

**Morphological and molecular evidence of cryptic speciation in sympatric colour morphotypes of
Mycale (Carmia) cecilia (Porifera: Poecilosclerida) from the Mexican Pacific**

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SUPPLEMENTARY MATERIAL

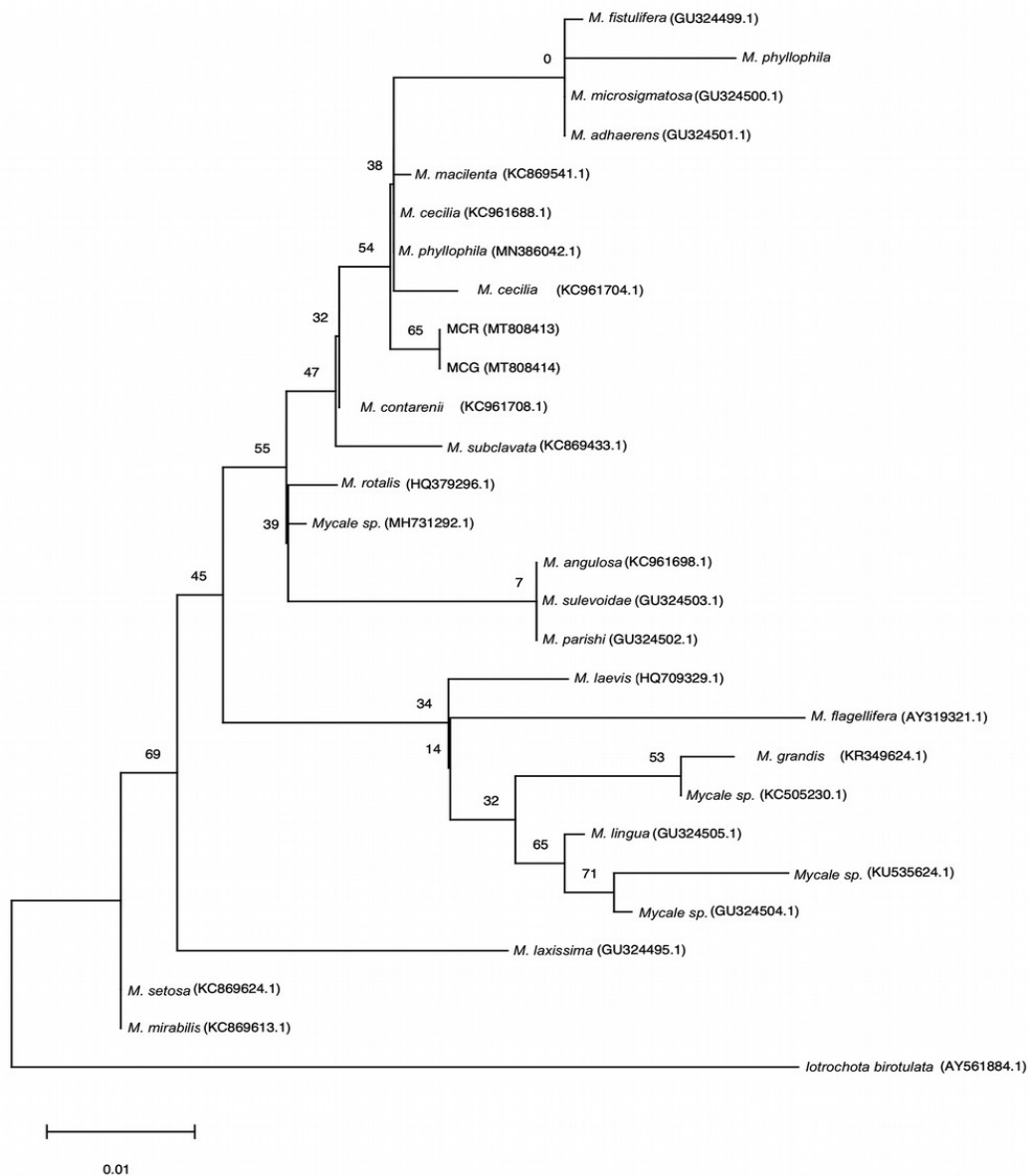


Fig. S1. – Maximum likelihood phylogenetic reconstruction of the partial D3-D5 domain of the 28S gene among morphotypes of *Mycale* (*C.*) *cecilia* (MCR, red individuals; MCG, green individuals) and other species of *Mycale*. Values