Caribbean Candidatus Aquarickettsia rohweri metagenome-assembled genomes

Website: https://www.bco-dmo.org/dataset/924330
Data Type: experimental, Synthesis
Version: 1
Version Date: 2024-04-03

Project
» Collaborative Research: Tracking the interacting roles of the environment, host genotype, and a novel Rickettsiales in coral disease susceptibility (Coral Rickettsiales)

Contributors	Affiliation	Role
Vega Thurber, Rebecca	Oregon State University (OSU)	Principal Investigator
Muller, Erinn M.	Mote Marine Laboratory (Mote)	Co-Principal Investigator
Baker, Lydia	Oregon State University (OSU)	Scientist
Klinges, Grace J.	Oregon State University (OSU)	Scientist
Gerlach, Dana Stuart	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

Abstract
The symbiont “Candidatus Aquarickettsia rohweri” infects a diversity of aquatic hosts. In the threatened Caribbean coral, Acropora cervicornis, Aquarickettsia proliferates in response to increased nutrient exposure, resulting in suppressed growth and increased disease susceptibility and mortality of coral. This study evaluated the extent, as well as the ecology and evolution of Aquarickettsia infecting threatened corals, Ac. cervicornis, and Ac. palmata and their hybrid (“Ac. prolifera”). Aquarickettsia was found in all acroporids, with coral host and geographic location impacting the infection magnitude. Phylogenomic and genome-wide single-nucleotide variant analysis of Aquarickettsia found phylogenetic clustering by geographic region, not by coral taxon. Analysis of Aquarickettsia fixation indices suggests multiple sequential infections of the same coral colony are unlikely. Furthermore, relative to other Rickettsiales species, Aquarickettsia is undergoing positive selection, with Florida populations experiencing greater positive selection relative to other Caribbean locations. This may be due in part to Aquarickettsia proliferating in response to greater nutrient stress in Florida, as indicated by greater in situ replication rates in these corals. Aquarickettsia was not found to significantly codiversify with either the coral animal or the coral’s algal symbiont (Symbiodinium “fitti”). Quantitative PCR analysis showed that gametes, larvae, recruits, and juveniles from susceptible, captive-reared coral genets were not infected with Aquarickettsia. Thus, horizontal transmission of Aquarickettsia via coral mucocytes or an unidentified host is more likely. The prevalence of Aquarickettsia in Ac. cervicornis and its high abundance in the Florida coral population suggests that coral disease mitigation efforts focus on preventing early infection via horizontal transmission.

Table of Contents

[table of contents | back to top]

Related Publications

Baker, L. J., Reich, H. G., Kitchen, S. A., Klinges, J. G., Koch, H. R., Baums, I. B., Muller, E. M., & Thurber, R. V. (2021). The coral symbiont Candidatus Aquarickettsia is variably abundant in threatened Caribbean acroporids and transmitted horizontally. The ISME Journal, 16(2), 400–411. https://doi.org/10.1038/s41396-021-01077-8
Results

Bankevich, A., Nurk, S., Antipov, D., Gurevich, A. A., Dvorkin, M., Kulikov, A. S., … Pevzner, P. A. (2012). SPAdes: A New Genome Assembly Algorithm and Its Applications to Single-Cell Sequencing. Journal of Computational Biology, 19(5), 455–477. doi:10.1089/cmb.2012.0021
Software

Bateman, A., Martin, M.-J., Orchard, S., Magrane, M., Ahmad, S., Alpi, E., Bowler-Barnett, E. H., Britto, R., Bye-A-Jee, H., Cukura, A., Denny, P., Dogan, T., Ebenezer, T., Fan, J., Garmiri, P., da Costa Gonzales, L. J., Hatton-Ellis, E., Hussein, A., … Zhang, J. (2022). UniProt: the Universal Protein Knowledgebase in 2023. Nucleic Acids Research, 51(D1), D523–D531. https://doi.org/10.1093/nar/gkac1052
Software

Bushnell, B. (2014). BBMap: A Fast, Accurate, Splice-Aware Aligner. Lawrence Berkeley National Laboratory. LBNL Report #: LBNL-7065E. Retrieved from https://escholarship.org/uc/item/1h3515gn
Software

