



Certificate of Analysis

About this report

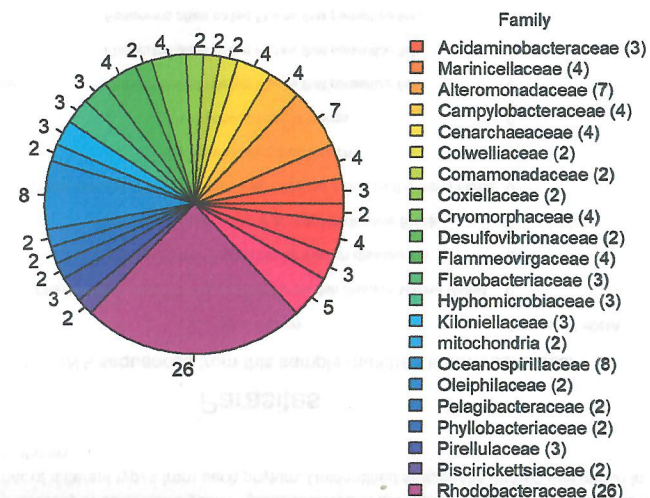
This report summarizes the results from DNA analysis of the community growing in and on a batch of live rock rubble. Universal genetic markers were amplified from microbial (prokaryotic) and other (eukaryotic) DNA in the sample, and thousands of individual DNA molecules from this mixture were sequenced. Each sequence was then compared with public DNA databases to identify its origin. This report summarizes the kinds of organisms detected in the sample, with a focus on beneficial microbes, pathogens, and parasites.

Information about this sample

Sample ID	rock5.1
Batch Name	1813350-1
Sample Date	2021-03-31 11:00 AM
Microbial DNA Sequences Analyzed	10155
Eukaryotic DNA Sequences Analyzed	2616

Microbial Diversity

This sample contained DNA from 382 different types of microbes.



This pie chart shows the diversity of each microbial family found in the sample. The size of each slice is proportional to the number of different types (labels on each slice). For clarity, only families containing 2 or more types are shown here. Unidentified sequences lacking any match in public databases are not shown.

Nitrifying Community

Ammonia-Oxidizing Microbes

Nitrosomonadaceae

Type	Percent of Community	Genus	Species
58445	0.29	Unknown	Unknown

Cenarchaeaceae

Type	Percent of Community	Genus	Species
31953	1.06	Nitrosopumilus	Unknown
760	0.25	Nitrosopumilus	Unknown
2860	0.19	Nitrosopumilus	Unknown
73	0.12	Nitrosopumilus	Unknown

Nitrite-Oxidizing Bacteria

Nitrospiraceae

Type	Percent of Community	Genus	Species
3471	0.98	Unknown	Unknown

The nitrifying community in this sample included 6 different types of microbes.

Bacterial Pathogens

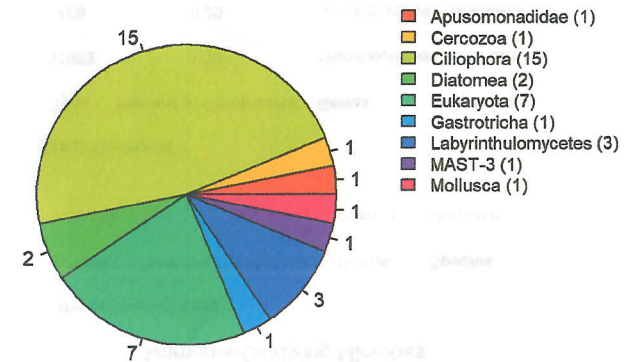
None found.

Complete list of pathogens we screened for:

Eubacterium tarantellae, Lactococcus garvieae, Enterococcus seriolicida, Streptococcus parauberis, Streptococcus iniae, Mycobacterium chelonae, Mycobacterium fortuitum, Mycobacterium marinum, Mycobacterium neoaurum, Nocardia asteroides, Nocardia salmonicida, Nocardia seriolae, Renibacterium salmoninarum, Aeromonas jandaei, Aeromonas salmonicida, Serratia liquefaciens, Chryseobacterium balustinum, Chryseobacterium scophthalmum, Tenacibaculum maritimum, Tenacibaculum ovolyticum, Pasteurella skyensis, Pseudomonas anguilliseptica, Moritella marina, Moritella viscosa, Photobacterium damsela, Shewanella putrefaciens, Vibrio alginolyticus, Vibrio cholerae, Vibrio fischeri, Vibrio furnissii, Vibrio harveyi, Vibrio carchariae, Vibrio trachuri, Vibrio ichthyenteri, Vibrio logei, Vibrio ordalii, Vibrio pelagius, Vibrio salmonicida, Vibrio splendidus, Halomonas cupida, Piscirickettsia salmonis, Vibrio shiloi, Vibrio coralliilyticus, Vibrio harveyi, Aurantimonas corallicida, Vibrio rotiferianus, Vibrio alginolyticus, Vibrio proteolyticus, Vibrio charcharvina, Serratia marcescens, Aquarickettsia rohweri

Eukaryotic Biodiversity

This sample contained DNA from 32 different Eukaryotic sources.



This pie chart shows the diversity of each Eukaryotic Phylum detected in the sample. The size of each slice is proportional to the number of different types from each phylum. Unidentified sequences lacking any match in public databases are not shown.

