

GenBank accession links to DNA sequences for 4 genes (COI, 16S, 28S, H3) from ~200 species of order Sacoglossa: Krug et al (2015) Syst. Biol. Supp. Table 3 (PLDvFST project)

Website: <https://www.bco-dmo.org/dataset/682475>

Data Type: Other Field Results

Version:

Version Date: 2017-02-08

Project

» [Quantifying larval behavior to reconcile genetic connectivity with biophysical model predictions](#) (PLDvFST)

| Contributors | Affiliation | Role |
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Dataset Description

This dataset includes species names, sample codes and GenBank accession links for genes COI, 16S, 28S, H3 for ~200 species of order Sacoglossa (Gastropoda).

Related Reference:

Supplemental Table 3 from Krug, P.J., Vendetti, J.E., Ellingson, R.A., Trowbridge, C.D., Hirano, Y.M., Trathen*, D.Y., Rodriguez*, A.K., Swennen, C., Wilson, N.G., and A.A. Valdés. Species selection favors dispersive life histories in sea slugs, but higher per-offspring investment drives shifts to short-lived larvae. *Systematic Biology* (2015) 64(6): 983-999.

DOI: <https://doi.org/10.1093/sysbio/syv046>

These data are also available from Krug PJ, Vendetti JE, Ellingson RA, Trowbridge CD, Hirano YM, Trathen DY, Rodriguez AK, Swennen C, Wilson NG, Valdés AA (2015) Data from: Species selection favors dispersive life histories in sea slugs, but higher per-offspring investment drives shifts to short-lived larvae. Dryad Digital Repository. <http://dx.doi.org/10.5061/dryad.88mv3.2>

Taxa arranged according to traditional systematics as given in Table S2.

Methods & Sampling

For full details on sampling and analytical methodology, see Krug et al, *Systematic Biology*, 2015.

The data were for a global study of diversity in clade Sacoglossa; all temperate and tropical oceans were sampled. Specimens came from the authors' collections or from museum collections.

Excerpt: "For one to two exemplars per taxon, portions of four loci were sequenced: (i) COI; (ii) mitochondrial large ribosomal subunit rRNA (16S); (iii) nuclear histone III (H3); and (iv) nuclear large ribosomal subunit rRNA (28S). Amplifications and sequencing followed published protocols, with 28S amplified as three overlapping

fragments and assembled prior to alignment (Krug et al. 2008; Händeler et al. 2009). Data matrix completeness was 94% (840 cells, locus × taxon). Initial alignments of all loci were done using MUSCLE with default settings in Geneious v6.1.6. Based on published models for rRNA genes (Lydeard et al. 2000; Medina and Walsh 2000; Mallatt et al. 2010), we developed secondary structure models to refine alignments of 16S (Supplementary Figs. S1 and S2) and 28S (Supplementary Fig. S3). Adjustments were made by eye to maintain predicted base pairing interactions in stem regions conserved across Mollusca. Loop regions of ambiguous alignment were removed, as were sequence blocks masked by the least stringent criteria in Gblocks v.0.91b (Castresana 2000). Final aligned sequence partitions were 658 bp (COI), 404 bp (16S), 1392 bp (28S), and 328 bp (H3); NCBI accession numbers are given in Supplementary Table S3. Individual gene trees were built for all loci using Bayesian Inference (BI) and maximum likelihood (ML) as detailed below, to ensure no rogue sequences or unstable taxa were included; topologies were consistent among gene trees except in unresolved regions (Supplementary Fig. S4a-d)."

Data Processing Description

BCO-DMO Processing notes:

- added conventional header with dataset name, PI name, version date
- modified parameter names to conform with BCO-DMO naming conventions
- replaced '-' with nd (no data). These did not amplify successfully
- added clade and family columns
- added links to GenBank accession pages

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Data Files

| File |
|---|
| dataset1_tableS3.csv (Comma Separated Values (.csv), 98.38 KB) MD5:2a772c571d0ba00526397ce5f63c37fe |
| Primary data file for dataset ID 682475 |

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Parameters

| Parameter | Description | Units |
|---------------------|---|----------|
| clade | taxonomic clade | unitless |
| family | taxonomic family | unitless |
| species | species name | unitless |
| sample_code | sample identifier | unitless |
| collection_locality | place of collection | unitless |
| collector | collector's name | unitless |
| date_collected | date collected | 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 |
| accession_COI_link | link to COI gene GenBank accession page | unitless |
| accession_16S_link | link to 16S gene GenBank accession page | unitless |
| accession_H3_link | link to H3 gene GenBank accession page | 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. |

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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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