

## Supplementary material

### **An integrated morphological–molecular approach reveals new insights on the systematics of the octocoral *Telestula humilis* (Thomson, 1927) (Octocorallia : Alcyonacea : Clavulariidae)**

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**Table S1. List of the indexes (BGI platform) used for each sequenced samples**

Sample ID	Species	Sequencing index (BGI platform)
027-DR06	<i>Pseudotelestula humilis</i> comb. nov.	BGI_24: ATGTCGAAAC
011-DR08	<i>Pseudotelestula humilis</i> comb. nov.	BGI_25: TCGGGGTCCC
05ROV2B	<i>Pseudotelestula humilis</i> comb. nov.	BGI_27: GGTTGGGTCT
FC07 L131	<i>Telestula septentrionalis</i>	BGI_29: AAAGTAGTGT
073-DR02	<i>Telestula</i> cf. <i>batoni</i>	BGI_28: AATCTCGAGG

**Table S2. Best substitution models and partition schemes selected with PartitionFinder for *Cox1*, *mtMutS* and 28S rRNA gene**

Protein-coding gene	Codon position	Best model	Subset partitions (SP)
<i>cox1</i>	cox1_1	SYM+I+G	SP3
	cox1_2	GTR+I	SP4
	cox1_3	GTR+I+G	SP2
<i>mtMutS</i>	mtMutS_1	GTR+I+G	SP1
	mtMutS_2	GTR+I+G	SP1
	mtMutS_3	GTR+I+G	SP2
28S rRNA	28S	GTR+I+G	SP5

**Table S3. Species and accession numbers used for mitogenomic analyses**

Family	Genus or species	Specimen voucher	Accession number
Acanthogorgiidae	<i>Calicogorgia granulosa</i>		GU047880
Alcyoniidae	<i>Anthomastus</i> sp.	USNM 1171062	KM015352
Alcyoniidae	<i>Anthomastus</i> sp.	USNM 1081145	KM015353
Alcyoniidae	<i>Sinularia peculiaris</i>		JX023274
Alcyoniidae	<i>Paraminabea aldersladei</i>	NTM C14895	JX508792
Briareidae	<i>Briareum asbestinum</i>		DQ640649
Clavulariidae	<i>Incrustatus comauensis</i>	ANT48	MT254531
Clavulariidae	<i>Pseudotelestula humilis</i> comb. nov.	05ROV2B	MT254527
Clavulariidae	<i>Pseudotelestula humilis</i> comb. nov.	027-DR06	MT254529
Clavulariidae	<i>Pseudotelestula humilis</i> comb. nov.	011-DR08	MT254528
Clavulariidae	<i>Telestula</i> cf. <i>batoni</i>	073-DR02	MT254530
Clavulariidae	<i>Telestula septentrionalis</i>	FC07 L131	MT254532
Coralliidae	<i>Corallium rubrum</i>		AB700136
Coralliidae	<i>Hemicorallium imperiale</i>	USNM 1072449	KC782355
Coralliidae	<i>Hemicorallium imperiale</i>	USNM 1072448	KC782352
Coralliidae	<i>Hemicorallium laauense</i>		KC782348
Coralliidae	<i>Pleurocorallium elatius</i>		AB700134
Coralliidae	<i>Pleurocorallium elatius</i>		AB700135
Coralliidae	<i>Pleurocorallium kishinouyei</i>	USNM 1072441	KC782353
Coralliidae	<i>Pleurocorallium konojoi</i>		AB595190
Coralliidae	<i>Pleurocorallium secundum</i>		KC782347
Coralliidae	<i>Paracorallium japonicum</i>		AB595189
Ellisellidae	<i>Junceella fragilis</i>		KJ541509
Gorgoniidae	<i>Eugorgia mutabilis</i>	SNSB-BSPG 2015 XXXI GW1806	NC035665
Gorgoniidae	<i>Eunicella albicans</i>	SNSB-BSPG 2015 XXXI GW1815	KY559407
Gorgoniidae	<i>Eunicella cavolini</i>	SNSB-BSPG 2015 XXXI GW4597	KY559408
Gorgoniidae	<i>Leptogorgia alba</i>	SNSB-BSPG 2015 XXXI GW4709	KY559410
Gorgoniidae	<i>Leptogorgia capversensis</i>	SNSB-BSPG 2015 XXXI GW1780	KY553145
Gorgoniidae	<i>Leptogorgia gaini</i>	SNSB-BSPG 2015 XXXI GW1777	KY559404