Parasites

None of the DNA sequences from this sample matched known parasites.

Group	Description	Percent of eDNA
Amyloodinium	Dinoflagellate parasites responsible for the fish disease Marine Velvet	0
Cryptocaryon	Ciliate parasites responsible for the fish disease Ich	0
Brooklynella	Ciliate parasites responsible for the fish disease Brook	0
Uronema	Ciliate parasites responsible for a fish disease called by the same name	0
Phestilla	Montipora-eating Nudibranchs	0
Amakusaplana	Acropora-eating Flatworms	0
Ancyrocephalidae	Flatworms often called Flukes that parasitize fish	0
Gyrodactylidae	Flatworms often called Flukes that parasitize fish	0
Capsalidae	Flatworms often called Flukes that parasitize fish	0
Turbonilla	Snails in the family Pyramidellidae that parasitize giant clams	0
Trichodina	A ciliated protozoan parasite of fish	0

Other Animal Pests

None of the DNA sequences from this sample matched known animal pests.

Group	Description	Percent of eDNA
Aiptasia	The glass anemone, a ubiquitous pest	0
Thylacodes	Vermetid snails	0
Asterina	A group of sea stars that includes coral predators	0

Complete list of Eukaryotes identified

These tables, arranged by Phylum, list all Eukaryotic species that were detected in the sample and identified based on comparison with public DNA sequence databases. DNA sequences that lacked any matches in public databases could not be identified, and are not shown here.

Multimonas koreensis (Apusomonadidae), Gromia oviformis (Cercozoa), Philaster sinensis (Ciliophora), uncultured ciliate 73 (Ciliophora), Urorychia transfuga (Ciliophora), Pseudodiophrys nigricans (Ciliophora), Epicarchesium abrae (Ciliophora), uncultured marine 694 (Ciliophora), Caryotricha sp. (Ciliophora), Aspidisca aculeata (Ciliophora), Paranophrys magna (Ciliophora), Euplotes dammamensis (Ciliophora), Aristerostoma sp. (Ciliophora), Paranophrys magna (Ciliophora), Trochochilodon flavus (Ciliophora), Varistrombidium kielum (Ciliophora), Plagiocampa sp. (Ciliophora), Entomoneis sp. (Diatomea), Halamphora subtropica (Diatomea), Lithotrichon pulchrum (Eukaryota), Lithotrichon pulchrum (Eukaryota), Paraphysomonas foraminifera (Eukaryota), metagenome (Eukaryota), uncultured eukaryote 88 (Eukaryota), Placidia cafeteriopsis (Eukaryota), Paramoeba branchiphila (Eukaryota), uncultured eukaryote 275 (Gastrotricha), uncultured eukaryote 275 (Labyrinthulomycetes), Thraustochytriidae sp. (Labyrinthulomycetes), Ulkenia profunda (Labyrinthulomycetes), uncultured eukaryote 275 (MAST-3), Malleus albus (Mollusca)

Complete List of Microbes Identified

This list includes all microbes (Bacteria & Archae) that were detected in the sample and identified based on comparison with public DNA sequence databases. DNA sequences that lacked any matches in public databases could not be identified, and are not shown here. The list is sorted by abundance, from highest to lowest.

Unclassified Oceanospirillaceae 28100, Unclassified Rhodobacteraceae 226, Unclassified Hyphomicrobiaceae 273, Unclassified Desulfovibrionaceae 96, Marivita sp., Unclassified Pelagibacteraceae 52067, Thalassospira sp., WH1-8 sp., Hirschia baltica, Unclassified Oceanospirillaceae 58088, Unclassified Legionellaceae 11183, Unclassified J115 14108, Unclassified Hyphomicrobiaceae 58162, Unclassified Endozoicimonaceae 62045, Unclassified Coxiellaceae 1075, Oceanospirillum sp., Unclassified Oceanospirillaceae 9768, Unclassified Bacteria 19902, Unclassified Bacteria 61945, Unclassified Oleiphilaceae 175, Arcobacter sp., Arcobacter sp., Arcobacter sp., BD2-13 sp., Arcobacter sp., Unclassified Desulfovibrionaceae 58195, Ferrimonas sp., Sediminicola sp., Unclassified Alteromonadaceae 16245, Neptunomonas sp., Vibrio sp., HTCC sp., Nitrosopumilus sp., Unclassified Francisellaceae 11816, Fusibacter sp., Unclassified Bacteria 2964, Unclassified Bacteria 30, Unclassified Marinilabiaceae 60116, Unclassified Alteromonadaceae 823, Unclassified Cryomorphaceae 13973, Unclassified Bacteria 20436, Mycobacterium sp., Unclassified Bacteria 2327, Unclassified Rhodospirillaceae 2867, Unclassified wb1_P06 965, Unclassified Bacteria 1502, Moritella sp.,

Unclassified Bacteria 10614, Unclassified Bacteria 64192, Unclassified Coxiellaceae 3856, Unclassified Rhodospirillaceae 33459, Unclassified Bacteria 14395, Unclassified Bacteria 20967, Unclassified Chitinophagaceae 837, Unclassified Bacteria 3467, Unclassified Cryomorphaceae 12269, Aeromicrobium sp.

DNA analysis conducted by [AquaBionics LLC](#).