Haloptilus longicornis population structure (Atlantic Ocean) - Microsatellite data.

Website: https://www.bco-dmo.org/dataset/699458
Data Type: experimental
Version: 1
Version Date: 2017-03-20

Project
» Basin-scale genetics of marine zooplankton (Plankton Population Genetics)
» Does habitat specialization drive population genetic structure of oceanic zooplankton? (Plankton_PopStructure)

Contributors	Affiliation	Role
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Abstract
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Coverage

Temporal Extent: 2012-01-01 - 2012-12-31

Dataset Description

These microsatellite data derive from individual copepods collected on Atlantic Meridional Transect cruise 22 (AMT22) in 2012 (RRS James Cook).

These data are reported on in Goetze, E., Andrews, K., Peijnenburg, K. T. C. A., Portner, E., Norton, E. L. (2015) Temporal Stability of Genetic Structure in a Mesopelagic Copepod. *PLoS One* 10(8): e0136087. doi:10.1371/journal.pone.0136087

These microsatellite data are also available under supporting information S1 File.csv at *PLoS One*.

Mitochondrial cytochrome c oxidase subunit II (mtCOII) sequence data from this study are available at NCBI under accession numbers KR872026-KR872295 and KC713636-KC713781. Oceanographic data from the Atlantic Meridional Transect cruises are available through the British Oceanographic Data Center.

Abstract: Although stochasticity in oceanographic conditions is known to be an important driver of temporal genetic change in many marine species, little is known about whether genetically distinct plankton populations can persist in open ocean habitats. A prior study demonstrated significant population genetic structure among oceanic gyres in the mesopelagic copepod *Haloptilus longicornis* in both the Atlantic and Pacific Oceans, and we hypothesized that populations within each gyre represent distinct gene pools that persist over time. We tested

this expectation through basin-scale sampling across the Atlantic Ocean in 2010 and 2012. Using both mitochondrial (mtCOII) and microsatellite markers (7 loci), we show that the genetic composition of populations was stable across two years in both the northern and southern subtropical gyres. Genetic variation in this species was partitioned among ocean gyres (F_{CT} = 0.285, P < 0.0001 for mtCOII, F_{CT} = 0.013, P < 0.0001 for microsatellites), suggesting strong spatial population structure, but no significant partitioning was found among sampling years. This temporal persistence of population structure across a large geographic scale was coupled with chaotic genetic patchiness at smaller spatial scales, but the magnitude of genetic differentiation was an order of magnitude lower at these smaller scales. Our results demonstrate that genetically distinct plankton populations persist over time in highly-dispersive open ocean habitats, and this is the first study to rigorously test for temporal stability of large-scale population structure in the plankton.

Methods & Sampling

Refer to the following publication for complete methodology details:

Goetze, E., Andrews, K., Peijnenburg, K. T. C. A., Portner, E., Norton, E. L. (2015) Temporal Stability of Genetic Structure in a Mesopelagic Copepod. PLoS One 10(8): e0136087. doi:10.1371/journal.pone.0136087

In summary (excerpted from above):

For H. longicornis species 1, deviations from Hardy-Weinberg equilibrium (HWE) and linkage disequilibrium were examined using ARLEQUIN v3.5.1.3 and GENEPOP v4.2 for all microsatellite loci [36–38]. We tested for the presence of null alleles in microsatellite data using MICROCHECKER v2.2.3 [39], and estimated null allele frequencies and calculated population pairwise FST values with correction for null alleles in FreeNA [40]. Microsatellite genetic diversity indices of observed and expected heterozygosity, average alleles per locus, and allele richness were calculated in GENETIX v4.05 and FSTAT [35,41]. Pairwise FST values were calculated among all sample sites using both microsatellite and mtCOII data, as a measure of population subdivision across samples (ARLEQUIN v3.5.1.3, [38]). Significance was assessed following correction for multiple comparisons using the false discovery rate (FDR, [42,43]). Pairwise ΦST values also were calculated for the mtCOII data. We identified the nucleotide substitution model that best fit our mtCOII data using the Akaike Information Criterion, as implemented in jModelTest v2.1.4 [44], and the K81 or three-parameter model was selected as the best model (TPM3uf+G). The Tamura and Nei substitution model, which was the closest available model in Arlequin, was used to calculate pairwise and global ΦST values, and to estimate genetic diversity at each site. Hierarchical Analyses of Molecular Variance (AMOVA) based on FST were carried out to partition the genetic variance across both space (ocean gyres) and time (sampling years), for both marker types. In these analyses, we tested for population structure under the following groupings: with samples stratified by (1) northern and southern subtropical gyres (2 gyres), and (2) across two sampling years (2010, 2012). Global FST values were estimated using non-hierarchical AMOVAs among all samples, as well as among subsets of the data across ocean gyres and sampling years. Significance was tested with 10,000 permutations of genotypes or haplotypes among populations. Principal coordinate analysis (PCA) plots of linearized pairwise FST values based on both mtCOII and microsatellite data were used to visualize spatial and temporal genetic differentiation among samples. Population structure was further examined using a Bayesian clustering method implemented in STRUCTURE [45,46] for microsatellite loci. We used admixture and correlated allele frequency models, with a burn-in of 105 steps followed by 106 steps, with and without using sampling location as a prior. We ran these analyses for each of the 2010 and 2012 datasets using K = 1 to K = 10, and for the dataset of combined years using K = 1 to K = 20. We ran three separate replicates for each K to investigate consistency of Pr(X|K). The true K was evaluated by visual inspection of barplots and comparing Pr(X|K) across K values.

