Pool-seq data from wild populations of copepods in the North Sea from May 2014 (Evolutionary genomics of a copepod project)

Website: https://www.bco-dmo.org/dataset/897977
Data Type: Other Field Results
Version: 1
Version Date: 2023-06-27

Project
» Evolutionary Responses to Global Changes in Salinity and Temperature (Evolutionary genomics of a copepod)

Contributors	Affiliation	Role
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Abstract
This dataset was generated from studies of wild populations of Eurytemora affinis (E. affinis). Copepod populations were collected from three locations in the North Sea using bongo nets with 100 micrometer (µm) mesh and stored in RNAlater. Sampling locations included two freshwater lakes and one brackish estuary. Individual copepods (100 individuals, 50:50 male:female) were pooled and their DNA was extracted. Paired-end whole-genome sequencing libraries were prepared using the Illumina Nextera DNA kit (Illumina, Inc.) and sequenced on three lanes of an Illumina HiSeq 2000 sequencer, generating an average of approximately 158 million paired-end (100 bp) reads per pool. These data have been deposited in the National Center for Biotechnology Information (NCBI) under BioProject number PRJNA923656.

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Coverage

Spatial Extent: **N**:52.699 **E**:5.29 **S**:51.302 **W**:4.286
Temporal Extent: 2014-05 - 2014-05

Dataset Description

These data have been deposited in NCBI under BioProject number PRJNA923656.

Methods & Sampling

Methods and Sampling:

Wild *Eurytemora affinis* populations were collected from three locations in the North Sea using bongo nets with 100 micrometer (µm) mesh. Copepods were stored in RNAlater. Sampling locations included two fresh water lakes and one brackish estuary. From each population, individual copepods (100 individuals, 50:50 male:female) were pooled and their DNA was extracted using the DNeasy Blood and Tissue Extraction kit (Qiagen, Inc.). Paired-end whole-genome sequencing libraries were prepared using the Illumina Nextera DNA kit (Illumina, Inc.) and sequenced on three lanes of an Illumina HiSeq 2000 sequencer at the Maryland Institute of Genome Science, generating an average of approximately 158 million paired-end (100 bp) reads per pool.

Data Processing Description

Processing notes from researcher:

Raw sequence reads were mapped to a reference genome to call SNPs. We then detected SNPs with significant signatures of selection across temperature and salinity gradients. Signatures of selection were detected using an outlier approach and an association with an environmental variable (i.e., temperature or salinity) approach.

The following software was used:
BayPass v.2.2, BEDOPS v.2.4.39, BITE v.1.2.8, BLAST 2.7.1+, BWA-MEM v.0.7.17, GATK v.3.8, Gowinda v.1.12, ggplot2 v.3.3.5, gplots v.3.1.3, OptM v.0.1.6, PHYLIP v.3.697, Picard v. 2.18.27, poolfstat v.1.0, poolfstat v.2.1.1, PoPoolation v.1.2.2, PoPoolation2 v.1.201, SAMtools v.1.3.1, stats v.4.1.2, TreeMix v.1.13, Trimmomatic v.0.39, VarScan v.2.4.3, vegan v.2.6-2, https://github.com/TheDBStern/Baltic_Lab_Wild (DOI:10.5281/zenodo.6615047), https://github.com/juanitadiaz/Europe_Wild_LocalAdaptation_GeneFlow (DOI:10.5281/zenodo.7819560), https://github.com/carolindahms/TreeMix

BCO-DMO Processing Notes:

- The submitted data file (named jdiaz_04.23_bco-dmo_metadatasheet-1.xlsx changed to 897977_v1_wild_pool-seq_data.csv post-processing

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Related Publications

Diaz, J., Stern, D., & Lee, C. E. (2023). Local adaptation despite gene flow in copepod populations across salinity and temperature gradients in the Baltic and North Seas.
https://doi.org/10.22541/au.168311545.58858033/v1
Results

Diaz, Juanita & Stern, D. B. (2022). TheDBStern/Baltic_Lab_Wild: First release (Version v0.0.1)[Computer software]. Zenodo. https://doi.org/10.5281/ZENODO.6615047
https://doi.org/https://doi.org/10.5281/zenodo.6615047
Software

Diaz, Juanita (2023). juanitadiaz/Europe_Wild_LocalAdaptation_GeneFlow: v0.0.1 (Version v0.0.1) [Computer software]. Zenodo. https://doi.org/10.5281/ZENODO.7819560
https://doi.org/http://doi.org/10.5281/zenodo.7819560
Software

