

Average daily sea surface temperature from Florida to Prince Edward Island in 2004-2008 (Local adaptation in Menidia project)

Website: <https://www.bco-dmo.org/dataset/562834>

Version: 2015-07-27

Project

» [Local adaptation across latitudes: spatial scales, gene flow, and correlates of countergradient growth variation](#) (Local adaptation in Menidia)

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Dataset Description

This dataset is the average daily temperature from 2-3 years of data for each location. For example, January, Calendar Day 1, Julian Day 1 is the average temperature for all recordings from Jan. 1 averaged over years 2005, 2006, and 2007.

To determine the latitudinal pattern of sex determination, embryos from *M. menidia* were collected from 31 locations along the species' range from Amelia Island, FL (30° 31.13' N, 081° 27.78' W) to the Magdalen Islands, Quebec, Canada (47° 23.60' N, 061° 50.76' W) (Table 1, See Hice et al. (2012) for detailed methods). This resulted in collection sites that averaged 60-80 km from each other for complete coverage of *M. menidia*'s range (Figure 1). Briefly, spawning adult *M. menidia* were collected with a 30m seine net, stripped spawned following the methods employed by Lagomarsino and Conover (1993) and embryos were transported to Flax Pond Laboratory in Old Field, NY or the Bluepoint Laboratory in West Sayville, NY. Larvae of mixed parentage were pooled and randomly allocated into 15 °C or 28 °C in triplicate containers prior to sex determination (Conover and Fleisher 1986). Density per container was periodically adjusted and fish were euthanized when they reached a minimum of 21-23 mm TL. Time to reach this size ranged from one to six months, depending on growth rate and temperature treatment.

Sex was determined macroscopically with a dissecting microscope and total lengths were recorded. Females were identified by opaque or lightly pigmented fragile ovaries, as compared to thin, translucent and flexible testes in males (Conover and Fleisher 1986). In some replicates (27%), a few individuals did not reach a size at which sex could be definitively assessed, but this accounted for a small proportion (1.2%) of all fish. An average of 228 + 36 fish were sexed from each location.

Sea surface temperature (SST) data was collected from the NOAA National Buoy Data Center archives for estuarine or nearshore sites within the U.S.A. and from the Oceanographic Database maintained by the Dept. of Fisheries and Oceans, Canada. Data from two to three years between 2004 and 2007 were used to calculate the average SST (to reduce noise of an anomalous year), as well as mean values for the absolute range (maximum summer temperature - minimum winter temperature), summer temperature (July through September), and 30 day winter minimum temperature (coldest 30 day period). Season length was calculated as

the mean number of days that SST within the estuary was ≥ 12 °C, as somatic growth is approximately zero below this temperature (Conover and Heins 1987a). Data for SST was available for 19 of the 31 sites.

Level of TSD was calculated as the difference in sex ratios of juvenile *M. menidia* reared at feminizing (15 °C) and masculinizing (28°C) temperatures (defined as, $[F/(F+M)$ at 15 °C]- $[F/(F+M)$ at 28 °C], Conover and Heins 1987a). Sex ratios were calculated by weighting the sex ratio from each replicate by the number of individuals. Measurements of TSD were repeated during an additional year for two populations that experienced high mortality during the common garden rearing (Norfolk, VA and Patchogue, NY). The repeated calculations of TSD were used in the data presented here. Piecewise linear regression was applied to the latitudinal distribution of TSD to determine breakpoints in the form of sex determination. The validity of five models (1 to 5 segments) was assessed using the methods in Hice et al. (2012). Confidence limits (95th percentile) were calculated using Sigmaplot (version 10.1, Systat Software, San Jose, CA, USA).

