Endozoicomonas gorgoniicola from Plexaura sp. in Bimini, Tuna Alley, Bahamas

Endozoicomonas euniceicola from Eunicea fusca in Florida, USA

Endozoicomonas montiporae CL-33 from Montipora aequituberculata in Kenting, Taiwan

Endozoicomonas sp. from a sea cucumber pond in China

Endozoicomonas sp. from Pecten maximus (king scallop) in United Kingdom

Endozoicomonas montiporae from Arenosclera brasiliensis (marine sponge) in Rio de Janeiro, Brazil

Endozoicomonas sp. from Halichondria panicea in South-West Iceland

Endozoicomonas numazuensis from Haplosclerida gen. et sp. in Shizuoka, Numazu, Japan

Endozoicimonas elysicola from Elysia ornata (sea slug) in Izu-Miyake Island, Japan

Endozoicomonas sp. from Diplodus puntazzo larva in eastern Mediterranean sea

Endozoicomonas ascidiicola from Ascidiella sp. In Gullmarsfjorden, Sweden

Endozoicomonas atrinae from Atrina pectinata (comb pen) in South Korea

Endozoicomonas sp. Acr-14 from Acropora sp. in Kenting, Taiwan

Endozoicomonas sp. Acr-14 from Acropora sp. in Kenting, Taiwan
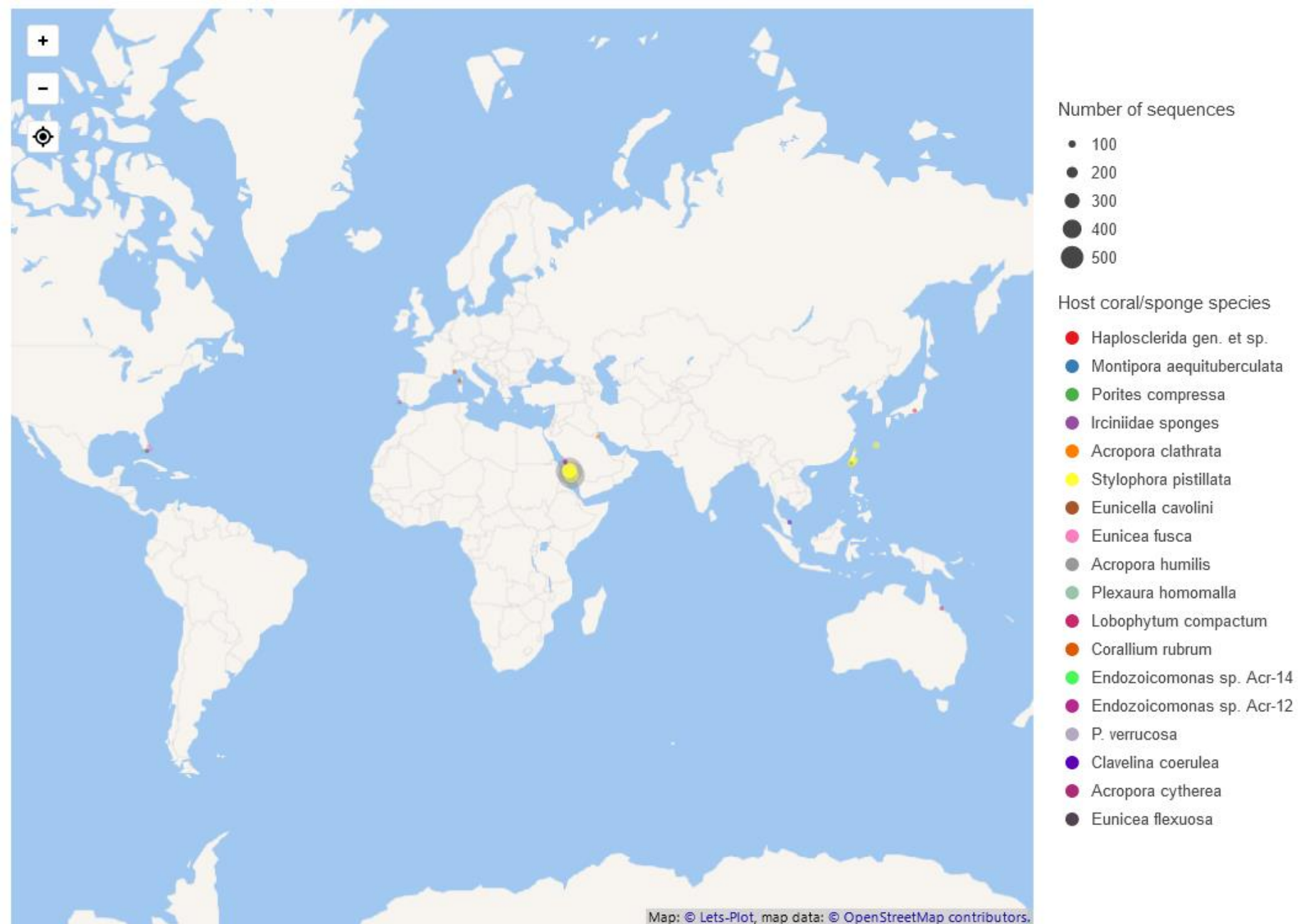
Endozoicomonas sp. From China

Endozoicomonas bacteria phylogeny inferred in a likelihood analysis of 15 16S rRNA sequences using TIM3+I+G4 model. Bootstrap values are labeled on the branches, orange being above 90%, and red being 100% support values. Taxon label includes the location of sampling, as well as the species from which it was sampled from (the host). The list was based off of Picking sequences was influenced by Pike et al. (2013).

