

# Phylogenetic Analysis of Co-diversification Between the Bacterial Order Oceanospirillales and Anthozoans

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## Abstract

Associations between marine organisms and prokaryotes have been widely studied. One of these associations is the interaction between anthozoans (mainly reef-building coral species) and bacteria. One order of bacteria, Oceanospirillales, has been shown to compose a large portion of the bacterial consortium associated with many species of corals. This study analyzed the co-diversification patterns of Oceanospirillales between coral species through a culture independent method. We used 16S ribosomal DNA sequences for inferring phylogenetic relationships among the different identified strains of Oceanospirillales from both hard and soft corals. Sequences were collected from scientific literature relevant to Oceanospirillales and used to construct Maximum Likelihood and Bayesian Inference phylogenetic trees.

The resultant grouping of species demonstrated a high species selectivity pattern, which suggests there is non-random assortment of Oceanospirillales depending on the coral species, additionally clades appear to be separated by a predominant coral species. Furthermore, there is a distinctive separation between hard and soft corals, which may support the hypothesis of co-diversification at higher taxonomic level.



<http://reefguide.org/mustardhill.html>



<http://www.scientificamerican.com/slideshow/gulf-oil-eating-microbes-slide-show/>



<http://reefal33.overblog.com/acropora>



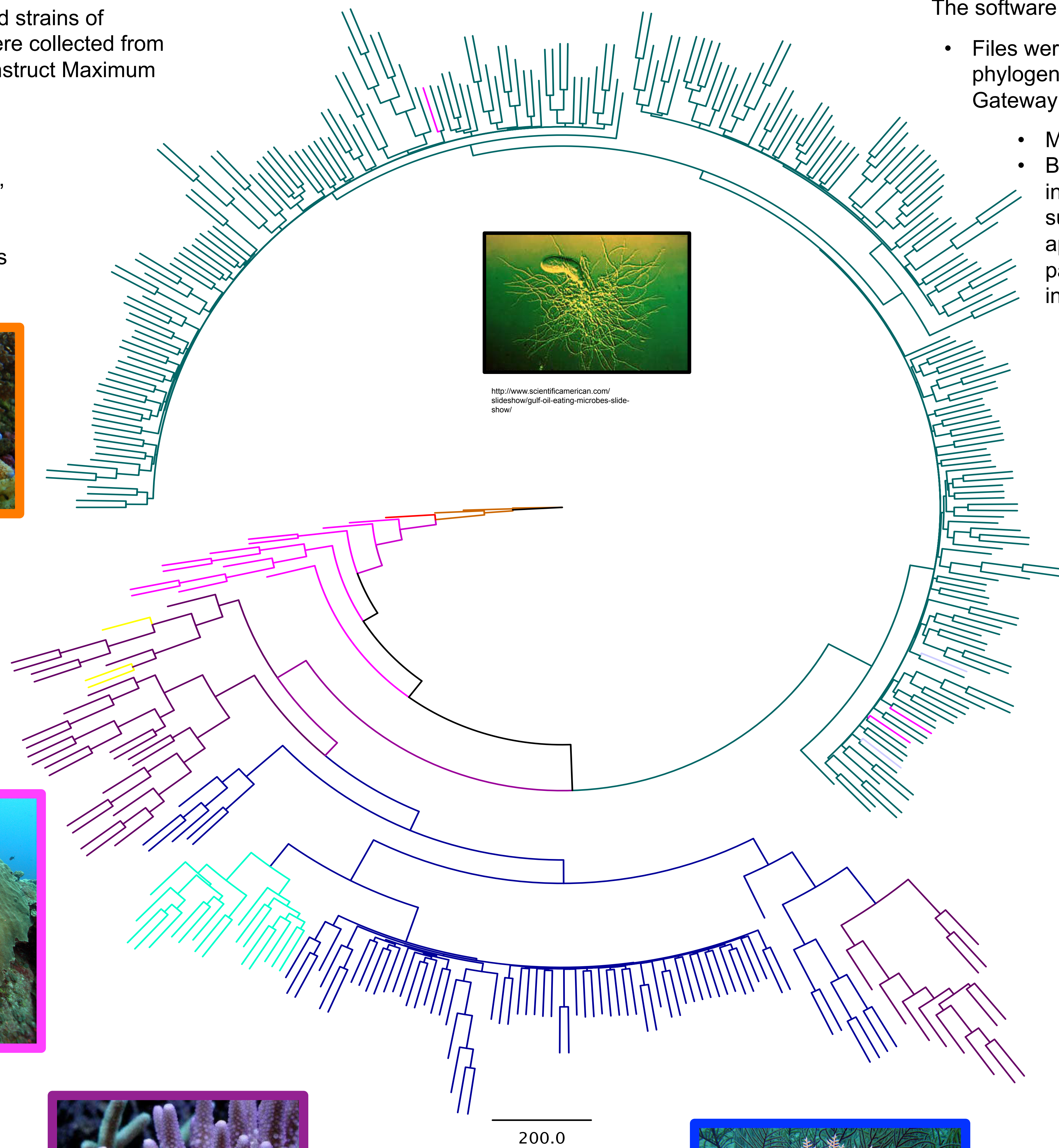
<http://forum.marinedepot.com/PrintTopic37429.aspx>