Camacho, C., Coulouris, G., Avagyan, V., Ma, N., Papadopoulos, J., Bealer, K., & Madden, T. L. (2009). BLAST+: architecture and applications. BMC Bioinformatics, 10(1). doi:10.1186/1471-2105-10-421
Software

Conway, J. R., Lex, A., & Gehlenborg, N. (2017). UpSetR: an R package for the visualization of intersecting sets and their properties. Bioinformatics, 33(18), 2938–2940. https://doi.org/10.1093/bioinformatics/btx364
Software

Emms, D. M., & Kelly, S. (2019). OrthoFinder: phylogenetic orthology inference for comparative genomics. Genome Biology, 20(1). https://doi.org/10.1186/s13059-019-1832-y
Software

Finn, R. D., Clements, J., & Eddy, S. R. (2011). HMMER web server: interactive sequence similarity searching. Nucleic Acids Research, 39(suppl), W29–W37. https://doi.org/10.1093/nar/gkr367
Software

Kitchen, S. A., Ratan, A., Bedoya-Reina, O. C., Burhans, R., Fogarty, N. D., Miller, W., & Baums, I. B. (2019). Genomic Variants Among ThreatenedAcroporaCorals. G3 Genes|Genomes|Genetics, 9(5), 1633–1646. https://doi.org/10.1534/g3.119.400125
Methods

Klinges, J. G., Rosales, S. M., McMinds, R., Shaver, E. C., Shantz, A. A., Peters, E. C., Eitel, M., Wörheide, G., Sharp, K. H., Burkepile, D. E., Silliman, B. R., & Vega Thurber, R. L. (2019). Phylogenetic, genomic, and biogeographic characterization of a novel and ubiquitous marine invertebrate-associated Rickettsiales parasite, Candidatus Aquarickettsia rohweri, gen. nov., sp. nov. The ISME Journal, 13(12), 2938–2953. https://doi.org/10.1038/s41396-019-0482-0
Results
,
Methods

Langmead, B., & Salzberg, S. L. (2012). Fast gapped-read alignment with Bowtie 2. Nature Methods, 9(4), 357–359. doi:10.1038/nmeth.1923
Software

Lee, I., Ouk Kim, Y., Park, S.-C., & Chun, J. (2016). OrthoANI: An improved algorithm and software for calculating average nucleotide identity. International Journal of Systematic and Evolutionary Microbiology, 66(2), 1100–1103. https://doi.org/10.1099/ijsem.0.000760
Software

Mukhopadhyay, C.S. and Choudhary, R.K (2017) BLASTx. In C.S. Mukhopadyay, R.K. Choudhary, & M.A. Iquebal (Eds.) Basic Applied Bioinformatics (Chapter 14, p.103-108). Hoboken, New Jersey: John Wiley & Sons, Inc (Wiley) https://isbnsearch.org/isbn/9781119244417
Software

Parks, D. H., Imelfort, M., Skennerton, C. T., Hugenholtz, P., & Tyson, G. W. (2015). CheckM: assessing the quality of microbial genomes recovered from isolates, single cells, and metagenomes. Genome Research, 25(7), 1043–1055. https://doi.org/10.1101/gr.186072.114
Software

Reich, H. G., Kitchen, S. A., Stankiewicz, K. H., Devlin-Durante, M., Fogarty, N. D., & Baums, I. B. (2021). Genomic variation of an endosymbiotic dinoflagellate (Symbiodinium ‘fitti’) among closely related coral hosts. Molecular Ecology, 30(14), 3500–3514. Portico. https://doi.org/10.1111/mec.15952
Methods

Seemann, T. (2014). Prokka: rapid prokaryotic genome annotation. Bioinformatics, 30(14), 2068–2069. https://doi.org/10.1093/bioinformatics/btu153
Software

[table of contents | back to top]

Related Datasets

IsRelatedTo

Oregon State University. Candidatus Aquarickettsia rohweri strain:a_cerv_44 Genome sequencing and assembly. 2018/12. In: BioProject [Internet]. Bethesda, MD: National Library of Medicine (US), National Center for Biotechnology Information; 2011-. Available from: http://www.ncbi.nlm.nih.gov/bioproject/PRJNA507282. NCBI:BioProject: PRJNA507282.