Data Processing Description

BCO-DMO Processing:
- modified parameter names to conform with BCO-DMO naming conventions
- "0" missing value code changed to "nd"

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Data Files

File
HALO_population.csv (Comma Separated Values (.csv), 62.88 KB) MD5:4e57454d30bfa84541f83000f415d4ff Primary data file for dataset ID 699458

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Related Publications

Goetze, E., Andrews, K. R., Peijnenburg, K. T. C. A., Portner, E., & Norton, E. L. (2015). Temporal Stability of Genetic Structure in a Mesopelagic Copepod. PLOS ONE, 10(8), e0136087. doi:10.1371/journal.pone.0136087
General

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Parameters

Parameter	Description	Units
sample_id	PI issued sample ID number	unitless
station	Station number where sampling occurred	unitless
diploidGenotype1_HALOMS175	Diploid genotypes reported for each locus and individual	count
diploidGenotype2_HALOMS175	Diploid genotypes reported for each locus and individual	count
diploidGenotype1_HALOMS27	Diploid genotypes reported for each locus and individual	count
diploidGenotype2_HALOMS27	Diploid genotypes reported for each locus and individual	count
diploidGenotype1_HALOMS32	Diploid genotypes reported for each locus and individual	count
diploidGenotype2_HALOMS32	Diploid genotypes reported for each locus and individual	count
diploidGenotype1_HALOMS86	Diploid genotypes reported for each locus and individual	count
diploidGenotype2_HALOMS86	Diploid genotypes reported for each locus and individual	count
diploidGenotype1_HALOM264	Diploid genotypes reported for each locus and individual	count
diploidGenotype2_HALOM264	Diploid genotypes reported for each locus and individual	count
diploidGenotype1_HALOMS91	Diploid genotypes reported for each locus and individual	count
diploidGenotype2_HALOMS91	Diploid genotypes reported for each locus and individual	count
diploidGenotype1_HALOMX66	Diploid genotypes reported for each locus and individual	count
diploidGenotype2_HALOMX66	Diploid genotypes reported for each locus and individual	count

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Instruments

Dataset-specific Instrument Name	ABI3730 Genetic Analyzer
Generic Instrument Name	Thermal Cycler
Dataset-specific Description	PCR products were genotyped
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.

JC053

Website	https://www.bco-dmo.org/deployment/737883
Platform	RRS James Cook
Start Date	2010-10-12
End Date	2010-11-25
Description	From: https://www.bodc.ac.uk/resources/inventories/cruise_inventory/report/9969/ AMT20 (JC053) is the third cruise of the third phase of the Atlantic Meridional Transect (AMT) programme. The programme is hosted by Plymouth Marine Laboratory in collaboration with the National Oceanography Centre, Southampton, provides an exceptional opportunity for nationally and internationally driven collaborative research, and provides a platform for excellent multi-disciplinary oceanographic research. As an in situ observation system, AMT informs on changes in biodiversity and function of the Atlantic ecosystem during this period of rapid change to our climate and biosphere. The aims of the AMT programme [www.amt-uk.org] are to quantify the nature and causes of ecological and biogeochemical variability in the planktonic ecosystems of the Atlantic Ocean, and to assess the effects of this variability on biological carbon cycling and air-sea exchange of radiatively active gases and aerosols. Between 1995 and 2005 marine and atmospheric data were collected twice a year along a 13,500 km transect in the Atlantic Ocean. The cruise track enabled biogeochemical measurements to be made within the poorly studied North and South Atlantic oligotrophic gyres as well as within equatorial and coastal upwelling regions. The range of ecosystems sampled has facilitated the calibration and validation of newly developed techniques, provided a testbed for comparative ecology and enabled the development of atmospheric and oceanographic models. The unique AMT dataset continues to be deposited and made available to the wider community through the British Oceanographic Data Centre.

