Sample and genetic accession information for RNA-seq data from whole Atlantic silverside (Menidia menidia) larvae from two populations and their F1 hybrids reared under different temperatures in 2017

Website: https://www.bco-dmo.org/dataset/854887
Data Type: experimental
Version: 1
Version Date: 2021-06-29

Project
» Collaborative research: The genomic underpinnings of local adaptation despite gene flow along a coastal environmental cline (GenomAdapt)

Contributors	Affiliation	Role
Therkildsen, Nina Overgaard	Cornell University (Cornell)	Principal Investigator
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Abstract
Sample and genetic accession information for RNA-seq data from whole Atlantic silverside (Menidia menidia) larvae from two populations and their F1 hybrids. Larvae were reared under two different temperatures to study temperature-dependent gene regulatory divergence between locally adapted Atlantic silverside populations in 2017. The data are deposited in the National Center for Biotechnology Information (NCBI) Sequence Read Archive (SRA) with accession numbers SRR13523227- SRR13523268 associated with BioProject PRJNA694674 and BioSamples SAMN17531688 - SAMN17531729.

Table of Contents

Coverage

Spatial Extent: **N**:40.75 **E**:-73 **S**:31.02 **W**:-81.43
Temporal Extent: 2017-04 - 2017-08

Methods & Sampling

Sampling and analytical procedures:

Wild adults were caught at spawning time using seine nets at Jekyll Island, Georgia (GA; 3103N, 8126W) and Patchogue, New York (NY; 4045N, 7300W) in spring 2017. Individuals were transported live to the Rankin Seawater Facility at the University of Connecticuts Avery Point campus. A full reciprocal crossing design was

set up by strip-spawning multiple males and females in batches onto mesh screens submerged in plastic dishes in seawater. We created reciprocal F1 crosses: NY♀ x NY♂ (NY), NY♀ x GA♂ (NYxGA), GA♀ x NY♂ (GAxNY), and GA♀ x GA♂ (GA). Fertilized eggs were kept in 20L rearing containers placed in large temperature-controlled water baths at constant salinity (30psu) and photoperiod (15L:9D). We split the fertilized eggs of each pure cross (NY and GA) into four batches, and hatched and reared two batches per cross at 20C and two batches at 26C. The hybrid crosses were each split into two batches, with one batch for each crossing direction incubated at either 20C or 26C. The two temperatures, 20C and 26C, were chosen to reflect the common rearing temperatures at both parental spawning locations (NY and GA), respectively. Individuals were reared to an approximate total length of 30mm, with the rearing durations differing between populations and temperature regimes. Most individuals from the GAxNY cross died at 26C and all at 20C and thus we could not include these crosses in present study. From the remaining crosses, we randomly selected 6-8 individuals for RNA-sequencing.

Total RNA was extracted from whole larvae (n=42) using the ZymoResearch Direct-zol Miniprep RNA plus kit. Whole larvae were homogenized in Trizol using a pestle prior to RNA extraction. During the extraction, an optional in-column DNAse I treatment step was performed to remove traces of genomic DNA from the sample, and samples were eluted in 50l of RNAse-free water and stored at -70C. RNA quantity was determined using the HS Assay kit for the Qubit 3.0 fluorometer (Life Technologies, Carlsbad, CA) and quality was assessed using a Fragment Analyzer (Agilent, Santa Clara, CA) at the Cornell University Biotechnology Resource Centre. RIN values ranged from 5.3 to 8.3, with an average RIN of 6.9. RNA-seq libraries were prepared at BGI Genomics using the stranded Illumina TruSeq mRNA sequencing kit with Poly-A selection.

Instruments:

Each library was sequenced to an average of 37.1M 2x150bp paired-end reads (0.194M s.d.) using an Illumina HiSeq 4000 sequencer at BGI Genomics.

Location:
The larvae reared in the laboratory were F1 offspring of parents collected either in :

1) Jekyll Island, Georgia (31.02,-81.43), or
2) Patchogue, New York (40.75,-73.00)

Data Processing Description

No processing.

BCO-DMO data manager processing notes:
* Extracted excerpts of sample information from NCBI in XML format. Converted it to a tabular dataset (csv) and imported into BCO-DMO's data system to aid in dataset discovery and data reuse.

[table of contents | back to top]

Data Files

File	
854887_v1_silverside_rnaseq_info.csv	(Comma Separated Values (.csv), 7.13 KB) MD5:1a6d5d38aa091bfd6c0b989ae86ef471
Primary data file for dataset ID 854887, version 1	

[table of contents | back to top]

Related Datasets

IsRelatedTo

Bethesda, MD: National Library of Medicine (US), National Center for Biotechnology Information; Available from: http://www.ncbi.nlm.nih.gov/bioproject/PRJNA694674.

Therkildsen, N. O., Baumann, H. (2021) **Methodology information and links to data access for allele frequencies and FST estimates for 1,904,119 SNPs analyzed in five population samples of Atlantic silverside (Menidia menidia) collected along the east coast of North America between 2005 to 2007.** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2021-06-29 http://lod.bco-dmo.org/id/dataset/854895 [view at BCO-DMO]
Relationship Description: The RNA-seq dataset compares gene expression differences between two of the populations that we provide population genomic data for in the "Allele frequencies and FST estimates" dataset.