Number of sequences
- 100
- 200
- 300
- 400
- 500

Host coral/sponge species
- Haplosclerida gen. et sp.
- Montipora aequituberculata
- Porites compressa
- Irciniidae sponges
- Acropora clathrata
- Stylophora pistillata
- Eunicella cavolini
- Eunicea fusca
- Acropora humilis
- Plexaura homomalla
- Lobophytum compactum
- Corallium rubrum
- Endozoicomonas sp. Acr-14
- Endozoicomonas sp. Acr-12
- P. verrucosa
- Clavelina coerulea
- Acropora cytherea
- Eunicea flexuosa

Map: © Lets-Plot, map data: © OpenStreetMap contributors.

Mapping of location of included a mix of 140 *Endozoicomonas* and bacterial clone (not explicitly uploaded as Endozoicomonas sp.) 16S sequences with latitude and longitudinal on a map using pandas, geopandas, lat_long_parser and Lets-Plot (with OpenStreetMap). Size of dot correlates to number of sequences, while color indicate the sample's host species. Samples come from Australia, France, Portugal, US (Florida and Hawai'i), Bahamas, Malaysia, Saudi Arabia, Kuwait, Taiwan (Kenting, Yeh Liu, Green Island) and Japan (Shizuoka and Okinawa).

Uncultured bacterial clones from Stylophora pistillata in Southern Red Sea, Saudi Arabia

Uncultured bacterial clones from Stylophora pistillata in Southern Red Sea, Saudi Arabia

Uncultured bacterial clones from P. verrucosa in Al-Fahal reef, Saudi Arabia

Uncultured bacterial clones from P. verrucosa in Al-Fahal reef, Saudi Arabia

Uncultured bacterial clones from Stylophora pistillata in Southern Red Sea, Saudi Arabia

Endozoicomonas montiporae CL-33 from Montipora aequituberculata in Kenting, Taiwan

Uncultured bacterial clones from Acropora humilis in Red Sea, Brown reef, Saudi Arabia

Uncultured Endozoicomonas from Corallium rubrum in Porticcio, Corsica Island, France

Endozoicimonas from Irciniidae sponges in Algarve, Gale Alta, Armacao de Pera, Portugal

Uncultured bacterial clones from Eunicella cavolini in Bay of Villefranche-sur-Mer, France

Uncultured bacterial clones from Clavelina coerulea, Terengganu Malaysia

Uncultured bacterial clones from Acropora humilis in Red Sea, Brown reef, Saudi Arabia

Uncultured bacterial clones from Stylophora pistillata in Southern Red Sea, Saudi Arabia

Uncultured bacterial clones from Pocillopora damicornis in Red Sea, Brown reef, Saudi Arabia

Uncultured bacterial clones from Pocillopora damicornis in Red Sea, Brown reef, Saudi Arabia

Uncultured bacterial clones from P. verrucosa in Al-Fahal reef, Saudi Arabia

Uncultured bacterial clones from Pocillopora damicornis in Red Sea, Brown reef, Saudi Arabia

Uncultured Enzozoicomonas from Stylophora pistillata in Kenting, Taiwan

Endozoicomonas sp. from Acropora hemprichii in Red Sea, Saudi Arabia

Endozoicimonas from Acropora clathrata in Qit'at Bnaider, Kuwait

Uncultured Endozoicomonas from Stylophora pistillata in Kenting, Taiwan

Endozoicomonas sp. Acr-14 from Acropora sp. in Kenting, Taiwan

Endozoicomonas sp. Acr-12 from Acropora sp. in Kenting, Taiwan

Uncultured Enzozoicomonas from Stylophora pistillata in Kenting, Taiwan

Uncultured Enzozoicomonas from Stylophora pistillata in Kenting, Taiwan

Uncultured Enzozoicomonas from Stylophora pistillata in Kenting, Taiwan

Uncultured Enzozoicomonas from Stylophora pistillata in Okinawa, Japan

Endozoicomonas sp. from Acropora cytherea in Red Sea, Saudi Arabia

Uncultured Enzozoicomonas from Stylophora pistillata in Okinawa, Japan

Uncultured bacterial clones from Acropora humilis in Red Sea, Brown reef, Saudi Arabia

Endozoicomonas from Lobophytum compactum in Orpheus Island Great Barrier Reef, Australia

Endozoicomonas numazuensis from Haplosclerida gen. et sp. in Shizuoka, Numazu, Japan

Endozoicomonas euniceicola from Eunicea flexuosa in Florida, USA

Uncultured Endozoicomonas from Plexaura homomalla in Summerland Key, Florida, USA

Uncultured Endozoicomonas from Plexaura homomalla in Summerland Key, Florida, USA

Endozoicomonas gorgoniicola from Plexaura sp. in Bimini, Tuna Alley, Bahamas

Endozoicomonas montiporae CL-33 from Montipora aequituberculata in Kenting, Taiwan

Uncultured Enzozoicomonas from Stylophora pistillata in Kenting, Taiwan

Uncultured Endozoicomonas from Plexaura homomalla in Summerland Key, Florida, USA

140 *Endozoicomonas* and bacterial clone phylogeny inferred in a continuous Bayesian phylogeographic analysis using 16S rRNA sequences, their latitude and longitudinal information and sampling dates with BEAST v1.10.4, HKY substitution model and classic priors. Posterior values are labeled on the branches, with purple transitioning to pink being 80-90%, and red being above 90% in support values. Taxon label includes the location of sampling, as well as the species from which it was sampled from (the host). Some clades (filled colors) were collapsed for brevity. Picking sequences was intentionally global in scope.

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