Overview of population samples included in genetic analyses of Pleuromamma xiphias (Plankton Population Genetics)

Website: https://www.bco-dmo.org/dataset/699234
Data Type: Cruise Results
Version: 01 May 2017
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Project
» Basin-scale genetics of marine zooplankton (Plankton Population Genetics)

Contributors	Affiliation	Role
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Coverage

Spatial Extent: **N**:39.6470388 **E**:-22.4662575 **S**:-40.0732082 **W**:-42.3712545
Temporal Extent: 2012-10-16 - 2012-11-17

Dataset Description

Overview of population samples that were included in genetic analyses of Pleuromamma xiphias from across the Atlantic Ocean. Specimens were collected on the Atlantic Meridional Transect 22 (AMT22) cruise on RRS James Cook from Oct-Nov 2012. Data columns include collection location and date, ocean biome, number of individuals sampled (N), number of haplotypes observed (H), the ratio of haplotypes to sample size (H/N), haplotype diversity (h) and nucleotide diversity (π) for each site. 'Pop' indicates whether the sample was included in population genetic analyses (Yes/No, see Goetze et al. 2016 for explanation).

These data are also published in Table 1 of:
Goetze, E., Hüdepohl, P., Chang, C., Iacchei, M., Van Woudenberg, L., Peijnenburg, K. T. C. A. (2016) Ecological dispersal barrier across the equatorial Atlantic in a migratory planktonic copepod. *Progress in Oceanography – AMT special issue.* doi: 10.1016/j.pocean.2016.07.001

Refer to the related dataset "Pxiphias PopStructure mtDNA" for data files generated by the genetic analyses.

Methods & Sampling

Refer to the following publication for complete methodology details:
Goetze, E., Hüdepohl, P., Chang, C., Iacchei, M., Van Woudenberg, L., Peijnenburg, K. T. C. A. (2016) Ecological

dispersal barrier across the equatorial Atlantic in a migratory planktonic copepod. *Progress in Oceanography – AMT special issue.* doi: 10.1016/j.pocean.2016.07.001

In summary (excerpted from above):
Bulk plankton samples were collected on Atlantic Meridional Transect Cruise 22 (AMT22) between 10/13/2012 and 11/19/2012. Oblique tows were conducted with bongo nets (200 um, 333 um), towed between on average 324 m depth and the sea surface. A General Oceanics flowmeter (2030RC) mounted in the mouth of the 200 um net was used to measure seawater filtered during the tow. Plankton from the 200 um mesh net was bulk preserved immediately in 100% ethyl alcohol, the alcohol was changed to fresh within 12–24 h of collection, and samples were stored at -20 C. Plankton from the 333 um mesh net was sorted live at sea, and Pleuromamma xiphias specimens were preserved immediately in RNALater (Ambion), followed by cryopreservation in liquid nitrogen, and long-term storage at -80 C.

Specimens included in the genetic analyses in this study were collected at 18 stations, located between 39 38.82N and 40 4.39S latitude. The majority of genetic analyses focused on stations with sufficient sample size for population-level inference (N > 42), including AMT22-09 through AMT22-29 and AMT22-45 through AMT22-68. Specimens used in genetic analyses were primarily RNALater-preserved, but some specimens were included from ethanol-preserved samples to achieve the minimum target sample size of 45 individuals per station. When a major genetic break across the equatorial region was identified, we included samples from stations AMT22-31 through AMT22-43 to assess the genetic composition of populations across this region. Population-level analyses were not conducted on these latter stations due to small sample sizes and low abundance in this region, but sequences from these animals were included in the haplotype network. DNA was extracted from individual P. xiphias adults using the DNeasy Blood & Tissue kit (Qiagen), following the manufacturer's protocol, with the exception of longer elution incubation times (Goetze, 2011). The second of two elutions for each individual was used in this study. Polymerase Chain Reaction (PCR) amplification of a 681-bp fragment of mtCOI was conducted with primers and PCR and sequencing protocols as described in (Goetze, 2011). Forward and reverse sequences from each individual were aligned and checked for errors in Geneious (v7.1.8, Biomatters). Consensus sequences for all individuals were aligned using MUSCLE (Edgar, 2004), and unique mtCOI haplotypes were identified using FABox (http://users-birc.au.dk/biopv/php/fabox/). MtCOI sequences representing unique haplotypes are available under GenBank accession numbers KT429028–KT429159. A minimum spanning haplotype network was inferred for all mtCOI sequences using Population Analysis with Reticulate Trees (PopART; http://popart.otago.ac.nz), in order to investigate geographic patterns in the distribution of haplotypes across the Atlantic.

Data Processing Description

BCO-DMO Processing:
- modified parameter names to conform with BCO-DMO naming conventions;
- converted lat and lon from degrees and decimal minutes to decimal degrees;
- changed date format to yyyy-mm-dd.

