Supplemental tables for Krug et al (2015) Syst. Biol. (PLDvFST project)

Website: https://www.bco-dmo.org/dataset/679901
Data Type: Other Field Results
Version:
Version Date: 2017-02-01

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

Contributors	Affiliation	Role
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Dataset Description

BCO-DMO versions downloaded from Dryad on 2017-02-01:

Table S1, Sampled taxa and collection details: Table_S1_sampled_taxa_collection_details_v6.doc (323.0 Kb)
Species names, sample codes and collection details for sequenced taxa used in phylogenetic analyses. Blank cells reflect missing information for sequence data obtained from a public database.

Table S2, Developmental character data for Sacoglossa: Table_S2_devel_data_v7_refs.xls (94.20 Kb)
Developmental character data for Sacoglossa including larval development mode, presence/absence and pattern of extra-capsular yolk (ECY), mean egg diameter (± SD), and mean larval shell width (± SD) at hatching. Taxa are listed alphabetically by traditional family within higher clades, and then by binomial name within family. Generic names in quotation marks denote taxa that do not group with most other members of the genus to which they are traditionally assigned.

Table S3, NCBI accession numbers: Table_S3_accession_nos.xls (82.94 Kb)
Accession numbers from the National Center for Bioinformatics database for sequences generated and/or analyzed in this study.

Table S4, BiSSE model fit using a pruned input tree and global estimate of unsampled taxa: Table S4_split_BiSSE_model fit_pcent_missin...xa.doc (40.44 Kb)
Comparison of BiSSE models correcting for missing data with a pruned input tree and one overall estimate of the percentage of unsampled taxa (69%), with either (a) one rate of character change, or (b) rates of reversal (q10) constrained to be rare (<1%) relative to gains of lecithotrophy (q01).

Table S5, BiSSE parameter estimates using a percentage of unsampled taxa to correct for missing data: Table_S5_split_BiSSE_params_pcent_missing_taxa.doc (50.17 Kb)
Maximum-likelihood parameter estimates for BiSSE models, correcting for missing data using an overall percentage of unsampled taxa (69%). The ML tree (Fig. 3) was pruned of terminals missing character data, and used as the input tree for BiSSE analyses with three phylogenetic partitions across Sacoglossa, and either (A) one rate of character change, or (B) rates of reversal to planktotrophy (q10) constrained to be rare (<1%) relative to forward rates (q01). Estimates from the preferred model are bolded, with alternatives shown in descending order of AIC scores.

Table S6, References cited in Table 4: Table_S6_references_v2.doc (37.88 Kb)
References cited in Table 4, from which data on development modes were taken for select clades in Heterobranchia and Caenogastropoda.

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Data Files

File
suppl_tables.csv (Comma Separated Values (.csv), 871 bytes) MD5:1938fb67b66d5d5aae6def4dfc093c9d
Primary data file for dataset ID 679901

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Related Datasets

Results

Krug, P. J., Vendetti, J. E., Ellingson, R. A., Trowbridge, C. D., Hirano, Y. M., Trathen, D. Y., … Valdés, Á. A. (2015). Data from: Species selection favors dispersive life histories in sea slugs, but higher per-offspring investment drives shifts to short-lived larvae [Data set]. Dryad Digital Repository. https://doi.org/10.5061/dryad.88mv3.2

Different Version

Krug, P. J., Vendetti, J. E., Ellingson, R. A., Trowbridge, C. D., Hirano, Y. M., Trathen, D. Y., … Valdés, Á. A. (2015). Data from: Species selection favors dispersive life histories in sea slugs, but higher per-offspring investment drives shifts to short-lived larvae [Data set]. Dryad Digital Repository. https://doi.org/10.5061/dryad.88mv3.2

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Parameters

Parameter	Description	Units
suppl_table	Supplemental Table number	unitless
table_link	link to download file	unitless
size_kb	file size	kilobytes
description	description of data in the file	unitless

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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.

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.

Funding

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