Family	Genus or species	Specimen voucher	Accession number
Gorgoniidae	<i>Leptogorgia cf. palma</i>	SNSB-BSPG 2015 XXXI GW1810	KY559406
Gorgoniidae	<i>Leptogorgia sarmentosa</i>	SNSB-BSPG 2015 XXXI GW4737	KY559411
Gorgoniidae	<i>Leptogorgia</i> sp.	USNM 1437444	KY559412
Gorgoniidae	<i>Pacifigorgia cairnsi</i>	SNSB-BSPG 2015 XXXI GW4656	KY559409
Gorgoniidae	<i>Pseudopterogorgia bipinnata</i>		DQ640646
Isididae	<i>Acanella eburnea</i>	YPM:IZ:44537	EF672731
Isididae	<i>Keratoisidinae</i> sp.	BAL208-1	EF622534
Nephtheidae	<i>Dendronephthya castanea</i>		GU047877
Nephtheidae	<i>Dendronephthya gigantea</i>		FJ372991
Nephtheidae	<i>Dendronephthya mollis</i>		HQ694725
Nephtheidae	<i>Dendronephthya putteri</i>		HQ694726
Nephtheidae	<i>Dendronephthya suenisoni</i>		GU047878
Nephtheidae	<i>Dendronephthya suenisoni</i>		JQ290079
Nephtheidae	<i>Scleronephthya gracillimum</i>		GU047879
Paragorgiidae	<i>Paragorgia coralloides</i>		KF785800
Paragorgiidae	<i>Paragorgia coralloides</i>		KF785801
Paragorgiidae	<i>Paragorgia</i> sp.	USNM 1075769	KC782349
Paragorgiidae	<i>Paragorgia</i> sp.	USNM 1072339	KC782354
Paragorgiidae	<i>Paragorgia</i> sp.	USNM 1075761	KC782350
Paragorgiidae	<i>Paragorgia</i> sp.	USNM 1072362	KC782351
Paragorgiidae	<i>Paragorgia</i> sp.	USNM 1075741	KC782356
Paragorgiidae	<i>Sibogagorgia cauliflora</i>	USNM 1122229	KM015354
Plexauridae	<i>Echinogorgia complexa</i>		HQ694727
Plexauridae	<i>Euplexaura crassa</i>		HQ694728
Plexauridae	<i>Muricea crassa</i>		LT174652
Plexauridae	<i>Muricea purpurea</i>		LT174653
Plexauridae	<i>Paramuricea clavata</i>	GW4701	LT576167
Plexauridae	<i>Paramuricea macrospina</i>	GW4713	LT576168
Primnoidae	<i>Narella hawaiiensis</i>	USNM 1072109	KM015351
Renillidae	<i>Renilla muelleri</i>		JX023273
Virgulariidae	<i>Stylatula elongata</i>		JX023275

**Table S4. Best substitution models and partition schemes selected with PartitionFinder for the 14 mitochondrial protein-coding genes**

Protein-coding gene	Codon position	Best model	Subset partitions (SP)
<i>cox1</i>	cox1_1	GTR+I+G	SP1
	cox1_2	HKY+I+G	SP2
	cox1_3	GTR+G	SP3
<i>nad1</i>	nad1_1	GTR+I+G	SP1
	nad1_2	GTR+I+G	SP6
	nad1_3	HKY+G	SP7

Protein-coding gene	Codon position	Best model	Subset partitions (SP)
<i>cob</i>	cob_1	GTR+I+G	SP5
	cob_2	HKY+I+G	SP2
	cob_3	GTR+G	SP3
<i>nad6</i>	nad6_1	GTR+I+G	SP5
	nad6_2	GTR+I+G	SP6
	nad6_3	GTR+G	SP3
<i>nad3</i>	nad3_1	GTR+I+G	SP1
	nad3_2	GTR+I+G	SP6
	nad3_3	GTR+G	SP3
<i>nad4l</i>	nad4l_1	GTR+I+G	SP1
	nad4l_2	HKY+I+G	SP2
	nad4l_3	GTR+G	SP3
<i>mtMutS</i>	mtMutS_1	GTR+I+G	SP4
	mtMutS_2	GTR+I+G	SP4
	mtMutS_3	GTR+I+G	SP4
<i>nad2</i>	nad2_1	GTR+G	SP3
	nad2_2	GTR+I+G	SP1
	nad2_3	GTR+I+G	SP6
<i>nad5</i>	nad5_1	GTR+I+G	SP5
	nad5_2	GTR+I+G	SP6
	nad5_3	HKY+G	SP7
<i>nad4</i>	nad4_1	GTR+I+G	SP6
	nad4_2	GTR+G	SP3
	nad4_3	GTR+I+G	SP1
<i>cox3</i>	cox3_1	GTR+I+G	SP1
	cox3_2	HKY+I+G	SP2
	cox3_3	GTR+G	SP3
<i>atp6</i>	atp6_1	GTR+I+G	SP1
	atp6_2	HKY+I+G	SP2
	atp6_3	GTR+G	SP3
<i>atp8</i>	atp8_1	GTR+I+G	SP4
	atp8_2	GTR+I+G	SP5
	atp8_3	GTR+G	SP3
<i>cox2</i>	cox2_1	GTR+I+G	SP1
	cox2_1	HKY+I+G	SP2
	cox2_1	GTR+G	SP3