<http://flowergarden.noaa.gov/about/cnidarianlist.html>

## Legend

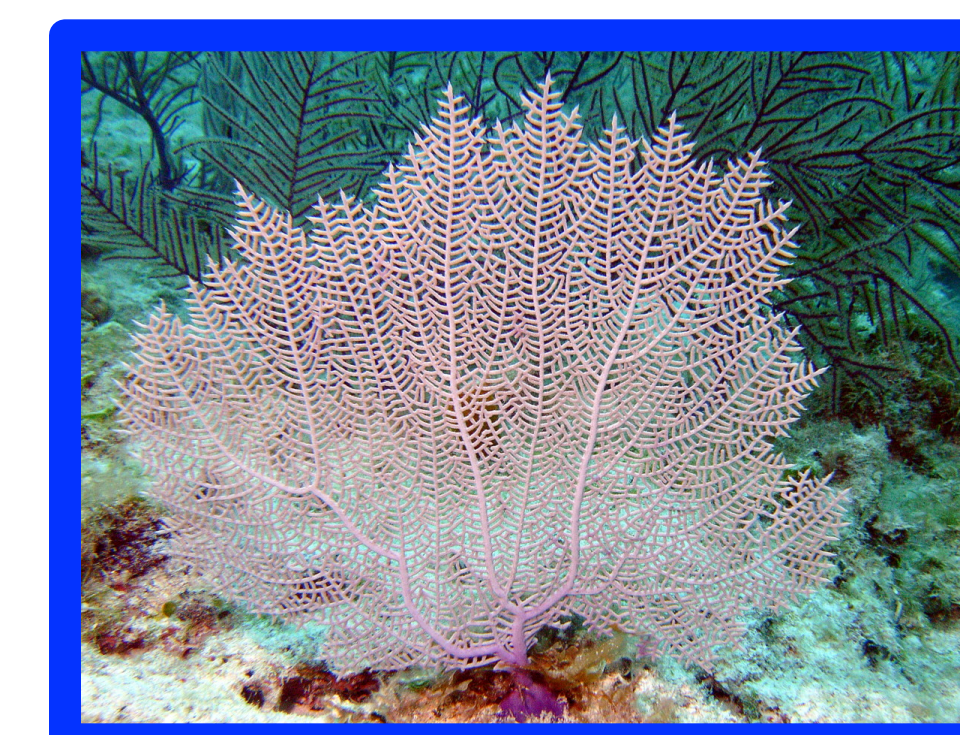
- *Porites astreoides*
- *Acropora humilis*
- *Orbicella faveolata*
- *Eunicella cavolini*
- *Gorgonia ventalina*
- *Acropora digitifera*
- *Muricea elongata*



<http://animal-world.com/Aquarium-Coral-Reefs/Finger-Staghorn-Coral>



<http://www.nonsolomaldive.net/galerie/Catalfuria/slides/045%20Eunicella%20Cavolini.html>



<http://reefguide.org/pv/commentair5.pg>

## Methods

- 16S Ribosomal DNA sequences of Oceanospirillales bacteria associated with corals and softcorals were obtained from NCBI accession numbers found in relevant scientific literature. These sequences were then used as queries to continue mining the NCBI GenBank database, and only those belonging to Oceanospirillales and associated with corals and softcorals were included in the data set. The classification of each sequence was also confirmed using the classification algorithm of the Ribosomal Database Project (1).
- From the original sequence data set, only sequences of >700 base pairs were kept for further analyses. The software utilized for the sequence alignment was MAFFT (2).
- Files were formatted to Phylip and Nexus for Maximum Likelihood (ML) and Bayesian Inference (BI) phylogenetic methods, respectively. The two phylogenies were constructed on the CIPRES Science Gateway portal (3).
  - ML phylogenies were built using RAxML (4) with 858 bootstrap replicates.
  - BI analysis were conducted in Mr. Bayes (5) on XSEDE. The model for this analysis included Invariant Gamma rate variation with six substitutions and 4x4 nucleotide substitution model. Parameters also include a Markov Chain Monte Carlo (MCMC) approach with 1,000,000 generations and sampled every 100<sup>th</sup> cycles. The burn-in parameter was set at 25% of the sampled trees. The trees were viewed and later modified in FigTree (6).

## Results

- The superimposition of host identity on the bacterial 16S rDNA phylogenetic tree reveals a pattern of co-diversification between Anthozoan hosts and Oceanospirillales bacteria.
- There is a distinct pattern of bacterial clade separation amongst each predominant coral host species.
- The phylogenetic trees show an evolutionary divergence of bacteria associated between hard and soft corals.

## Conclusions

- The high specificity level of association between bacteria and anthozoan hosts suggests that there is a non-random assortment and therefore, there may be certain evolutionary advantages when it comes to choosing a coral host.
- There is a distinctive separation of the Oceanospirillales bacteria hosted between hard and soft corals, which may support the hypothesis of co-diversification at higher taxonomic level. Alternatively, this separation may be driven by geographical factors; certain environmental conditions may act as an evolutionary pressure that is reflected on the affinity of the order Oceanospirillales for certain coral species.

## Relevant references

- Speck MD, et al. (2012) *Widespread Oceanospirillaceae Bacteria in Porites spp.* Journal of Marine Biology, Article ID 746720.
- Rodriguez-Lanetty M, et al. (2013) *Ecological Inferences from a deep screening of the Complex Bacterial Consortia associated with the coral, Porites astreoides.* Molecular Ecology 22: 4349–4362.
- Morrow KM, et al. (2012) *Bacterial associates of two Caribbean coral species reveal species-specific distribution and geographic variability.* Applied and Environmental Microbiology 78: 6438–6449.

## Introduction

- The bacterial order, Oceanospirillales makes up a large portion of the bacterial consortium in many species of corals, specifically *Porites astreoides*.
- In order to better aid coral conservation efforts, we must first understand the highly complex symbiotic relationship between microbes and the coral host. This phylogenetic analysis illustrates the co-evolving relationship of this symbiosis.
- A non-random distribution of the bacterial consortium could suggest a pattern of evolutionary advantage between the coral host and the bacterial order.