GenBank accessions and links for sequences of three genes (COI, 16S, H3) for five Elysia spp., chiefly E. pusilla: Vendetti et al (2012) Integ. and Comp. Biol. (PLDvFST project)

Website: https://www.bco-dmo.org/dataset/682268
Data Type: Other Field Results
Version:
Version Date: 2017-01-26

Project
» Quantifying larval behavior to reconcile genetic connectivity with biophysical model predictions (PLDvFST)

Contributors	Affiliation	Role
Krug, Patrick	California State University Los Angeles (Cal State LA)	Principal Investigator
Copley, Nancy	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

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Dataset Description

Sequences for three genes (COI, 16S, H3) were generated for five Elysia species sampled across the Pacific (E. pusilla, E. stylifera) and Caribbean (other species). Collection information, accessions, and links to the GenBank pages are provided.

'did_not_amplify ' means that a locus that did not amplify;
'n/a' means that no amplification was attempted in the present study
'nd' means that the allelic phase was not resolved from genotypic sequence data

Related Reference: Vendetti, J.E., Trowbridge, C.D., and P.J. Krug. 2012. Poecilogony and population genetic structure in Elysia pusilla (Heterobranchia: Sacoglossa), and reproductive data for five sacoglossans that express dimorphisms in larval development. Integrative and Comparative Biology, 52: 138-150. doi: 10.1093/icb/ics077

Methods & Sampling

Purified PCR products were directly cycle-sequenced in both directions using PCR primers and Big Dye Terminator 3.1 Cycle Sequencing chemistry at the High-Throughput Genomics Unit, University of Washington or on an ABI PrismTM 377 DNA Sequencer (Applied Biosystems). Chromatograms were edited and primer sequences removed in GeneiousPro 4.8 software.

For full details on sampling and analytical methodology, see Vendetti et al (2012).

Data Processing Description

Sequences were edited to remove primer sequences.

BCO-DMO Processing notes:
- added conventional header with dataset name, PI name, version date
- modified parameter names to conform with BCO-DMO naming conventions
- added links to NCBI accessions
- replaced hyphens with 'did_not_amplify'
- copied information from previous haplotype or allele to fill out table; if none matched, nd (no data) was entered into blank cells in accession columns

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Data Files

File	
dataset5_Vendetti_2012.csv	(Comma Separated Values (.csv), 12.02 KB) MD5:0c4812c7831ffbb6ab2c37f67474e8b5
Primary data file for dataset ID 682268	

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Parameters

Parameter	Description	Units
species	specimen identifier code	unitless
collection_locality	place of collection	unitless
date_collected	date collected	unitless
specimen_code	in-house specimen identifier	unitless
haplotype_COI	haplotype COI identifier	unitless
accession_COI	COI gene GenBank accession number	unitless
accession_COI_link	link to COI gene GenBank accession page	unitless
haplotype_16S	haplotype 16S identifier	unitless
accession_16S	16S gene GenBank accession number	unitless
accession_16S_link	link to 16S gene GenBank accession page	unitless
Histone_3_allele	Histone 3 allele identifier	unitless
accession_H3	H3 gene GenBank accession number	unitless
accession_H3_link	link to H3 gene GenBank accession page	unitless

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Instruments

Dataset-specific Instrument Name	
Generic Instrument Name	Automated DNA Sequencer
Dataset-specific Description	Big Dye Terminator 3.1 Cycle Sequencing chemistry at the High-Throughput Genomics Unit, University of Washington or on an ABI PrismTM 377 DNA Sequencer (Applied Biosystems).
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	Thermal Cycler
Generic Instrument Description	A thermal cycler or "thermocycler" is a general term for a type of laboratory apparatus, commonly used for performing polymerase chain reaction (PCR), that is capable of repeatedly altering and maintaining specific temperatures for defined periods of time. The device has a thermal block with holes where tubes with the PCR reaction mixtures can be inserted. The cycler then raises and lowers the temperature of the block in discrete, pre-programmed steps. They can also be used to facilitate other temperature-sensitive reactions, including restriction enzyme digestion or rapid diagnostics. (adapted from http://serc.carleton.edu/microbelife/research_methods/genomics/pcr.html)

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Deployments

Krug_lab

Website	https://www.bco-dmo.org/deployment/679311
Platform	Cal State LA
Start Date	2011-09-01
End Date	2016-07-31
Description	Studies on ecology and evolution of marine animals, focusing on larval stages.

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Project Information

Quantifying larval behavior to reconcile genetic connectivity with biophysical model predictions (PLDvFST)

Coverage: Florida and Caribbean

Dispersal is a critical life-history trait linking ecological and evolutionary processes. Transport of planktonic larvae affects colonization success and population persistence for benthic animals, and influences genetic subdivision of populations, local adaptation, and speciation. However, recent studies question the long-held assumption that pelagic larval duration (PLD) determines how far larvae are advected. This has applied significance, as oceanographic models used to predict exchange among marine protected areas often use PLD as the key larval parameter. The investigators' data for Caribbean gastropods show genetic breaks that are not congruent with model predictions, and levels of structure that are inconsistent with larval lifespan, highlighting a need for new theory.

This research will integrate molecular and larval ecology to test the link between dispersal and larval duration in a phylogenetic framework, and determine whether Individual Based Models (IBMs) accurately predict exchange for Caribbean reef ecosystems. The PI will collect multi-locus genetic data and quantify larval behavior for 14 related, ecologically similar species of sea slugs with PLDs from 0-30 days. The PI predicts that larval behavior explains why some species are under- or over-dispersed relative to their PLD; this work will reveal key parameters needed for biophysical-coupling models to predict connectivity for coastal invertebrates. The proposal will address 3 inter-related objectives: (1) Are genetic connectivity estimates from mtDNA and nuclear markers congruent, and consistent with model predictions? Data for mitochondrial and nuclear loci will be used to test for selection on mtDNA, estimate rates of gene flow and times of divergence, and assess levels of connectivity within each species. Matrices of model-predicted exchange will be compared with genetic similarity matrices to test whether breaks in gene flow occur where predicted. (2) Are genetic connectivity and PLD correlated? More broadly, the PI will test the assumption that larval period determines dispersal, using comparative methods in a phylogenetic framework to correct for effects of relatedness among species. The PI will compare models of trait evolution with Bayesian Markov chain Monte Carlo (MCMC) methods to determine if gene flow is correlated or uncorrelated with PLD, using a molecular phylogeny and multi-locus genetic data. (3) Does larval behavior explain genetic structure in species with long PLD? At least two of the focal species selected for this study are under-dispersed, with genetically isolated demes despite a 30-day PLD. Conversely, at least one short-PLD species has no genetic structure over large regions of the Caribbean. The PI will build on past work quantifying larval behavior to ask if species-specific differences in larval swimming facilitate local retention, making species deviate from expected connectivity patterns. The PI will also test whether pre-competent larvae respond to habitat cues in a way that influences dispersal, as occurs in fish. This work will reconcile life-history theory, oceanographic models, and genetics by mechanistically explaining breaks in connectivity; the results will deepen our understanding of how larval behavior can determine the pace of divergence among populations.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1130072

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