The complete mitochondrial genome of *Montipora vietnamensis* (Scleractinia, Acroporidae)

Wei Wang‡, Bingbing Cao‡, Ziqing Xu‡, Zhiyu Jia‡, Shuangen Yu§, Peng Tian‡, Wentao Niu‡, Jiaguang Xiao‡

‡ Third Institute of Oceanography, Ministry of Natural Resources, Xiamen, China
§ Key Laboratory of Mariculture of Ministry of Education, College of Fisheries, Ocean University of China, Qingdao, China

Corresponding author: Wei Wang (<wangwei@tio.org.cn>), Wentao Niu (<wentaoniu@tio.org.cn>), Jiaguang Xiao (<xiaojiaguang@tio.org.cn>)

Academic editor: Danwei Huang

Received: 11 Aug 2022 | Accepted: 02 Sep 2022 | Published: 13 Sep 2022

Citation: Wang W, Cao B, Xu Z, Jia Z, Yu S, Tian P, Niu W, Xiao J (2022) The complete mitochondrial genome of *Montipora vietnamensis* (Scleractinia, Acroporidae). Biodiversity Data Journal 10: e91531. [https://doi.org/10.3897/BDJ.10.e91531](https://doi.org/10.3897/BDJ.10.e91531)

### Abstract

*Montipora vietnamensis* Veron, 2000 (Cnidaria, Anthozoa, Scleractinia, Acroporidae) is an uncommon, but distinctive species of stony coral. The complete mitochondrial genome of *M. vietnamensis* was sequenced in this study for the first time, based on 32 pairs of primers newly designed according to seven species in the family Acroporidae. The mitogenome of *M. vietnamensis* has a circular form and is 17,885 bp long, including 13 protein-coding genes (PCGs), 2 tRNA (tRNA\textsubscript{Met}, tRNA\textsubscript{Tyr}), 2 rRNA genes and a putative control-region. The base composition of the complete mitogenome was 24.8% A, 14.2% C, 24.2% G and 36.8% T, with a higher AT content (61.6%) than GC content (38.4%). Based on 13 protein-coding genes, a Maximum Likelihood phylogenetic analysis showed that *M. vietnamensis* is clustered in the genus *Montipora* which belongs to the family Acroporidae. More stony coral species should be sequenced for basic molecular information and to help confirm the taxonomic status and evolutionary relationships of Scleractinia in the future.

### Keywords

mitochondrial genome, primers, Acroporidae, *Montipora vietnamensis*
Introduction

Reef-building coral species of the order Scleractinia play an important role in shallow tropical seas by providing an environmental foundation for the ecosystem (Fukami et al. 2000, Sheppard et al. 2017). While traditional morphology-based systematics cannot clearly reflect all the evolutionary relationships of Scleractinia, molecular data have become increasingly important in recent years to help overcome the limitations of morphological analyses amongst scleractinians (Arrigoni et al. 2017, Terraneo et al. 2017).

Cnidarian mitogenome data contain important phylogenetic information for understanding its evolutionary history (Kayal et al. 2013). The utility of integrating morphological and genetic datasets also facilitates the taxonomic revisions of scleractinian taxa (Juszkiewicz et al. 2022). There are more than 1600 Scleractinia species, whereas only approximately 100 complete mitogenomes of Scleractinia species are currently available in NCBI (https://www.ncbi.nlm.nih.gov/) (Hoeksema and Cairns 2022).

Montipora vietnamensis Veron, 2000 (Cnidaria, Anthozoa, Scleractinia, Acroporidae) is a species of stony coral, which is uncommon, but distinctive and usually inhabits shallow reef environments and rocky foreshores. Its colonies have an encrusting or laminar base, with closely compacted short upright branches; their coenosteum ridges are mostly vertical, but may be irregular; their corallites are large and prominent and their colours are dark brown, usually with white coenosteum ridges and branch tips (Veron 2000).

In this research, the complete mitochondrial genome of M. vietnamensis was sequenced for the first time, based on 32 pairs of primers designed according to seven species in the family Acroporidae. The phylogenetic position of M. vietnamensis within the family Acroporidae, based on protein coding genes of the mitogenome, will help determine its taxonomic status and facilitate further study on stony coral evolutionary and phylogenetic relationships (Tian et al. 2022). Ultimately, this information can aid in species monitoring and conservation efforts (Colin et al. 2021).