Oregon State University. Caribbean Candidatus Aquarickettsia rohweri metagenome-assembled genomes. 2020/09. In: BioProject [Internet]. Bethesda, MD: National Library of Medicine (US), National Center for Biotechnology Information; 2011-. Available from: http://www.ncbi.nlm.nih.gov/bioproject/PRJNA666461. NCBI:BioProject: PRJNA666461.

[table of contents | back to top]

Parameters

Parameters for this dataset have not yet been identified

[table of contents | back to top]

Project Information

Collaborative Research: Tracking the interacting roles of the environment, host genotype, and a novel Rickettsiales in coral disease susceptibility (Coral Rickettsiales)

Coverage: at Oregon State University and in the Florida Keys at Mote Marine Laboratory

NSF Award Abstract:
Historically one of the most abundant reef-building corals in Florida and the wider Caribbean, the staghorn coral, *Acropora cervicornis*, is now listed as critically endangered primarily because of previous and reoccurring disease events. Understanding the holistic mechanisms of disease susceptibility in this coral is a top concern of practitioners engaged in conservation and restoration. The investigators recently discovered a group of parasitic bacteria common within the microbial community of *A. cervicornis* that can reduce the growth and health of corals when reefs are exposed to nutrient polluted waters. Determining how interactions among the coral host, this parasitic microbe, and the environment are linked to disease susceptibility provides critical insight and greater success of future restoration efforts. Yet the complexity of animal microbiomes and the contextual nature of disease make it difficult to identify the specific cause of many disease outbreaks. In this project, the investigators conduct experiments to explore the interactions among different genetic strains of coral and these bacteria in various nutrient scenarios to better understand how this bacterium affects the susceptibility of staghorn coral to diseases. This project also characterizes the genomics, host range, and local and global distribution of this bacterial coral parasite to determine how its evolutionary history and physiology drive disease susceptibility in this important coral species. The project trains two postdocs, one technician, and seven students (one graduate, six undergraduates) in integrative sciences that span marine science, physiology, genetics, microbiology, omics, and statistical modeling. A research-based after school program in Florida is expanded to include microbiology and create a new program module called Microbial warriors, with a focus on women in science. The investigators produce documentary style films and outreach materials to broadly communicate the project science and conservation efforts to local and national communities via presentations at Mote Marine Lab and the Oregon Museum of Science and Industry. This project is co-funded by the Biological Oceanography Program in the Division of Ocean Sciences and the Symbiosis, Defense, and Self-recognition Program in the Division of Integrative Organismal Systems.

The investigators recently identified a marine *Rickettsiales* bacterium that, in corals, can be stimulated to grow in the presence of elevated nitrogen and phosphorous species. Based on genomic reconstruction and phylogeography, this bacteria is classified as a novel bacterial genus, *Candidatus Aquarickettsia*, and showed that it is broadly associated with scleractinian corals worldwide. Importantly, using a model system, the endangered *Acropora cervicornis* coral, the team has also shown that the growth of this bacterium in vivo is associated with reduced host growth and increased disease susceptibility. This project aims to more completely evaluate the mechanisms behind and impacts of these inducible infections on coral physiology and host-bacterial symbiosis. The investigators conduct nutrient dosing experiments on different coral genotypes with various *Rickettsiales* abundances. Using a range of omics and microscopy techniques, the team quantifies the resulting effects on holobiont phenotypes. The investigators are also comparing the genomes of these bacteria in the different Acroporid hosts and other coral genera to evaluate facets of the bacterium's evolutionary history, as well as to identify possible mechanisms of its proliferation, virulence, and host specificity. This interdisciplinary project mechanistically links nutrients to temporal changes in host, algal symbiont, and bacterial parasite physiology and also explain why there is natural variation in these responses by exploring how host and parasite genotypes and growth dynamics combined with environmental contextuality alter holobiont phenotypes.

This award reflects NSF's statutory mission and has been deemed worthy of support through evaluation using the Foundation's intellectual merit and broader impacts review criteria.

[table of contents | back to top]

Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1923836
NSF Division of Ocean Sciences (NSF OCE)	OCE-1923926

[table of contents | back to top]