in the nodes indicate bootstrap support (300 replicates). GenBank accession numbers are in parentheses. No bootstrap values because they are less than 75%.

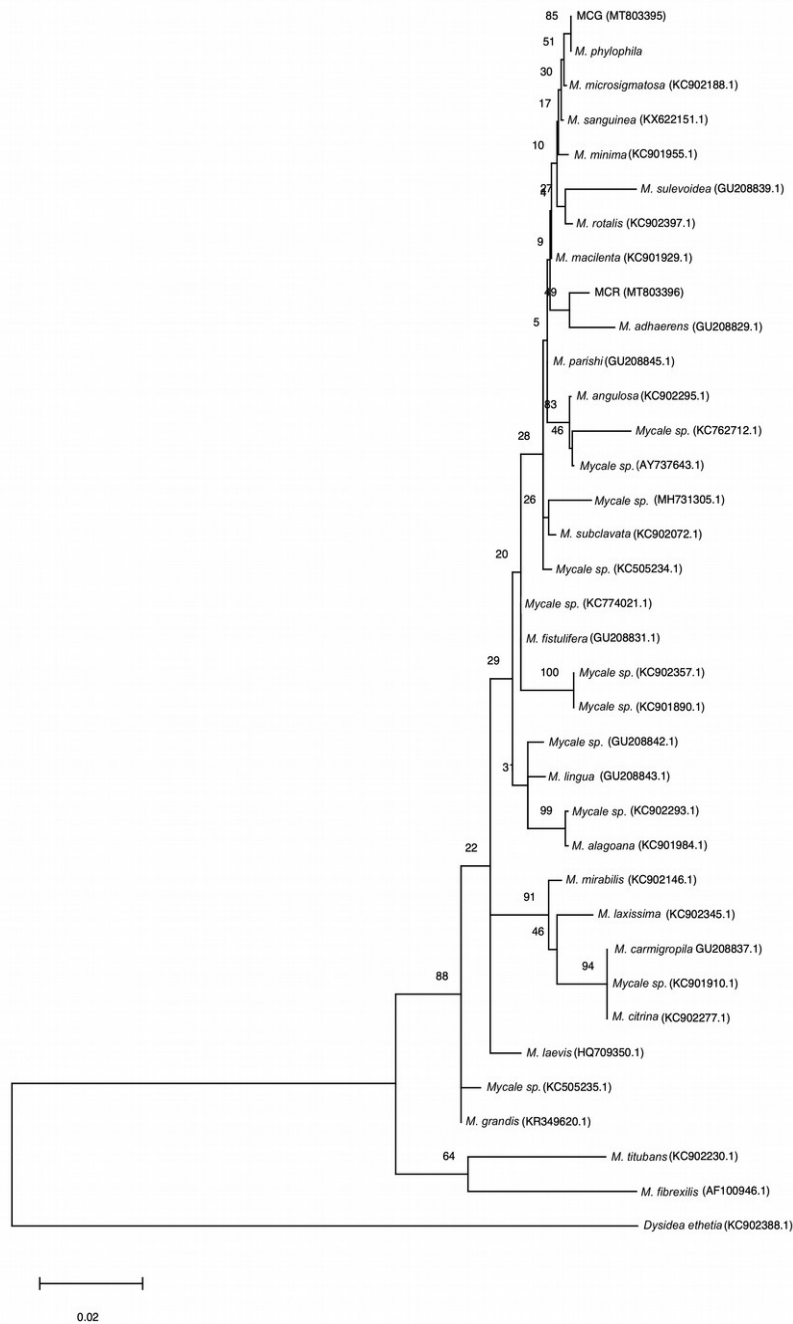


Fig. S2. – Maximum likelihood phylogenetic reconstruction of the nuclear 18S gene among morphotypes of *Mycale* (*C.*) *cecilia* (MCR, red individuals; MCG, green individuals) and other species of *Mycale*. Values in the nodes indicate bootstrap support (>75%, 300 replicates). GenBank accession numbers are in parentheses.