Material and methods

Two samples of M. vietnamensis (Fig. 1) were collected from Houhai, Sanya, Hainan Province, China (109°44’ 55.91”E, 18°16’ 28.58” N); one of them was immediately placed in a single vial in ethanol (+99%) and labelled with a unique identifier E38. This sample was then stored at -20°C until extraction. The other one was bleached by soaking in 5% sodium hypochlorite and then the specimen was kept in our Coral Sample Repository with a special code, 20181124-E38 (contact the first author to view or loan this specimen). Species identification was conducted according to the photographs and description of Veron (2000) (http://www.coralsoftheworld.org/species_factsheets/species_factsheet_summary/montipora-vietnamensis/). Complete genomic DNA (gDNA) was extracted using the DNeasy Blood and Tissue Kit (Qiagen, Shanghai, China), following the protocol at https://www.qiagen.com/cn/resources/resourcedetail?id=68f29296-5a9f-40fa-8b3d-1c148d0b3030&lang=en. Electrophoresis with 1% agarose gel was used to estimate the integrity
of the gDNA and the spectrophotometer NanoDrop 2000 (Thermo Scientific, USA) was used to measure the gDNA concentration.

The mitogenome sequence fragments were obtained through a PCR approach using 32 pairs of primers (Table 1) designed through primer-blast (https://www.ncbi.nlm.nih.gov/tools/primer-blast/), based on seven Acroporidae species that had been sequenced and data available in https://www.ncbi.nlm.nih.gov/genbank/ (NC_029251, KF448533, C_024092, NC_040137, MG851913, KJ634269, NC_006902). The PCR used 25 μl mixtures containing 2.5 μl of 10x ExTaq Buffer (20 mM), 2 μl dNTP, 1 μl of each primer(10 μM), 0.13 μl ExTaq DNA polymerase (Takara Product Code No. RR001Q, Beijing, China) and approximately 0.5 μg of gDNA. Cycling conditions consisted of 5 min at 95°C; then 30 cycles of 30 s at 95°C, 45 s at 50°C and 1 min at 72°C; followed by a final extension at 72°C for 10 min. The PCR products were directly sequenced using an ABI 3730XL automated DNA sequencer (Applied Biosystems, Sangon Biotech, Shanghai, China). We assembled all the sequencing fragments as a circularised contig using ContigExpress v. 3.0.0. The circularised contig was then submitted to MITOS (Bernt et al. 2013) WebServer (http://mitos.bioinf.uni-leipzig.de/index.py) for preliminary mitochondrial genome annotation. We then identified and annotated the 13 PCGs and RNA genes by alignments of homologous mitogenomes of other scleractinians that had been uncovered through BLAST searches in NCBI (https://blast.ncbi.nlm.nih.gov/Blast.cgi). The genomic structure was mapped using the online CGView Server (https://proksee.ca/) (Stothard and Wishart 2004).

Table 1.
Total of 32 pairs of primers designed, based on seven Acroporidae species.

