Pool-seq data from wild populations of copepods in the Baltic Sea from May 2018 through August 2019

Website: https://www.bco-dmo.org/dataset/878322
Data Type: Other Field Results
Version: 1
Version Date: 2022-08-11

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 represents data from wild populations of E. affinis. Copepod populations were collected from eight locations in the Baltic Sea using bongo and WP2 nets with 100 µm mesh and stored in RNAlater. Sampling locations spanned a range of mean annual salinities from low (~3 PSU) to higher salinity (~19 PSU). Individual copepods (ranging from 50 to 200 in number) 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 five lanes of an Illumina HiSeq 4000 sequencer, generating an average of approximately 176 million paired-end (100 bp) reads per pool. These genomic data have been deposited in NCBI under BioProject number PRJNA844002.

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Coverage

Spatial Extent: **N**:65.3836 **E**:23.7097 **S**:54.3333 **W**:10.15
Temporal Extent: 2018-05 - 2019-08

Acquisition Description

Sampling and analytical procedures:
Wild *E. affinis* populations were collected from eight locations in the Baltic Sea using bongo and WP2 nets with 100 micrometer (µm) mesh. Copepods were stored in RNAlater. Sampling locations spanned a range of mean annual salinities from low (~3 PSU) to higher salinity (~19 PSU). From each population, individual copepods (ranging from 50 to 200 in number) 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 five lanes of an Illumina HiSeq 4000 sequencer at the University of Chicago Genomics Facility, generating an average of approximately 176 million paired-end (100 bp) reads per pool.

Processing Description

Raw sequence reads were mapped to a reference genome to call SNPs. We then detected SNPs and genomic regions under natural selection in response to salinity change.

The following software were used:
BLAST 2.7.1+, BWA-MEM v0.7.17, CD-HIT v4.7, PoPoolation2, SAMBLASTER v0.1.26, Samtools v1.3.1, Trinity v2.6.6, VarScan v2.4.3, BioPython v1.78, numpy v1.15.2, lme4 v1.1.21, poolfstat v1.1.1, qvalue v2.14.1, ACER v1.0.2, haplovalidate v0.1.4, BBTools v38, BEDOPS v2.4.39, Bowtie v2.3.5, Gowinda v1.12, HMMER v3.2.1, SLiM v3.7, RSEM v1.3.1, Transdecoder v5.5, Trimmomatic v0.39, TreeMix v1.13, https://github.com/jjberg2/PolygenicAdaptationCode, wtdbg v2.5, Racon v1.4.3, LiftOff v1.6.1, https://github.com/TheDBStern/Baltic_Lab_Wild

These genomic data have been deposited in NCBI under BioProject number PRJNA844002.

BCO-DMO Processing Description:
- Adjusted field/parameter names to comply with BCO-DMO naming conventions
- Added a conventional header with dataset name, PI names, version date
- Replaced commas with semicolons in the "Location" column

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Related Publications

Stern DB, Anderson NW, Diaz JA, Lee CE. Genome-wide signatures of synergistic epistasis during parallel adaptation in a Baltic Sea copepod. Nature Communications. In press
Results

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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 http://lod.bco-dmo.org/id/dataset/878335 [view at BCO-DMO]

University of Wisconsin - Madison. Genome-wide signatures of synergistic epistasis during parallel adaptation in a Baltic Sea copepod. 2022/05. In: BioProject [Internet]. Bethesda, MD: National Library of Medicine (US), National Center for Biotechnology Information; 2011-. Available from: http://www.ncbi.nlm.nih.gov/bioproject/PRJNA844002. NCBI:BioProject: PRJNA844002.

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Parameters

Parameter	Description	Units
Location	Location of site, station ID	unitless
Collection_Date	Date of sample collection in format YYYY-MM	unitless
Sample_Code	unique identifier for sample	unitless
Sample_Salinity	Average water column salinity measured by CTD	Practical salinity units (PSU)
Latitude	Latitude North of collection location	decimal degrees
Longitude	Longitude East (West is negative) of collection location	decimal degrees
BioSample	NCBI BioSample	unitless
SRA_Run	SRA Run number	unitless

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Instruments

Dataset-specific Instrument Name	Bongo net
Generic Instrument Name	Bongo Net
Dataset-specific Description	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

Dataset-specific Instrument Name	WP-2 Net
Generic Instrument Name	WP-2 Plankton Net
Dataset-specific Description	WP2 net with 100 µm mesh
Generic Instrument Description	The WP-2 net is a variety of Ring Net for zooplankton but which is capable of being closed by means of a Nansen bottle-type release messenger weighing 0.8 kg and which can be equipped with a digital flow meter for determining the amount of water passing through the plankton net. The rings may have a variety of sizes (57cm, 70cm, 75 cm, or 1m internal diameter) and the nets which make up this device are in two parts, a cylindrical upper part and a conical lower part. The closing ring is between the two net segments. (more at KC Denmark)

Dataset-specific Instrument Name	Illumina HiSeq 4000 sequencer
Generic Instrument Name	Automated DNA Sequencer
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	
Generic Instrument Name	CTD
Generic Instrument Description	A reusable instrument that always simultaneously measures conductivity and temperature (for salinity) and pressure (for depth).

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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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