

# Accession numbers with links to GenBank sequences of labyrinthulomycete 18S rRNA genes from sediment and water column samples collected around Long Island, NY from 2005-2008 (LabyLI project)

**Website:** <https://www.bco-dmo.org/dataset/3974>

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## Project

» [Labyrinthulomycete diversity and abundance](#) (LabyLI)

Contributors	Affiliation	Role
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## Dataset Description

Accession numbers with links to GenBank sequences of labyrinthulomycete 18S rRNA genes from sediment and water column samples collected around Long Island, NY.

Collado Mercado et al, 2010 ABSTRACT: Labyrinthulomycetes (Labyrinthulea) are ubiquitous marine osmoheterotrophic protists that appear to be important in decomposition of both allochthonous and autochthonous organic matter. We used a cultivation-independent method based on the labyrinthulomycete-specific primer LABY-Y to PCR amplify, clone, and sequence 68 nearly full-length 18S rDNA amplicons from 4 sediment and 3 seawater samples collected in estuarine habitats around Long Island, New York, USA. Phylogenetic analyses revealed that all 68 amplicons belonged to the Labyrinthulea. Only 15 of the 68 amplicons belonged to the thraustochytrid phylogenetic group (Thraustochytriidae). None of these 15 were similar to cultivated strains, and 11 formed a novel group. The remaining 53 amplicons belonged either to the labyrinthulid phylogenetic group (Labyrinthulidae) or to other families of Labyrinthulea that have not yet been described. Of these amplicons, 37 were closely related to previously cultivated *Aplanochytrium* spp. and *Oblongichytrium* spp. Members of these 2 genera were also cultivated from 1 of the sediment samples. The 16 other amplicons were not closely related to cultivated strains, and 15 belonged to 5 groups of apparently novel labyrinthulomycetes. Most of the novel groups of amplicons also contained environmental sequences from surveys of protist diversity using universal 18S rDNA primers. Because the primer LABY-Y is biased against several groups of labyrinthulomycetes, particularly among the thraustochytrids, these results may underestimate the undiscovered diversity of labyrinthulomycetes.

## Methods & Sampling

Approximate sampling positions (latitude and longitude) were determined from navigational maps.

## Data Processing Description

See:

Collado Mercado, E., J. C. Radway, and J. L. Collier. 2010. Novel uncultivated labyrinthulomycetes revealed by 18S rDNA sequences from seawater and sediment samples. *Aquatic Microbial Ecology* 58: 215-228. [\[pdf\]](#)

Sequence accession numbers deposited in GenBank are indicated in the data file via hyperlinks.

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## Data Files

File
<b>labyLI.csv</b> (Comma Separated Values (.csv), 12.84 KB) MD5:fb89908aed6141c7c0ab976f4f4057ee Primary data file for dataset ID 3974

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## Parameters

Parameter	Description	Units
sample	sample identification	unitless
sample_type	type of sample: water or sediment	unitless
date	collection data: local time	dd-mmm-yyyy
site	collection site	unitless
lat	approximate latitude; north is positive	decimal degrees
lon	approximate longitude; east is positive	decimal degrees
depth_w	bottom depth	meters
size_fraction	size fraction of water samples	microns
sediment_description	sediment description	unitless
clone_number	clone identification number	unitless
accession_number	GenBank accession number	unitless

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## Deployments

### lab\_SBU\_Collier

<b>Website</b>	<a href="https://www.bco-dmo.org/deployment/59045">https://www.bco-dmo.org/deployment/59045</a>
<b>Platform</b>	Long_Island_shore
<b>Start Date</b>	2005-10-13
<b>End Date</b>	2008-04-29
<b>Description</b>	Water and sediment collections from around Long Island, NY, for laboratory-based study.

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## Project Information

### Labyrinthulomycete diversity and abundance (LabyLI)

**Coverage:** Long Island, NY, USA

*The following description is an excerpt from the NSF award abstract:*

The Labyrinthulomycetes (labyrinthulids, thraustochytrids, and aplanochytrids) are ubiquitous, diverse, and abundant marine protists. They are thought to live mainly as saprobes, obtaining their nutrition from non-living particulate organic matter (POM) of algal, higher plant, or animal origin. Thus, while Labyrinthulomycetes are not "fungi" in a taxonomic sense, they may function as "fungi" in an ecological sense, playing similar roles in the decomposition of POM. Because of their high content of essential polyunsaturated fatty acids (PUFAs), Labyrinthulomycetes may also play a role in the nutrition of marine metazoans by improving the food quality of detritus ("trophic upgrading"). However, evidence of their role decomposing marine POM is somewhat circumstantial, and thus does not support quantitative conclusions about their function or importance. The long-term goal of this project is to gather the evidence about Labyrinthulomycete abundance and diversity that will be needed to better understand their role in marine ecosystems.

This project aims to develop molecular genetic methods based on the polymerase chain reaction (PCR) to investigate the diversity and abundance of Labyrinthulomycetes. The existing Labyrinthulomycete-specific PCR primers for 18S ribosomal DNA (rDNA) cannot recognize a potentially important component of Labyrinthulomycete diversity (some groups of thraustochytrids). The investigators will develop new 18S rDNA primers that will allow better estimation of the diversity of the Labyrinthulomycetes, and then use these primers to gather 18S rDNA sequence data from a variety of habitats. The resulting sequence data will diversity of these organisms to be quantified in the field relative to the representatives currently in culture. These primers (or others designed in the course of the project) will be used to develop quantitative real-time PCR assays to determine the abundance of Labyrinthulomycetes (and subgroups of Labyrinthulomycetes) in environmental samples. Methods will also be developed to cultivate novel Labyrinthulomycetes detected in local sediments during the preliminary sequencing efforts.

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## Funding

Funding Source	Award
<a href="#">NSF Division of Ocean Sciences (NSF OCE)</a>	<a href="#">OCE-0726702</a>

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