| No. | Name   | primer sequences         |
|-----|--------|--------------------------|
| 1   | Acro16SF1 | 5'-ATTCCGTAAGTAGCAGGGAG-3' |
| 2   | Acro16SR1 | 5'-TTGTCTAAATCCCCATACTCC-3' |
| No. | Name       | Primer Sequences               |
|-----|------------|--------------------------------|
| 3   | Acro16SF2  | 5'-TTCGAAGTAGACAGACGAC-3'      |
| 4   | Acro16SR2  | 5'-GCAGGTCTCCACCTCTCATAC-3'    |
| 5   | Acro16SF3  | 5'-TAAGGAACTCGGACAGTAT-3'      |
| 6   | Acro16SR3  | 5'-GACGTTATTACGCTTATAT-3'      |
| 7   | Acro16SF4  | 5'-GAGCAGACACTTATCTTTGG-3'     |
| 8   | Acro16SR4  | 5'-CTTTATAATCAACAGGCTTAAG-3'   |
| 9   | AcroND5F5  | 5'-GTTGGAGGAAGAAAATTAGG-3'     |
| 10  | AcroND5R5  | 5'-AGCCCCAAGCTGTGACAGACTT-3'   |
| 11  | AcroND5F6  | 5'-GGTCTTTAGATTTCTTCT-3'       |
| 12  | AcroND5R6  | 5'-CTTCTCATAACTATCTTTGGAC-3'   |
| 13  | AcroND1F7  | 5'-GGCTGTTTTCTCGATAAGTG-3'     |
| 14  | AcroND1R7  | 5'-ACGCCTTTCATAAAAGACAC-3'     |
| 15  | AcroND1F8  | 5'-GCTCTTCTTCTCTGATT-3'        |
| 16  | AcroND1R8  | 5'-CCTCAGGTAGCATAGGCAC-3'      |
| 17  | AcroCytbF9 | 5'-CCGTTTGGCGAGTGGC-3'         |
| 18  | AcroCytbR9 | 5'-CGTCCAATTGAGCAAAAG-3'       |
| 19  | AcroCytbF10| 5'-GCACTTCAAGCTGAGT-3'         |
| 20  | AcroCytbR10| 5'-CTCCGTAACCCACACAT-3'        |
| 21  | AcroND2F11 | 5'-CTTCAAGTAGTTAGCCTTG-3'      |
| 22  | AcroND2R11 | 5'-ACCTCTATTTCCAAAAGAC-3'      |
| 23  | AcroND2F12 | 5'-TTGGGCTCTTCTTTTCGAT-3'      |
| 24  | AcroND2R12 | 5'-CCATAACATAACACCAC-3'        |
| 25  | AcroND2F13 | 5'-CTTTTCTGATAAGCTCAAAG-3'     |
| 26  | AcroND2R13 | 5'-CCAAATGAGAAGATAATTTATG-3'   |
| 27  | AcroND6F14 | 5'-CGCTCAATCTTGCAATG-3'        |
| 28  | AcroND6R14 | 5'-CCCAATTCTTTGAGTTAACAC-3'    |
| 29  | AcroND6F15 | 5'-GCAGATTGATTTGTATAGCCTTG-3'  |
| 30  | AcroND6R15 | 5'-CCAAACCGCTAAATAGC-3'        |
| 31  | AcroATP6F16| 5'-GTAAAGTTTTATCCAGGGC-3'      |
| 32  | AcroATP6R16| 5'-TCAAGCATAAAACACTCC-3'       |
| 33  | AcroND4F17 | 5'-AAAGTTGAAAGTCCATTAGGC-3'    |
| 34  | AcroND4R17 | 5'-TGTGCAACGAGAAATAAAGC-3'     |
| 35  | AcroND4F18 | 5'-TTTCTTGGCCGATTGGCC-3'       |
| 36  | AcroND4R18 | 5'-TTACCCATTCTTCAACAGG-3'      |
| 37  | AcroND4F19 | 5'-CTTCCGTTATGTTCTTTGCC-3'     |
| 38  | AcroND4R19 | 5'-TGGACACTTATTTGACGGAC-3'     |
| No. | Name          | Primer sequences                          |
|-----|---------------|-------------------------------------------|
| 39  | Acro12SF20    | 5’-AGGCCACATTTCACCTGAGAC-3’               |
| 40  | Acro12SR20    | 5’-AAACCACGTGTAAATCTG-3’                  |
| 41  | Acro12SF21    | 5’-AGAGACCTACCACAACTTG-3’                 |
| 42  | Acro12SR21    | 5’-CTCTAATAACATCTCGTAC-3’                 |
| 43  | AcroCO3F22    | 5’-GGTGAAGCCTTCTGCTGGCC-3’                |
| 44  | AcroCO3R22    | 5’-AATGCCCAATACACACTG-3’                  |
| 45  | AcroCO3F23    | 5’-TTTCACTATTCGGATCCG-3’                  |
| 46  | AcroCO3R23    | 5’-CTAACACATGGATTCG-3’                    |
| 47  | AcroCO2F24    | 5’-GGACATCAATGGGTATTCG-3’                 |
| 48  | AcroCO2R24    | 5’-ACCCGGAGTGAACTAAAAG-3’                 |
| 49  | AcroND4LF25   | 5’-TTATGGTCTAACAATCAG-3’                  |
| 50  | AcroND4LR25   | 5’-AGGCAAATCCCTTTATGC-3’                  |
| 51  | AcroND3F26    | 5’-TTTCACTATTCGGATCCG-3’                  |
| 52  | AcroND3R26    | 5’-TTTCACTATTCGGATCCG-3’                  |
| 53  | AcroND5F27    | 5’-TTTCACTATTCGGATCCG-3’                  |
| 54  | AcroND5R27    | 5’-TTTCACTATTCGGATCCG-3’                  |
| 55  | AcroND5F28    | 5’-TTTCACTATTCGGATCCG-3’                  |
| 56  | AcroND5R28    | 5’-TTTCACTATTCGGATCCG-3’                  |
| 57  | AcroATP8F29   | 5’-TTTCACTATTCGGATCCG-3’                  |
| 58  | AcroATP8R29   | 5’-TTTCACTATTCGGATCCG-3’                  |
| 59  | AcroCO1F30    | 5’-TTTCACTATTCGGATCCG-3’                  |
| 60  | AcroCO1R30    | 5’-TTTCACTATTCGGATCCG-3’                  |
| 61  | AcroCO1F31    | 5’-TTTCACTATTCGGATCCG-3’                  |
| 62  | AcroCO1R31    | 5’-TTTCACTATTCGGATCCG-3’                  |
| 63  | AcroCO1F32    | 5’-TTTCACTATTCGGATCCG-3’                  |
| 64  | AcroCO1R32    | 5’-TTTCACTATTCGGATCCG-3’                  |

