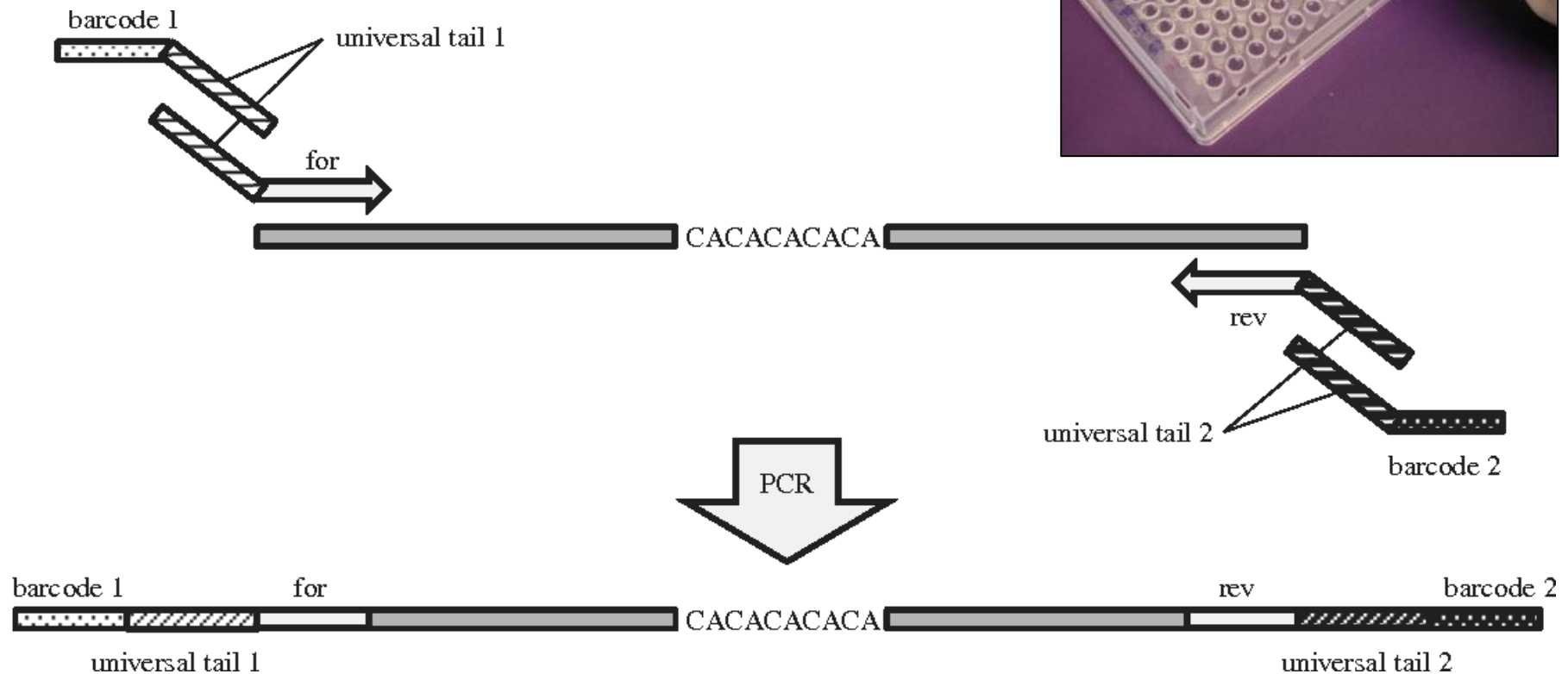
SELF-DIMER

HETERO-DIMER

NCBI BLAST

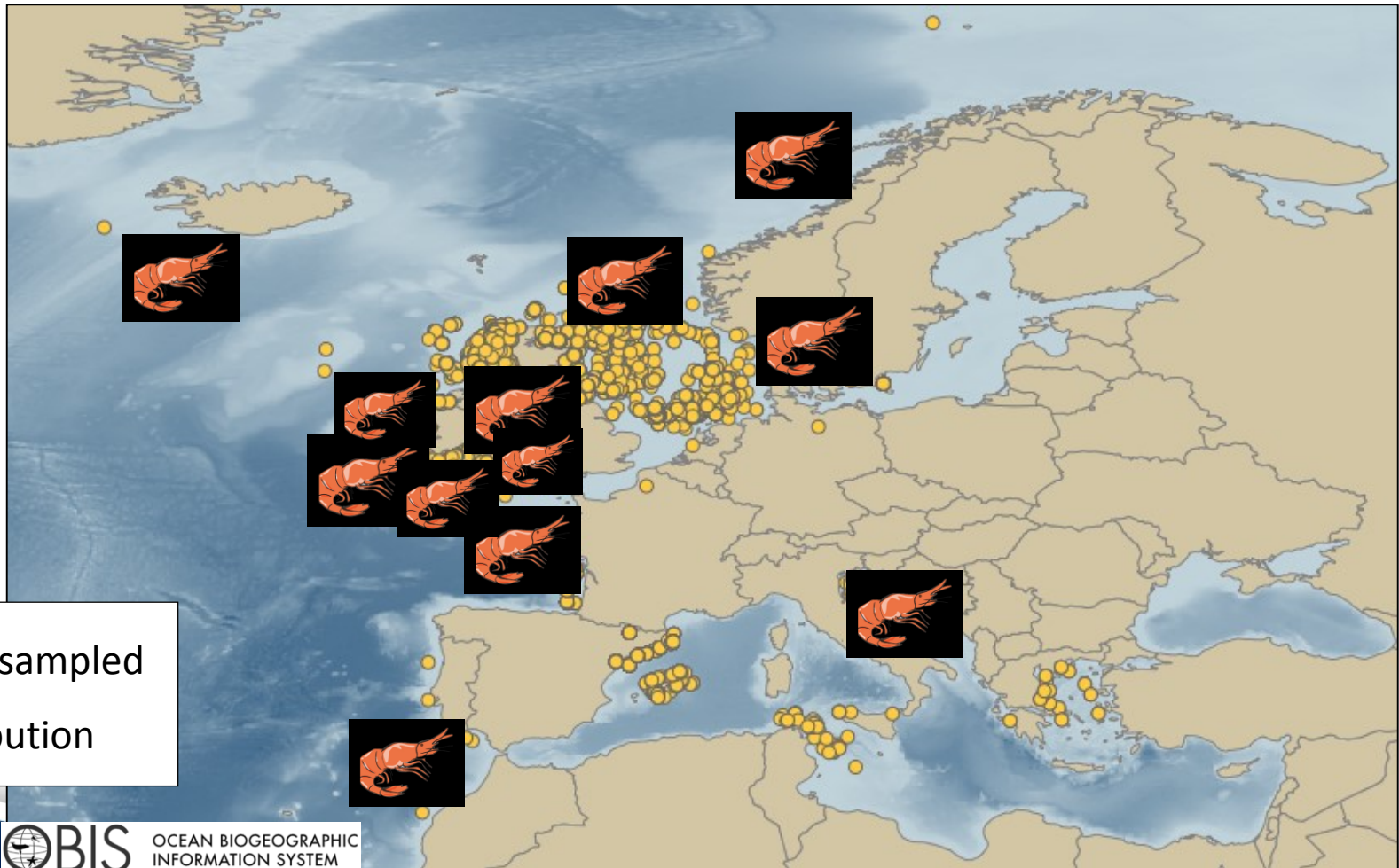
TM MISMATCH







## Population Genetics Mass Sampling

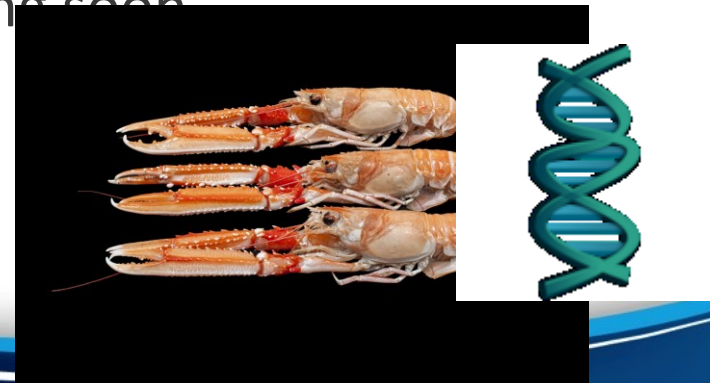




1200 samples → 60 plates → 106  
primer pairs → 1 tube



Results coming soon





# Thank You!



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