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Related Datasets

IsRelatedTo

Lee, C. E., Stern, D. B. (2022) **Pool-seq data from laboratory selection lines of copepods collected**

from Kiel Canal in Germany in 2017 and 2018. Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2022-08-29 doi:10.26008/1912/bco-dmo.878335.1 [view at BCO-DMO]

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Parameters

Parameter	Description	Units
Location	Location of sample site	unitless
Collection_Date	Date of sample collection in format YYYY-MM-DD	unitless
Sample_Code	Unique identifier for sample	unitless
Sample_Salinity	Sea surface salnity measured by refractometer	Practical salinity units (PSU)
Sample_Temperature	Sea surface temperature measured by thermometer	degrees Celsius
Latitude	Latitude of collection location in decimal degrees. A positive value indicates a Northern coordinate.	decimal degrees
Longitude	Longitude of collection location in decimal degrees. A positive value indicates an Eastern coordinate.	decimal degrees
BioSample	NCBI BioSample ID	unitless
SRA_Run	NCBI SRA Run number	unitless

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Instruments

Dataset-specific Instrument Name	Illumina HiSeq 2000 sequencer
Generic Instrument Name	Automated DNA Sequencer
Dataset-specific Description	Used to sequence pooled E. affinis samples.
Generic Instrument Description	General term for a laboratory instrument used for deciphering the order of bases in a strand of DNA. Sanger sequencers detect fluorescence from different dyes that are used to identify the A, C, G, and T extension reactions. Contemporary or Pyrosequencer methods are based on detecting the activity of DNA polymerase (a DNA synthesizing enzyme) with another chemoluminescent enzyme. Essentially, the method allows sequencing of a single strand of DNA by synthesizing the complementary strand along it, one base pair at a time, and detecting which base was actually added at each step.

Dataset-specific Instrument Name	Bongo net
Generic Instrument Name	Bongo Net
Dataset-specific Description	E. affinis samples were collected using a Bongo net with 100 µm mesh.
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

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Project Information

Evolutionary Responses to Global Changes in Salinity and Temperature (Evolutionary genomics of a copepod)

Coverage: St. Lawrence estuary, Gulf of Mexico, Great Lakes, Baltic Sea

NSF Award Abstract:

Drastic changes in the global water cycle and increases in ice melt are causing the freshening of Northern coastal seas. The combination of both reduced salinity and increased temperature will likely act in concert to reduce populations of estuarine and marine organisms. Data indicate that reduced salinity and high temperature would each increase the energy costs as well as reduce survival and reproduction of the common copepod Eurytemora affinis. This project will examine the joint effects of salinity reduction and temperature increase on the evolutionary responses of populations of E. affinis in the wild, as well as in selection experiments in the laboratory. This study will provide novel insights into responses of organisms to climate change, as no study has analyzed the joint impacts of salinity and temperature on evolutionary responses, and relatively few studies have examined the impacts of declining salinity. In general, how selection acts at the whole genome level is not well understood, particularly for non-model organisms. As a dominant estuarine copepod, E. affinis is among the most important species sustaining coastal food webs and fisheries in the Northern Hemisphere, such as salmon, herring, and anchovy. Thus, insights into its evolutionary responses with changing climate have important implications for sustainability of fisheries and food security. Two graduate students from historically underrepresented groups will be trained during this project. The project will have additional societal benefits, including development of educational modules for K-12 students and international collaboration.

This study will address the following questions: (1) To what extent could populations evolve in response to salinity and temperature change, and what are the fitness and physiological costs? (2) How will populations respond to the impacts of salinity-temperature interactions? (3) Do wild populations show evidence of natural selection in response to salinity and temperature? To analyze the evolutionary responses of E. affinis populations to the coupled impacts of salinity and temperature, the investigator will perform laboratory selection experiments and population genomic surveys of wild populations. Selection experiments constitute powerful tools for determining the rate, trajectory, and limits of adaptation. During laboratory selection, evolutionary shifts in fitness-related traits and genomic expression will be examined, as well as genomic signatures of selection in response to low salinity and high temperature selection regimes. The investigator will also conduct population genomic sequencing of E. affinis populations that reside along salinity and temperature

gradients in the St. Lawrence and Baltic Sea, and identify genes that show signatures of selection. The project will determine whether the loci that show signatures of selection in the wild populations are the same as those favored during laboratory selection. This reproducibility will provide greater confidence that the genes involved in adaptation to salinity and/or temperature have been captured.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1658517

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