Related Reference:

Lyndie A. Hice, Tara A. Duffy, Stephan B. Munch and David O. Conover (2014) Spatial scale and divergent patterns of variation in adapted traits in the ocean. *Ecology Letters* 15: 568-575 doi: 10.1111/j.1461-0248.2012.01769.x

Related Datasets:

[Menidia sex ratios - 2 temps](#)
[Temperature-dependent sex ratio of Menidia and SST data](#)

Data Processing Description

BCO-DMO Processing:

- added conventional header with dataset name, PI name, version date, reference information
- renamed parameters to BCO-DMO standard
- replaced blank cells with 'nd'
- removed special characters
- replaced spaces with underscores
- transposed site columns to rows
- added latitude and longitude for each site

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Data Files

File
mean_daily_sst_flat_site.csv (Comma Separated Values (.csv), 355.22 KB) MD5:9d91874024e3d9f280ceeab9ec2e0523
Primary data file for dataset ID 562834

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Parameters

Parameter	Description	Units
site	location of sampling	unitless
lat	latitude; north is positive	decimal degrees
lon	longitude; east is positive	decimal degrees
yrday	year-day of sea surface temperature reading. E.g. January 1 is 1 and November 1 is 305.	unitless
month	month of sea surface temperature reading	unitless
day	day of sea surface temperature reading	unitless
sst	sea surface temperature ; data from Long Term Ecological Research-LTER; Town of Islip shellfish hatchery; and Canadian databases have slightly different notations	degrees Celsius

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Deployments

Conover_lab

Website	https://www.bco-dmo.org/deployment/562661
Platform	lab StonyBrook_Conover
Start Date	2005-01-01
End Date	2008-12-31
Description	Study of fish traits in relation to temperature/latitude.

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Project Information

Local adaptation across latitudes: spatial scales, gene flow, and correlates of countergradient growth variation (Local adaptation in Menidia)

Coverage: Western N. Atlantic, N 30 31' to 47 23' (Florida to Magdalen Islands, Gulf of St. Lawrence)

Description from NSF award abstract:

Knowledge of geographic patterns in adaptive genetic variation is crucial to species conservation, yet in marine systems our understanding of this phenomenon is virtually nil. Until recently, the belief has been that because most marine species have highly dispersive or mobile life stages, local adaptation could occur only on broad geographic scales. This view is supported by comparatively low levels of genetic variation among populations as indexed by surveys of DNA markers neutral to selection. Phenotypic variation is expected to be largely of environmental origin, especially for physiological traits that are highly sensitive to environmental conditions. Stimulated by studies of the Atlantic silverside (*Menidia menidia*) and other species, these long-held beliefs are rapidly changing. The silverside shows dramatic evidence of highly structured local adaptation in a suite of coevolving physiological and morphological traits tightly associated with climate change across latitudes along the east coast of North America. Yet preliminary data from molecular genetic surveys suggest extensive gene flow along the entire latitudinal range.

This project will address two central problems. The first concerns the micro-geography of local adaptation. How finely scaled is it? How is it influenced by gene flow? Is it closely tied to physical features of the coastline? Do multiple traits co-vary similarly along the same gradient? The second problem focuses on the evolution of growth rate, a trait that strongly displays countergradient latitudinal variation not only in the silverside but also in numerous other taxa. Recent experiments show that growth rate can evolve very rapidly in response to

size-selective mortality, including genetic changes caused by fishing. This project will examine the correlates of growth rate evolution. We will study how trade-offs with growth rate influence development, behavior, morphology, and the ability of animals to defend against disease. This research integrates biogeography, physiology, quantitative and molecular genetics, behavior, immunology, and developmental biology. It draws upon natural and experimentally evolved populations, thereby allowing rigorous testing of hypotheses that would be impossible in most other marine species.

PLAN FOR ARCHIVING AND SHARING DATA AND SPECIMENS (from original proposal):

Preserved specimens: Specimens for genetic analysis will be stored whole at -80 C with replicate fin clips stored in 95% ethanol. Each sample from the field collections, those from the common garden experiments, and those from each generation of each population in the size selective harvest experiment will be subdivided and frozen or preserved in alcohol and archived at Stony Brook University and made available to other investigators. **Genetic sequence data:** All unique haplotypes will be submitted to Genbank as a population data set, annotated to reflect the frequency of each haplotype with respect to locality. Data sets will also be made available on Barber's website.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-0425830

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