The phylogenetic position of *M. vietnamensis* within the family Acroporidae was inferred using 13 tandem mitogenome PCG sequences, with 19 of the other 21 species of Scleractinia analysed in this study obtained from GenBank (https://www.ncbi.nlm.nih.gov/genbank/, Table 2). Two other species, *Acropora digitifera* (GenBank accession number: OP311587) and *Acropora hyacinthus* (GenBank accession number: OP311657), were sequenced using the same primers as *M. vietnamensis*. We used MEGA 7 (Kumar et al. 2016) to select the best-fitting model, based on the Akaike Information Criterion (AIC) and then constructed a Maximum Likelihood (ML) tree with 500 bootstrap replicates.
Table 2.
Representative species of Scleractinia included in this study.

| NO. | Species             | Family        | Length (bp) | GenBank accession number |
|-----|---------------------|---------------|-------------|--------------------------|
| 1   | Montipora vietnamensis | Acroporidae   | 17,885      | ON872180                 |
| 2   | Acropora aculeus     | Acroporidae   | 18,528      | NC_029251                |
| 3   | Acropora digitifera  | Acroporidae   | 18,480      | OP311587                 |
| 4   | Acropora digitifera  | Acroporidae   | 18,479      | NC_022830                |
| 5   | Acropora hyacinthus  | Acroporidae   | 18,567      | OP311657                 |
| 6   | Acropora hyacinthus  | Acroporidae   | 18,566      | NC_022826                |
| 7   | Acropora florida     | Acroporidae   | 18,365      | KF448533                 |
| 8   | Acropora horrida     | Acroporidae   | 18,480      | NC_022825                |
| 9   | Acropora nasuta      | Acroporidae   | 18,481      | NC_022831                |
| 10  | Acropora robusta     | Acroporidae   | 18,480      | NC_022833                |
| 11  | Astreopora myriophthalma | Acroporidae | 18,106      | NC_024092                |
| 12  | Montipora aequituberculata | Acroporidae | 17,886      | NC_037359                |
| 13  | Montipora efflorescens | Acroporidae | 17,886      | NC_040137                |
| 14  | Acropora aspera      | Acroporidae   | 18,479      | KF448532                 |
| 15  | Acropora humilis     | Acroporidae   | 18,479      | KF448528                 |
| 16  | Alveopora japonica   | Acroporidae   | 18,144      | MG851913                 |
| 17  | Astreopora explanata | Acroporidae   | 18,106      | KJ634269                 |
| 18  | Isopora palifera     | Acroporidae   | 18,725      | KJ634270                 |
| 19  | Isopora togianensis  | Acroporidae   | 18,637      | KJ634268                 |
| 20  | Montipora cactus     | Acroporidae   | 17,887      | NC_006902                |
| 21  | Pocillopora eydouxi  | Pocilporidae  | 17,422      | EF526303                 |
| 22  | Madracis mirabilis   | Pocilporidae  | 16,951      | NC_011160                |