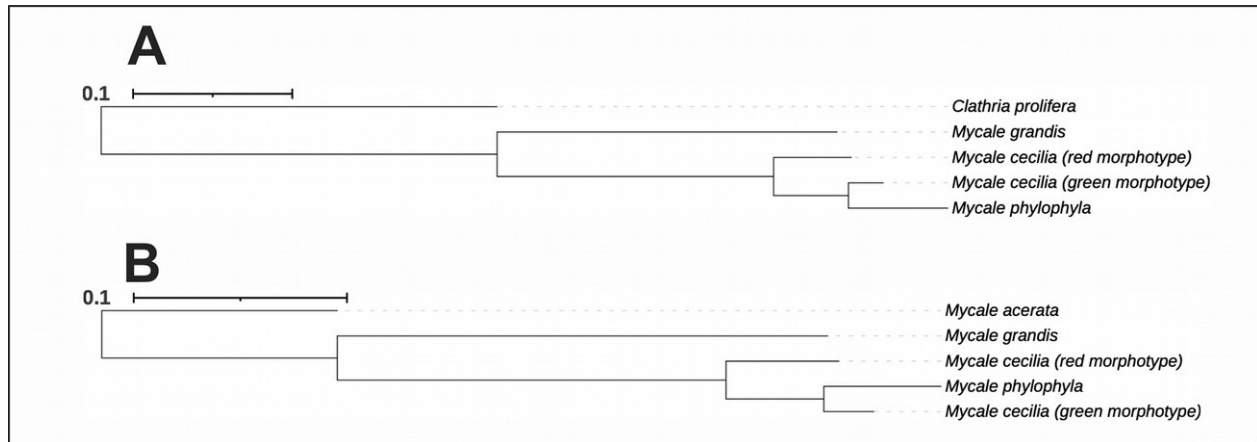


Fig. S4. – Species tree of complete single-copy orthologs using STAG inference, where branch lengths represent the average number of substitutions per site across a large range of gene families. A, 75 complete genes; B, 106 complete genes.

