

# Facultative Lifestyle Drives Diversity of Coral Alga Symbionts

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## Supplemental information

In our summary analysis, raw ITS2 data (BioProject: PRJNA761780) from 119 *Pocillopora acuta* and 132 *Montipora capitata* colonies collected from Kāneʻohe Bay, Hawaiʻi were retrieved from the Sequence Read Archive using fasterq-dump (sra-tools v3.0.3; <https://github.com/ncbi/sra-tools>) and processed using a local version of SymPortal v0.3.24 [1]. After minimum entropy decomposition (hereinafter, post-MED sequences), but before grouping into ITS2 type profiles, sequences were extracted from the Hawaiian sample results and from the list of published studies with data available *via* the SymPortal website (<https://symportal.org/>). The extracted post-MED sequences were aligned using MAFFT v7.453 ('--auto'; strategy FFT-NS-2 was chosen automatically by MAFFT) [2] and a maximum likelihood tree was constructed using iqtree v1.6.12 ('-bb 1000') [3] using the default (HKY) DNA substitution model and 1000 Ultrafast Bootstrap replicates (UFboot) [4].

## References

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3. Nguyen, L.T. *et al.* (2015) IQ-TREE: a fast and effective stochastic algorithm for estimating maximum-likelihood phylogenies. *Mol. Biol. Evol.* 32, 268–274.  
<https://doi.org/10.1093/molbev/msu300>
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