Therkildsen, N. O., Baumann, H. (2024) **Sample information and genetic accession information for raw low-coverage genomic sequence reads from 248 different Atlantic silverside (Menidia menidia) collected along the east coast of North America between 2005 to 2007.** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2021-06-30 doi:10.26008/1912/bco-dmo.854878.1 [view at BCO-DMO]
Relationship Description: The "Raw low-coverage whole genome sequencing reads" are from population samples from five locations, including the two populations studied in the RNA-seq dataset, but the individuals are not related (the fish used for low-coverage whole genome sequencing were sampled ~10 years before the fish used in the RNA-seq study).

[table of contents | back to top]

Parameters

Parameter	Description	Units
BioProject	NCBI BioProject Identifier	unitless
BioSample	NCBI BioSample Identifier	unitless
Sample_name	Sample name	unitless
SRA	Sequence read archive sample accession	unitless
taxonomy_id	NCBI taxonomy identifier	unitless
taxonomy_name	NCBI taxonomic name	unitless
ecotype	Population ancestry (pure F1 with both parents from Patchogue, New York, pure F1 with both parents from Jekyll Island, Georgia, and a hybrid F1 with one parent from each of the two populations)	unitless
dev_stage	Development stage	unitless
sex	Sex	unitless
tissue	Description of tissue sampled	unitless
sample_type	Sample type	unitless
cross	Information on the origin of parents (PANY = Patchogue, New York, JIGA = Jekyll Island, GA)	unitless
treatment	Treatment temperature	degrees Celsius

[table of contents | back to top]

Instruments

Dataset-specific Instrument Name	Illumina HiSeq 4000
Generic Instrument Name	Automated DNA Sequencer
Dataset-specific Description	Illumina HiSeq 4000 sequencer at BGI Genomics
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.

[table of contents | back to top]

Project Information

Collaborative research: The genomic underpinnings of local adaptation despite gene flow along a coastal environmental cline (GenomAdapt)

Website: https://befel.marinesciences.uconn.edu/2018/03/07/research-news-new-nsf-grant-to-study-silverside-genes/

Coverage: Eastern coastline of North America

NSF Abstract:

Oceans are large, open habitats, and it was previously believed that their lack of obvious barriers to dispersal would result in extensive mixing, preventing organisms from adapting genetically to particular habitats. It has recently become clear, however, that many marine species are subdivided into multiple populations that have evolved to thrive best under contrasting local environmental conditions. Nevertheless, we still know very little about the genomic mechanisms that enable divergent adaptations in the face of ongoing intermixing. This project focuses on the Atlantic silverside (Menidia menidia), a small estuarine fish that exhibits a remarkable degree of local adaptation in growth rates and a suite of other traits tightly associated with a climatic gradient across latitudes. Decades of prior lab and field studies have made Atlantic silverside one of the marine species for which we have the best understanding of evolutionary tradeoffs among traits and drivers of selection causing adaptive divergence. Yet, the underlying genomic basis is so far completely unknown. The investigators will integrate whole genome sequencing data from wild fish sampled across the distribution range with breeding experiments in the laboratory to decipher these genomic underpinnings. This will provide one of the most comprehensive assessments of the genomic basis for local adaptation in the oceans to date, thereby generating insights that are urgently needed for better predictions about how species can respond to rapid environmental change. The project will provide interdisciplinary training for a postdoc as well as two graduate and several undergraduate students from underrepresented minorities. The findings will also be leveraged to develop engaging teaching and outreach materials (e.g. a video documentary and popular science articles) to promote a better understanding of ecology, evolution, and local adaptation among science students and the general public.

The goal of the project is to characterize the genomic basis and architecture underlying local adaptation in M. menidia and examine how the adaptive divergence is shaped by varying levels of gene flow and maintained over ecological time scales. The project is organized into four interconnected components. Part 1 examines fine-scale spatial patterns of genomic differentiation along the adaptive cline to a) characterize the connectivity landscape, b) identify genomic regions under divergent selection, and c) deduce potential drivers and targets of selection by examining how allele frequencies vary in relation to environmental factors and biogeographic

features. Part 2 maps key locally adapted traits to the genome to dissect their underlying genomic basis. Part 3 integrates patterns of variation in the wild (part 1) and the mapping of traits under controlled conditions (part 2) to a) examine how genomic architectures underlying local adaptation vary across gene flow regimes and b) elucidating the potential role of chromosomal rearrangements and other tight linkage among adaptive alleles in facilitating adaptation. Finally, part 4 examines dispersal - selection dynamics over seasonal time scales to a) infer how selection against migrants and their offspring maintains local adaptation despite homogenizing connectivity and b) validate candidate loci for local adaptation. Varying levels of gene flow across the species range create a natural experiment for testing general predictions about the genomic mechanisms that enable adaptive divergence in the face of gene flow. The findings will therefore have broad implications and will significantly advance our understanding of the role genomic architecture plays in modifying the gene flow - selection balance within coastal environments.

This award reflects NSF's statutory mission and has been deemed worthy of support through evaluation using the Foundation's intellectual merit and broader impacts review criteria.

[table of contents | back to top]

Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1756316
NSF Division of Ocean Sciences (NSF OCE)	OCE-1756751

[table of contents | back to top]