**Table S5. Information on the length of the protein-coding genes, intergenic regions, DNA ambiguities and GC percentage of the mitogenomes of the specimens investigated**

Genes	<i>Incrustatus comauensis</i> (ANT48)	<i>Pseudotelestula humilis</i> comb. nov. (027-DR06)	<i>Pseudotelestula humilis</i> comb. nov. (011-DR08)	<i>Pseudotelestula humilis</i> comb. nov. (05ROV2B)	<i>Telestula cf. batoni</i> (073-DR02)	<i>Telestula septentrionalis</i> (FC07 L131)
<i>cox1</i>	1597	1597	1597	1597	1597	1597
<i>cox1-rns</i>	151	151	151	151	151	151
<i>rns</i>	926	926	926	926	933	934
<i>rns-nad1</i>	4	4	4	4	4	3
<i>nad1</i>	972	972	972	972	972	972
<i>nad1-cob</i>	49	62	62	62	65	62
<i>cob</i>	1158	1158	1158	1158	1161	1161
<i>cob-nad6</i>	313	42	42	45	40	39
<i>nad6</i>	558	558	558	558	558	558
<i>nad6-nad3</i>	43	43	43	43	43	43
<i>nad3</i>	354	354	354	354	354	354
<i>nad3-nad4l</i>	19	19	19	19	24	24
<i>nad4l</i>	294	294	294	294	294	294
<i>nad4l-mtMutS</i>	13	13	13	13	13	13
<i>mtMutS</i>	2982	2970	2970	2970	3000	2976
<i>mtMutS-rnl</i>	9	9	9	9	9	9
<i>rnl</i>	2195	2195	2195	2195	2177	2175
<i>rnl-nad2</i>	4	4	4	4	4	4
<i>nad2</i>	1158	1158	1158	1158	1158	1158
<i>nad2-nad5</i>	-13	-13	-13	-13	-13	-13
<i>nad5</i>	1818	1818	1818	1818	1818	1818
<i>nad5-nad4</i>	64	93	92	93	85	93
<i>nad4</i>	1449	1449	1449	1449	1449	1449
<i>nad4-trnM</i>	57	57	57	57	57	57

Genes	<i>Incrustatus comauensis</i> (ANT48)	<i>Pseudotelestula humilis</i> comb. nov. (027-DR06)	<i>Pseudotelestula humilis</i> comb. nov. (011-DR08)	<i>Pseudotelestula humilis</i> comb. nov. (05ROV2B)	<i>Telestula cf. batoni</i> (073-DR02)	<i>Telestula septentrionalis</i> (FC07 L131)
<i>trnM</i>	71	71	71	71	71	71
<i>trnM-cox3</i>	39	39	39	39	39	44
<i>cox3</i>	786	786	786	786	786	786
<i>cox3-atp6</i>	64	64	64	64	59	60
<i>atp6</i>	708	708	708	708	708	708
<i>atp6-atp8</i>	23	24	24	24	26	32
<i>atp8</i>	216	216	216	216	216	216
<i>atp8-cox2</i>	22	22	22	22	26	27
<i>cox2</i>	762	762	762	762	762	762
<i>cox2-cox1</i>	112	112	112	112	116	114
mt-genome size (bp)	18977	18737	18736	18740	18763	18751
pcg (bp)	18004	17992	17998	17992	18014	17989
igr (bp)	973	745	738	748	749	762
Number of ambiguities	1	9	12	20	61	76
GC%	36.5	36.3	36.3	37	37	36.9