Molecular species delimitation and gene flow in Oxynoe (PLDvFST project)

Website: https://www.bco-dmo.org/dataset/715506
Data Type: experimental
Version: 1
Version Date: 2017-09-22

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
Switzer, Megan	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

Abstract
Molecular species delimitation and gene flow in Oxynoe (PLDvFST project)

Table of Contents

Coverage

Temporal Extent: 1974 - 2014

Dataset Description

Species names, sample codes, and collection details for sequenced sea slugs in the family Oxynoidae that were used in phylogenetic analyses. Collections range from 1974 to 2014 from global locations near Florida, the Caribbean, and the East and West Pacific Ocean. Data are accessioned through the NCBI GenBank database.

Methods & Sampling

Purified PCR products were directly cycle-sequenced in both directions using PCR primers and Big Dye Terminator 3.1 Cycle Sequencing chemistry Retrogen, Inc. (San Diego). Chromatograms were edited and primer sequences removed in GeneiousPro 4.8 software. Samples for morphological analysis were deposited in museum collections, sequences were archived in GenBank for public access.

[table of contents | back to top]

Data Files

File
dataset8.csv (Comma Separated Values (.csv), 16.47 KB) MD5:9b4af5b5dcd8d610cf10429207e9d85b Primary data file for dataset ID 715506

[table of contents | back to top]

Related Publications

Berriman, J. S., Ellingson, R. A., Awbrey, J. D., Rico, D. M., Valdés, Á. A., Wilson, N. G., … Krug, P. J. (2018). A biting commentary: Integrating tooth characters with molecular data doubles known species diversity in a lineage of sea slugs that consume “killer algae.” Molecular Phylogenetics and Evolution, 126, 356–370. doi:10.1016/j.ympev.2018.02.027
Results

Krug, P. J., Berriman, J. S., & Valdés, Á. (2018). Phylogenetic systematics of the shelled sea slug genus Oxynoe Rafinesque, 1814 (Heterobranchia : Sacoglossa), with integrative descriptions of seven new species. Invertebrate Systematics, 32(4), 950. https://doi.org/10.1071/is17080 https://doi.org/10.1071/IS17080
Results

[table of contents | back to top]

Parameters

Parameter	Description	Units
species	Species	unitless
isolate_code	Isolate code	unitless
specimen_accession_numbers	Accession numbers. 1AM = Australian Museum (Sydney, Australia) malacology collection; LACM = Los Angeles County Museum of Natural History malacology collection.	unitless
collection_site	Collection site	unitless
date	Date	unitless
collector	Collector's name. AAV = Angel A. Valdes; AH = Alicia Hermosillo; CDT = Cynthia D. Trowbridge; DH = Dai Herbert; DJM = Dustin J. Marshall; MAP = Mark A. Phuong; NGW = Nerida G. Wilson; PJK = Patrick Joseph Krug; RAE = Ryan A. Ellingson; YB = Yan Buske; YMH = Yayoi M. Hirano	unitless
accession_COI	COI gene GenBank accession number	unitless
accession_16S	16S gene GenBank accession number	unitless
accession_H3	H3 gene GenBank accession number	unitless

[table of contents | back to top]

Instruments

Dataset-specific Instrument Name	Automated sequencer
Generic Instrument Name	Automated DNA Sequencer
Dataset-specific Description	Big Dye Terminator 3.1 Cycle Sequencing chemistry Retrogen, Inc. (San Diego)
Generic Instrument Description	A DNA sequencer is an instrument that determines the order of deoxynucleotides in deoxyribonucleic acid sequences.

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)

[table of contents | back to top]

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.

[table of contents | back to top]

Funding

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

[table of contents | back to top]