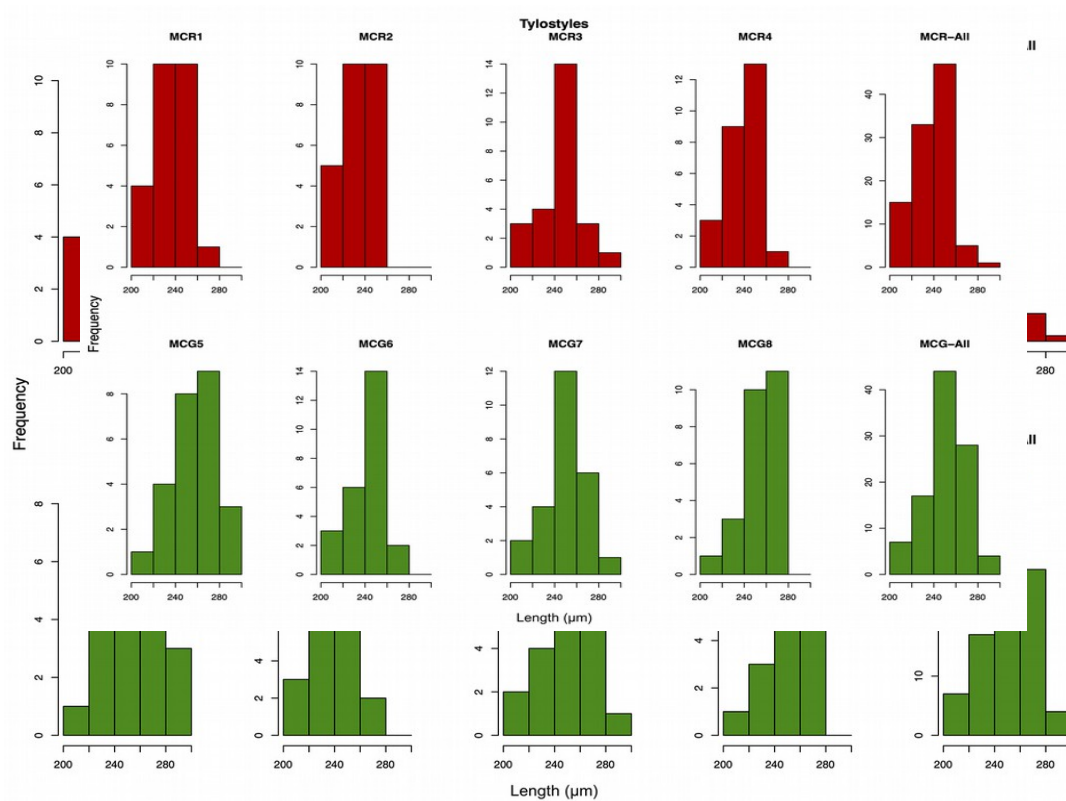


Fig. S5. – Length-frequency distribution of mycalostyles of each individual of *Mycale (C.) cecilia* (MC).

