

Genetic Identification of Planktotrophic Gastropod Veligers from Hawai'i Surface Slicks

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Introduction

- Surface slicks are patches of smooth surface water that act as biodiversity hotspots
- Provide nursery habitat for marine larvae including fish and invertebrates

Methods

- Sample collection:
 - Snails sorted from trawl samples that targeted surface slicks
- DNA Extractions:
 - Extractions performed on morphologically distinct snails
- Polymerase Chain Reaction (PCR):
 - Using Folmer (1994) primers to amplify the cytochrome c oxidase I (COI) gene fragment
- Agarose Mini-Gel Electrophoresis:
 - To visualize successful amplification
- Sanger Sequencing:
 - Sequences produced were blasted via NCBI GenBank Database using the Blastn function
- Phylogenetic analysis:
 - Matches determined w/reciprocal monophyly b/t our seq fragments and top GenBank matches
- Protoconch analysis:
 - Photomicrographs recorded for morphology analysis

Results

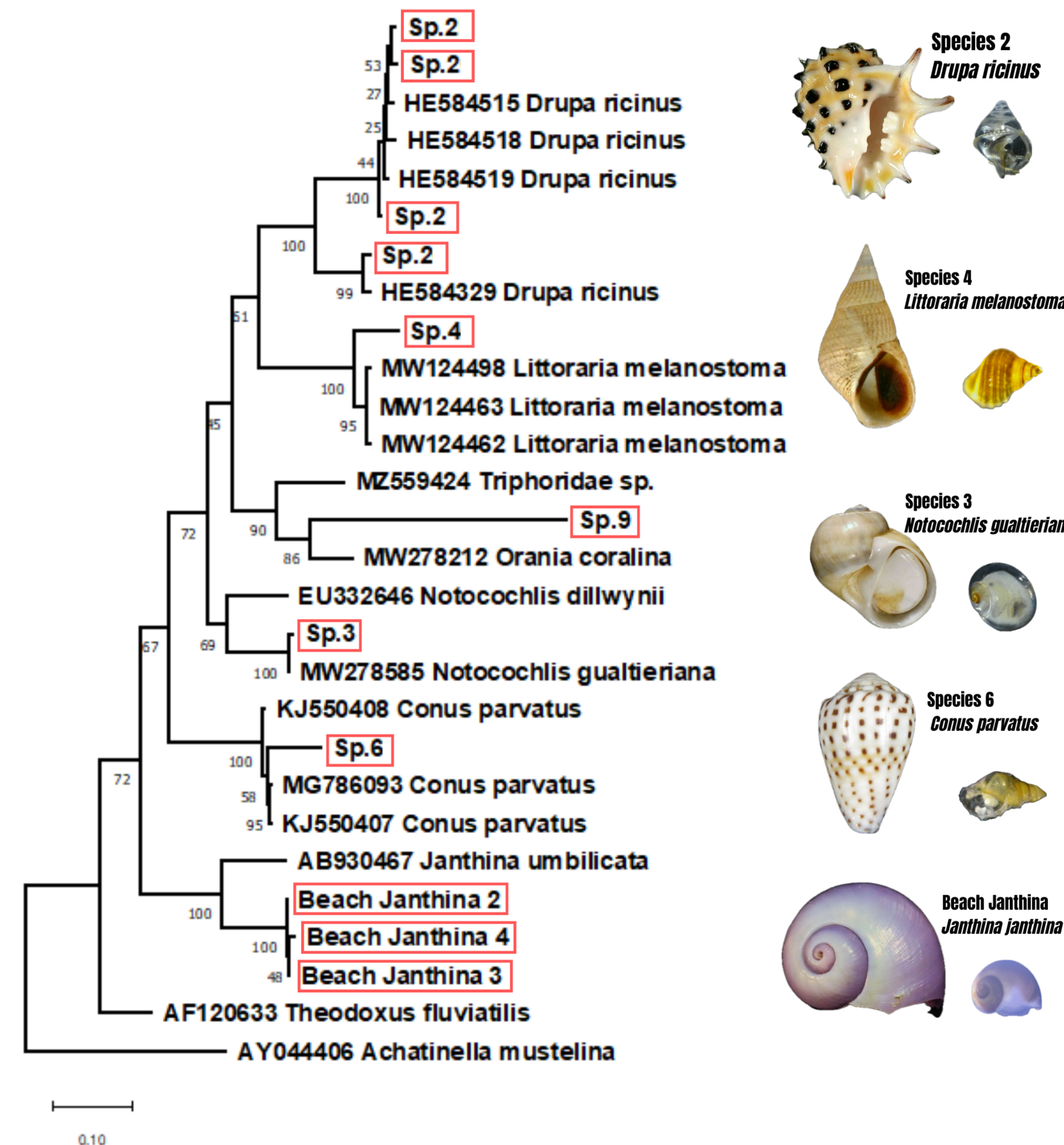


Figure 1. Phylogenetic Analysis. Tree was generated using Maximin-Likelihood and Hasegawa-Kishino-Yano model with 1000 bootstrap replicates. Operational taxonomic units w/ red boxes are surface slick larval snails: Sp. 2,3,4, and 6, and snails collected on Oahu's windward side, Beach Janthina 2,3, and 4. Additional sequences were from NCBI GenBank. Images depict surface slick protoconch veliger shells (right column) and adult shells of closest GenBank matches (left column).

• Genus level identifications:

- Littorinidae - Sp.4
- Janthinidae - Beach Janthina 2, 3, and 4
- Conidae - Sp.6

• Species level identifications:

- *Drupa ricinus* - Sp.2
- *Notocochlis gualtieriana* - Sp.3
- Sequence for species 9 does not show a close match to any GenBank sequence

Discussion

- Planktotrophic larvae sampled represent Hawaii intertidal marine gastropods
- Well-supported sister clades of *Drupa ricinus* samples represent two distinct populations
- Morphological assessment of Beach Janthina samples suggest it is *J. janthina*, a species lacking representative COI sequences in GenBank
- COI data for species 9 not currently providing a strong match and warrants additional sampling
- Assessment of shell characters was used with COI sequences because different biological species can, though rare, share haplotypes

Acknowledgements

- Advisor: Dr. Brenden Holland
- Dr. Matthew Iacchei, HPU
- Dr. Jessica Jacob, HPU
- Funding sources:
 - INBRE Hawaii
 - HUI SRC
- Author affiliations: 1. HPU; 2. NOAA; 3. Bailey-Matthews National Shell Museum & Aquarium; 4. Ocean Research Explorations



This project was supported by grants from the National Institutes of Health (NIH), National Institute of General Medical Sciences (NIGMS), IDeA Networks of Biomedical Research Excellence (INBRE), Award number: P20GM103466. The content is solely the responsibility of the authors and do not necessarily represent the official views of the National Institutes of Health