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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

Does habitat specialization drive population genetic structure of oceanic zooplankton? (Plankton_PopStructure)

Coverage: Global Ocean

Description from NSF award abstract:
This research will test whether habitat depth specialization is a primary trait driving large-scale population genetic structure in open ocean zooplankton species. Very little is known about population connectivity in marine zooplankton. Although zooplankton were long thought to be high-gene-flow systems with little genetic differentiation among populations, recent observations have challenged this view. In fact, zooplankton species may be genetically subdivided at macrogeographic, regional, or even smaller spatial scales. Recent studies also indicate that subtle, species-specific ecological factors play an important role in controlling gene flow among plankton populations. The investigator hypothesizes that depth-related habitat, including diel vertical migration (DVM) behavior, plays a critical role in controlling dispersal of plankton among ocean regions, through interactions with ocean circulation and bathymetry. This study will compare the population genetic structures of eight planktonic copepods that utilize different depth-related habitats, in order to test key predictions of genetic structure based on the interaction of organismal depth with the oceanographic environment. The objectives of the research are to:
1) Develop novel nuclear markers that can be used to resolve genetic structure and estimate gene flow among copepod populations,
2) Characterize the spatial patterns of gene flow among populations in distinct ocean regions of the Atlantic, Pacific, and Indian Oceans for eight target species using a multilocus approach, and
3) Test the central hypothesis that depth-related habitat will significantly impact the extent of genetic structure both across and within ocean basins, the magnitude and direction of gene flow among populations, and in the timing of major slitting events within species.

Drawing on genomic resources (cDNA libraries) recently developed by the PI, five (or more) polymorphic nuclear markers will be developed for each species. These new markers will be used, in combination with the mitochondrial gene cytochrome oxidase I, to characterize the population genetic structure of each species throughout its global distribution using graph theoretic and coalescent analytical techniques. Gene flow among populations and the timing of major splitting events will be estimated under a coalescent model (IMa), and empirical support for the hypothesis of depth-related trends in population structure will be assessed using graph theoretic congruence tests. Because the depth specialization and diel vertical migration behaviors of the target species are representative of distinct zooplankton species groups, the results of this study will have broad implications for understanding and predicting the genetic structure of these important grazers in pelagic ecosystems.

Publications produced with support from this award include:
Burridge, A., Goetze, E., Raes, N., Huisman, J., Peijnenburg, K. T. C. A. (in revision) Global biogeography and evolution of *Cuvierina* pteropods. *BMC Evolutionary Biology*.

Andrews, K. R., Norton, E. L., Fernandez-Silva, I., Portner†, E. Goetze, E. (in press) Multilocus evidence for globally-distributed cryptic species and distinct populations across ocean gyres in a mesopelagic copepod. *Molecular Ecology.*

Halbert , K. M. K., Goetze, E., Carlon, D. B. (2013) High cryptic diversity across the global range of the migratory planktonic copepods *Pleuromamma piseki* and *P. gracilis*. *PLOS One* 8(10): e77011. doi:10.1371/journal.pone.0077011

Norton , E. L., Goetze, E. (2013) Equatorial dispersal barriers and limited connectivity among oceans in a planktonic copepod. *Limnology and Oceanography* 58: 1581-1596.

Peijnenburg, K. T. C. A., Goetze, E. (2013) High evolutionary potential of marine zooplankton. *Ecology & Evolution* 3(8): 2765-2781. doi: 10.1002/ece3.644 (both authors contributed equally).

Fernandez-Silva, I., Whitney, J., Wainwright, B., Andrews, K. R., Ylitalo-Ward, H., Bowen, B. W., Toonen, R. J., Goetze, E., Karl, S. A. (2013) Microsatellites for Next-Generation Ecologists: A Post-Sequencing Bioinformatics Pipeline. *PLOS One* 8(2): e55990. doi:10.1371/journal.pone.0055990

Bron, J. E., Frisch, D., Goetze, E., Johnson, S. C., Lee, C. E., Wyngaard, G. A. (2011) Observing Copepods through a Genomic Lens. *Frontiers in Zoology* 8: 22.

Goetze, E. (2011) Population differentiation in the open sea: Insights from the pelagic copepod *Pleuromamma xiphias*. *Integrative and Comparative Biology* 51: 580-597.

Master's theses supported under this award include:

Emily L. Norton. *Empirical and biophysical modeling studies of dispersal barriers for marine plankton*. (2013). University of Hawaii at Manoa.

K. M. K. Halbert. *Genetic isolation in the open sea: Cryptic diversity in the Pleuromamma piseki - P. gracilis species complex*. (2013). University of Hawaii at Manoa.

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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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