Results and Discussion

The mitochondrial genome size of *M. vietnamensis* (GenBank accession number: ON872180, https://www.ncbi.nlm.nih.gov/nucleotide) was 17,885 bp, including 13 PCGs, 2 tRNA (tRNAMet, tRNATrp), 2 rRNA genes and a putative control-region (Fig. 2, Table 3). The mitogenome of *M. vietnamensis* offered no distinct structure and its gene order was the same as those of published mitogenomes of Acroporidae species, with all genes
encoded on the H-strand. The base composition of the complete mitogenome was 24.8% A, 14.2% C, 24.2% G and 36.8% T, with a higher AT content (61.6%) than GC content (38.4%). The total length of all 13 PCGs was 11,817 bp, with a base composition of 22.1%, 14.5%, 23.7% and 39.7% for A, C, G and T, respectively. ND5 gene had an intron insertion of 11,489 bp. The shortest gene was ATP8 (218 bp) and the longest gene was ND5 (1,836 bp). The putative control-region was 627 bp (Tables 3, 4).

Table 3.
Organisation of the mitochondrial genome of *M. vietnamensis*.

| Sequence | Position | Size (bp) | Amino | Gaps | Codon | Strand |
|----------|----------|-----------|-------|------|-------|--------|
| tRNA<sup>Met</sup> | 1 | 71 | 71 | 0 | GTG | H |
| 16s rRNA | 72 | 2331 | 2260 | 102 | H |
| ND5 5' | 2434 | 3153 | 720 | 240 | 322 | GTG |
| ND1 | 3476 | 4459 | 984 | 327 | 106 | GTG TAA |
| Cyt b | 4566 | 5723 | 1158 | 385 | 533 | ATG TAG |
| ND2 | 6257 | 7354 | 1098 | 365 | 32 | ATG TAA |
| ND6 | 7387 | 7980 | 594 | 197 | 71 | ATA TAA |
| ATP6 | 8052 | 8750 | 699 | 232 | 179 | ATG TAG |
| ND4 | 8930 | 10405 | 1476 | 491 | 28 | GTG TAA |
| 12S rRNA | 10434 | 11608 | 1175 | 0 | H |
| Control region | 11609 | 12235 | 627 | 0 | H |
| CO III | 12236 | 13024 | 789 | 262 | 55 | GTG TAG |
| CO II | 13080 | 13823 | 744 | 247 | 35 | ATG TAA |
| ND4L | 13859 | 14158 | 300 | 99 | 31 | GTG TAA |
| ND3 | 14190 | 14546 | 357 | 118 | 96 | GTG TAG |
| ND5 3' | 14643 | 15758 | 1116 | 371 | 29 | TAG |
| tRNA<sup>Trp</sup> | 15788 | 15857 | 70 | 32 | H |
| ATP8 | 15890 | 16108 | 219 | 72 | -19 | ATG TAG |
| COI | 16090 | 17691 | 1602 | 533 | 194 | ATG TAA |

Notes: The gaps are number of nucleotides between the given gene and the related gene behind, negative numbers indicating overlapping nucleotides; H indicated that the genes were transcribed on the heavy strand.

The encoding genes 12S rRNA and 16S rRNA in *M. vietnamensis* were 1,175 bp and 2,260 bp in size, respectively. Both the two rRNAs' base composition was 32.5% A, 14.5% C, 25.5% G and 27.5% T. The two tRNA encoding genes tRNA<sup>Met</sup> and tRNA<sup>Trp</sup> were 71 bp and 70 bp in size, respectively.
Table 4.
Nucleotide composition features in *M. vietnamensis*.

| Gene/Region | T%  | C%  | A%  | G%  | A+T% | size (bp) |
|-------------|-----|-----|-----|-----|------|-----------|
| Overall     | 36.8| 14.2| 24.8| 24.2| 61.6 | 17885     |
| Control region | 36.7| 12.8| 23.8| 26.8| 60.4 | 627       |
| rRNA        | 27.5| 14.5| 32.5| 25.5| 60   | 141       |
| tRNA        | 20.6| 23.4| 24.8| 31.2| 45.4 | 3435      |
| PCGs        | 39.7| 14.5| 22.1| 23.7| 61.8 | 11817     |
| 1st         | 32  | 13.5| 24.3| 30.2| 56.3 | 3939      |
| 2nd         | 45  | 19.9| 18.4| 16.7| 63.4 | 3939      |
| 3rd         | 42.1| 10.2| 23.7| 24  | 34.3 | 3939      |

The mitochondrial genome of *M. vietnamensis*. Gene order and positions are shown. COI, COII and COIII refer to the cytochrome oxidase subunits, Cyt b refers to cytochrome b and ND1-ND6 refers to NADH dehydrogenase components. All genes are encoded on the H-strand.