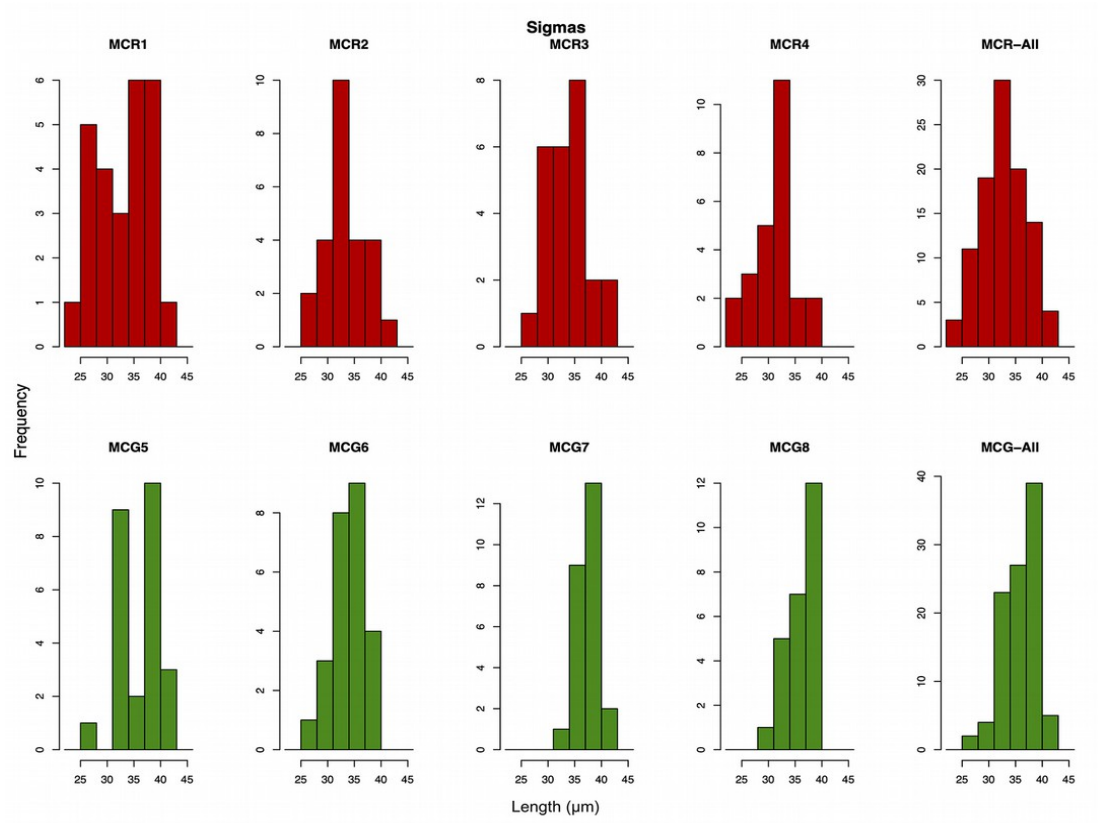


Fig. S6. – Length-frequency distribution of sigmas of each individual of *Mycale (C.) cecilia* (MC)

Table S1. – Source data for transcriptome phylogenetic analyses.

Species	Number of valid reads in assembly	Platform	Read format	Trinity transcripts	Trinity “genes”	contig N50	Complete proteins	SRA accession
<i>Mycale cecilia</i> (green morphotype)	23,029,532	Illumina HiSeq	2*150	200,223	149,755	1,286	52,152	SRR11291276
<i>Mycale cecilia</i> (red morphotype)	20,731,955	Illumina HiSeq	2*150	157,515	120,231	1,322	46,739	SRR13082359
<i>Mycale phylophyla</i>	23,846,465	Illumina HiSeq	2*100	143,136	97,331	1,079	34,431	SRR1711043
<i>Clathria prolifera</i>	20,633,098	Illumina HiSeq	2*150	85,915	55,185	1,934	24,930	SRR22301254
<i>Mycale grandis</i>	22,124,641	Illumina HiSeq	2*125	202,386	136,054	1,255	30,241	SRR3339399
<i>Mycale acerata</i>	23,029,532	Illumina NextSeq 550	2*150	111,427	75,267	884	17,184	SRR11291276
<i>Mycale tridens</i>	78,971,182	Illumina NextSeq 550	2*100	299,581	185,281	673	31,992	SRR11303650 SRR11303651 SRR11303652
<i>Mycale laevis</i>	82,306,782	Illumina NextSeq 550	2*110	1,108,117	817,212	462	54,915	SRR11294007 SRR11294008 SRR11294009

Table S2. – Commands used in the workflow for transcriptome analysis

Procedure	Script
<i>Transcriptomic assemblies per species</i>	trinityrnaseq-v2.15.1/Trinity --seqType fq --max_memory 100G --full_cleanup --trimmomatic --CPU 12 --left No.SRA.acc_1.fastq --right No.SRA.acc_2.fastq
<i>Protein sequences retrieval</i>	
Longest ORFs per species	TransDecoder-TransDecoder-v5.7.0/TransDecoder.LongOrfs -t trinity_out_dir.Trinity.fasta
Homology	
Swissprot (blast)	blastp -query trinity_out_dir.Trinity.fasta.transdecoder_dir/longest_orfs.pep -db /databases/trinotate_3.2.2_dbs/uniprot_sprot.pep -outfmt 6 -evalue 1e-5 -num_threads 24 -max_target_seqs 1 > blastp_longestOrfs
pFAM (HMMER)	hmmsearch --cpu 6 -E 1e-10 --domtblout pfam.domtblout /databases/trinotate_3.2.2_dbs/Pfam-A.hmm trinity_out_dir.Trinity.fasta.transdecoder_dir/longest_orfs.pep
Retention criteria	TransDecoder-TransDecoder-v5.7.0/TransDecoder.Predict -t trinity_out_dir.Trinity.fasta --retain_blastp_hits blastp_longestOrfs --retain_pfam_hits pfam.domtblout
Complete-only protein and renaming	fastagrep.pl "complete" trinity_out_dir.Trinity.fasta.transdecoder.pep seqkit replace -p ‘.+’ -r ‘***_{nr}’ > Cpro_CompleteCDS.pep where *** represents the species’ prefix