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Data Files

File	
genetic_samples.csv	(Comma Separated Values (.csv), 1.58 KB) MD5:0c83d223ce0dd5f9d281a8a7f5c2368d
Primary data file for dataset ID 699234	

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Related Publications

Goetze, E., Hüdepohl, P. T., Chang, C., Van Woudenberg, L., Iacchei, M., & Peijnenburg, K. T. C. A. (2017). Ecological dispersal barrier across the equatorial Atlantic in a migratory planktonic copepod. Progress in Oceanography, 158, 203–212. doi:10.1016/j.pocean.2016.07.001

Results

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Related Datasets

Different Version

Goetze, E., Hüdepohl, P. T., Chang, C., Van Woudenberg, L., Iacchei, M., & Peijnenburg, K. T. C. A. (2017). Data from: Ecological dispersal barrier across the equatorial Atlantic in a migratory planktonic copepod [Data set]. Dryad Digital Repository. https://doi.org/10.5061/dryad.s058r

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Parameters

Parameter	Description	Units
ID	Sample ID	unitless
cruise_station	Cruise and station number	unitless
latitude	Station latitude; positive values = North	decimal degrees
longitude	Station longitude; negative values = West	decimal degrees
date	Date of collection formatted as yyyy-mm-dd	unitless
ocean_biome	Description of ocean biome at the sampling station.	unitless
pop	'pop' indicates whether the sample was included in population genetic analyses (Yes/No)	unitless
N	Number of individuals sampled	unitless
H	Number of haplotypes observed	unitless
H_N	The ratio of haplotypes to sample size (H/N)	unitless
h	Haplotype diversity	unitless
pi	Nucleotide diversity	unitless

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Instruments

Dataset-specific Instrument Name	bongo net
Generic Instrument Name	Bongo Net
Dataset-specific Description	Oblique tows were conducted with bongo nets (200 um, 333 um), towed between on average 324 m depth and the sea surface.
Generic Instrument Description	A Bongo Net consists of paired plankton nets, typically with a 60 cm diameter mouth opening and varying mesh sizes, 10 to 1000 micron. The Bongo Frame was designed by the National Marine Fisheries Service for use in the MARMAP program. It consists of two cylindrical collars connected with a yoke so that replicate samples are collected at the same time. Variations in models are designed for either vertical hauls (OI-2500 = NMFS Pairovet-Style, MARMAP Bongo, CalVET) or both oblique and vertical hauls (Aquatic Research). The OI-1200 has an opening and closing mechanism that allows discrete "known-depth" sampling. This model is large enough to filter water at the rate of 47.5 m3/minute when towing at a speed of two knots. More information: Ocean Instruments, Aquatic Research, Sea-Gear

Dataset-specific Instrument Name	PCR
Generic Instrument Name	Thermal Cycler
Dataset-specific Description	Polymerase Chain Reaction (PCR) amplification of a 681-bp fragment of mtCOI was conducted with primers and PCR and sequencing protocols as described in (Goetze, 2011).
Generic Instrument Description	A thermal cycler or "thermocycler" is a general term for a type of laboratory apparatus, commonly used for performing polymerase chain reaction (PCR), that is capable of repeatedly altering and maintaining specific temperatures for defined periods of time. The device has a thermal block with holes where tubes with the PCR reaction mixtures can be inserted. The cycler then raises and lowers the temperature of the block in discrete, pre-programmed steps. They can also be used to facilitate other temperature-sensitive reactions, including restriction enzyme digestion or rapid diagnostics. (adapted from http://serc.carleton.edu/microbelife/research_methods/genomics/pcr.html)

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Deployments

JC079

Website	https://www.bco-dmo.org/deployment/540458
Platform	RRS James Cook
Report	http://dmoserv3.whoi.edu/data_docs/Goetze/AMT22_cruise/jc079.pdf
Start Date	2012-10-10
End Date	2012-11-24
Description	The AMT22 cruise set sail from Southampton in the UK on 10 October 2012 and arrived in Punta Arenas, Chile on 24 November 2012. The final cruise report and other cruise information, including all science components, can be found online at the Atlantic Meridional Transect webpage (http://www.amt-uk.org/Cruises), or through the British Oceanographic Data Centre (BODC) (http://www.bodc.ac.uk/projects/uk/amt/). Zooplankton ecology data from the project "Does habitat specialization drive population genetic structure of oceanic zooplankton?" (NSF OCE-1029478) were collected on this cruise.

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Project Information

Basin-scale genetics of marine zooplankton (Plankton Population Genetics)

Coverage: Atlantic Ocean, 46 N - 46 S

Description from NSF award abstract:
Marine zooplankton show strong ecological responses to climate change, but little is known about their capacity for evolutionary response. Many authors have assumed that the evolutionary potential of zooplankton is limited. However, recent studies provide circumstantial evidence for the idea that selection is a dominant evolutionary force acting on these species, and that genetic isolation can be achieved at regional spatial scales in pelagic habitats. This RAPID project will take advantage of a unique opportunity for basin-scale transect sampling through participation in the Atlantic Meridional Transect (AMT) cruise in 2014. The cruise will traverse more than 90 degrees of latitude in the Atlantic Ocean and include boreal-temperate, subtropical and tropical waters. Zooplankton samples will be collected along the transect, and mitochondrial and microsatellite markers will be used to identify the geographic location of strong genetic breaks within three copepod species. Bayesian and coalescent analytical techniques will test if these regions act as dispersal barriers. The physiological condition of animals collected in distinct ocean habitats will be assessed by measurements of egg production (at sea) as well as body size (condition index), dry weight, and carbon and nitrogen content. The PI will test the prediction that ocean regions that serve as dispersal barriers for marine holoplankton are areas of poor-quality habitat for the target species, and that this is a dominant mechanism driving population genetic structure in oceanic zooplankton.

Note: This project is funded by an NSF RAPID award. This RAPID grant supported the shiptime costs, and all the sampling reported in the AMT24 zooplankton ecology cruise report (PDF).

Online science outreach blog at: https://atlanticplankton.wordpress.com

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1338959
NSF Division of Ocean Sciences (NSF OCE)	OCE-1029478

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