Atlantic silverside genome

Website: https://www.bco-dmo.org/dataset/917790
Version: 1
Version Date: 2024-01-02

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

Abstract
Raw data and assembled scaffolds for the Atlantic silverside genome

---

Table of Contents

Coverage

Location: Jekyll Island,Georgia, and Mumford Cove,Connecticut
Spatial Extent: **N**:41.32 **E**:-72.02 **S**:31.02 **W**:-81.43

Methods & Sampling

Sampling and analytical procedures

The genomes of two different individuals were sequenced with different approaches:

1. An individual sampled at Jekyll Island, Georgia:

We built a reference genome for the Atlantic silverside through three steps. First, we created a draft assembly using 10x Genomics linked-reads technology (10x Genomics, Pleasanton, CA). Second, we used proximity-ligation data— ChicagoVR (Putnam et al. 2016) and Dovetail

Hi-C (Lieberman-Aiden et al. 2009)—from Dovetail Genomics (Santa Cruz, CA) to increase contiguity, break up mis-joins, and orient and join scaffolds into chromosomes. Finally, we used short-insert reads to close gaps in the scaffolded and error-corrected assembly. The data were generated from muscle tissue dissected from two lab-reared F1 offspring of Atlantic silversides collected from the wild on Jekyll Island, GA, USA (N31.02 ,W81.43 ; the southern end of the species distribution range) in May 2017. For 10x Genomics library preparation, we extracted DNA from fresh tissue from one individual using the MagAttract HMW DNA Kit (Qiagen). Prior to library preparation, we selected fragments longer than 30 kb using a BluePippin device (Sage Science). A 10x Genomics library was prepared following standard procedure and sequenced using two lanes of paired-end 150 bp reads on a HiSeq2500 (rapid run mode) at the Biotechnology Resource Center Genomics Facility at Cornell University. To assemble the linked reads, we ran the program Supernova 2.1.1 (Weisenfeld et al. 2017) from 10x Genomics with varying numbers of reads and compared assembly statistics to identify the number of reads that resulted in the most contiguous assembly. Tissue from the second individual was flash frozen in liquid nitrogen and shipped to Dovetail Genomics, where Chicago and Hi-C libraries were prepared for further scaffolding. These long-range libraries were sequenced on one lane of Illumina HiSeqX using paired-end 150 bp reads. Two rounds of scaffolding with HiRiseTM, a software pipeline developed specifically for genome

scaffolding with Chicago and Hi-C data, were run to scaffold and error-correct the best 10x Genomics draft assembly using Dovetail long-range data. Finally, the barcode-trimmed 10x Genomics reads were used to close gaps between contigs as the final step of the HiRise pipeline.

2. An individual sampled in Mumford Cove, Connecticut

This assembly was a lower-quality draft assembly used to identify structural variants in comparison to the chromosome-level assembly from the individual sampled in Georgia

The individual sampled for this assembly was sampled from Mumford Cove, Connecticut (N 41.32 , W 72.02) in June 2016. Genomic DNA was extracted from muscle tissue using the DNeasy Blood and Tissue kit (Qiagen) and normalized to 40 ng/ul. We prepared a genomic DNA library using the TruSeq DNA PCR-free library kit (Illumina) following the manufacturer's protocol for 550 bp insert libraries. The shotgun library was sequenced using paired-end 150 bp reads on an Illumina HiSeq4000. Mate-pair libraries with insert sizes of 3, 5.3, and 8.2 kb were prepared at the Huntsman Cancer Institute at the University of Utah using the Nextera Mate Pair Library Prep Kit (Illumina) and sequenced using paired-end 125 bp reads on an Illumina HiSeq2500. We used Trimmomatic 0.36 (Bolger et al. 2014) to remove adapter contamination and low-quality data from both the shotgun and the mate-pair libraries and used these filtered reads to assemble a draft assembly and fill assembly gaps with Platanus v.1.2.4 (Kajitani et al. 2014) with the commands assemble, scaffold, and gap_close. Finally,we filtered scaffolds shorter than 1 kb.

Data Processing Description

All files except those listed with "genome assembly" in the date type column are raw sequence data files that have not undergone any processing.

The two genome assemblies were processed as described under "Sampling and analytical procedures" described above.

More details in Tigano et al. 2021

Problem Description

No collection issues reported.

No quality issues reported.

[table of contents | back to top]

Parameters

Parameters for this dataset have not yet been identified

[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

[table of contents | back to top]