The ML bootstrap consensus tree shows that *M. vietnamensis* is clustered in the genus *Montipora* which belongs to the family Acroporidae with high bootstrap support (Fig. 3).
The mitochondrial genome data have provided important molecular information for understanding evolutionary relationships amongst stony corals (Kitahara et al. 2016, Arrigoni et al. 2020). In this research, the 32 pairs of primers we designed according to seven Acroporidae species comprised a useful tool to obtain the mitogenome of *M. vietnamensis*. With the same primer sets, we further obtained four mitogenomes of other Acroporidae species, *Acropora digitifera* (GenBank accession number: OP311587), *Acropora hyacinthus* (GenBank accession number: OP311657), *Acropora intermedia* (GenBank accession number: OP311588) and *Acropora microphthalma* (GenBank accession number: OP311656). These showed 99.82%, 99.99%, 99.79% and 99.98% sequence identity with conspecifics already sequenced and available in GenBank that were obtained by next-generation sequencing (NGS). The NGS method was convenient, fast and relatively accurate. However, it cost less and was more time-efficient when we sequenced these five samples using the current Sanger sequencing approach. More stony coral species should be sequenced for basic molecular information and to help confirm the taxonomic status and evolutionary relationships of Scleractinia in the future.

Figure 3. Inferred phylogenetic relationships, based on a Maximum-Likelihood analysis of concatenated nucleotide sequences of 13 mitochondrial PCGs. Numbers on branches are bootstrap percentages.
Acknowledgements

We are grateful to the National Key Research and Development Programme (2021YFC3100503); the Scientific Research Foundation of Third Institute of Oceanography, Ministry of Natural Resources (grant number 2022024; 2020006); and Nansha Islands Coral Reef Ecosystem National Observation and Research Station (NSICR).

Author contributions

Wei Wang, Shuangen Yu, Jiaguang Xiao and Wentao Niu conceived, designed and performed the study. Bingbing Cao, Ziqing Xu, Zhiyu Jia and Peng Tian processed and analysed the data. All authors contributed to the preparation of the manuscript.

Conflicts of interest

The authors report no conflicts of interest and are responsible for the content and writing of the paper.

References

- Arrigoni R, Berumen M, Huang D, Terraneo T, Benzoni F (2017) Cyphastrea (Cnidaria : Scleractinia : Merulinidae) in the Red Sea: phylogeny and a new reef coral species. Invertebrate Systematics 31 (2). https://doi.org/10.1071/is16035
- Arrigoni R, Berumen M, Mariappan K, Beck PA, Hulver AM, Montano S, Pichon M, Strona G, Terraneo TI, Benzoni F (2020) Towards a rigorous species delimitation framework for scleractinian corals based on RAD sequencing: the case study of Leptastrea from the Indo-Pacific. Coral Reefs 39 (4): 1001-1025. https://doi.org/10.1007/s00338-020-01924-8
- Bernt M, Donath A, Jühling F, Externbrink F, Florentz C, Fritzsch G, Pütz J, Middendorf M, Stadler P (2013) MITOS: Improved de novo metazoan mitochondrial genome annotation. Molecular Phylogenetics and Evolution 69 (2): 313-319. https://doi.org/10.1016/j.ympev.2012.08.023
- Colin L, Yesson C, Head CEI (2021) Complete mitochondrial genomes of three reef forming Acropora corals (Acroporidae, Scleractinia) from Chagos Archipelago, Indian Ocean. Biodiversity Data Journal 9: e72762. https://doi.org/10.3897/BDJ.9.e72762
- Fukami H, Omori M, Hatta M (2000) Phylogenetic relationships in the coral family acroporidae, reassessed by inference from mitochondrial genes. Zoological Science 17 (5): 689-96. https://doi.org/10.2108/zsj.17.689
- Hoeksema BW, Cairns S (2022) World list of Scleractinia. https://www.marinespecies.org/scleractinia/aphia.php?. Accessed on: 2022-8-06.
- Juszkiewicz D, White N, Stolarski J, Benzoni F, Arrigoni R, Hoeksema B, Wilson N, Bunce M, Richards Z (2022) Phylogeography of recent Plesiastrea (Scleractinia: Pariidae).
The complete mitochondrial genome of Montipora vietnamensis (Scleractinia, ...