DNA barcoding reveals the coral "laboratory-rat", *Stylophora pistillata* encompasses multiple identities

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Table S1. **Intra-clade (in grey) and inter-clade variation in COI [sequence diversity (p-distance)] for *Stylophora* samples**.

p-distance	Clade 1	Clade 2	Clade 3	Clade 4
Clade1	0.00017503± 0.00009578			
Clade 2	0.00378 ± 0.00248	0 ± 0		
Clade 3	0.01592 ± 0.00492	0.01584± 0.00495	0.00462174 ± 0.001932581	
Clade 4	0.01326 ± 0.00470	0.01317 ± 0.00465	0.01274 ± 0.00436	0.000175716 ±0.000117208

Table S2. **Information on COI base pair changes, length of CAD, tRNAW duplication and *Symbiodinium* clades in the four clades of Stylophora**. Asterix represent *Symbiodinium* data that was obtained from published databases.

Location	COI bp changes / Amino acid changes	Length of CAD 3	tRNAW duplication	*Symbiondinium* clades
Clade 1 Pacific Ocean				
Australia (GBR)	7/3	500bp	–	*C
Taiwan	7/3	500bp	Yes	C
Japan	7/3	500bp	Yes	C
Malaysia	7/3	500bp	Yes	C
Indonesia	7/3	500bp		C
New Caledonia	7/3	500bp		C
Clade 2 Indian Ocean				
Kenya	–	900bp	–	C
Tanzania	7 (3) / 4 (2)	500bp	–	C and D
South Africa	9 (4) / 4 (2)	500bp, or 400bp, 600bp, 900bp	–	C
Madagascar	9 (4) / 4 (2)	500bp, or 400bp, 600bp, 900bp	–	C
St. Brandon's (Mauritius)	7/3	500bp	–	C
Chagos Archipelago	7/3	500bp	Yes	C
Australia	7/3	500bp	–	*C
Clade 3 *Stylophora madagascarensis*				
Tanzania	7 (3) / 4 (2)	500bp	–	C and D
Madagascar	9 (4) / 4 (2)	500bp, or 400bp, 600bp, 900bp	–	C
South Africa	9 (4) / 4 (2)	500bp, or 400bp, 600bp, 900bp	–	C
Yemen	Morph S 6/2	900bp	No	A and C
Clade 4 Red Sea				
Saudi Arabia (Gulf of Aqaba)	–	900bp	No	A and A+C
Eilat (Red Sea)	–	900bp	No	A and A+C
Dijbouti	–	900bp	No	A and A+C
Yemen	Morph M, L	900bp	No	A and C
Oman	–	900bp	No	A and A+C

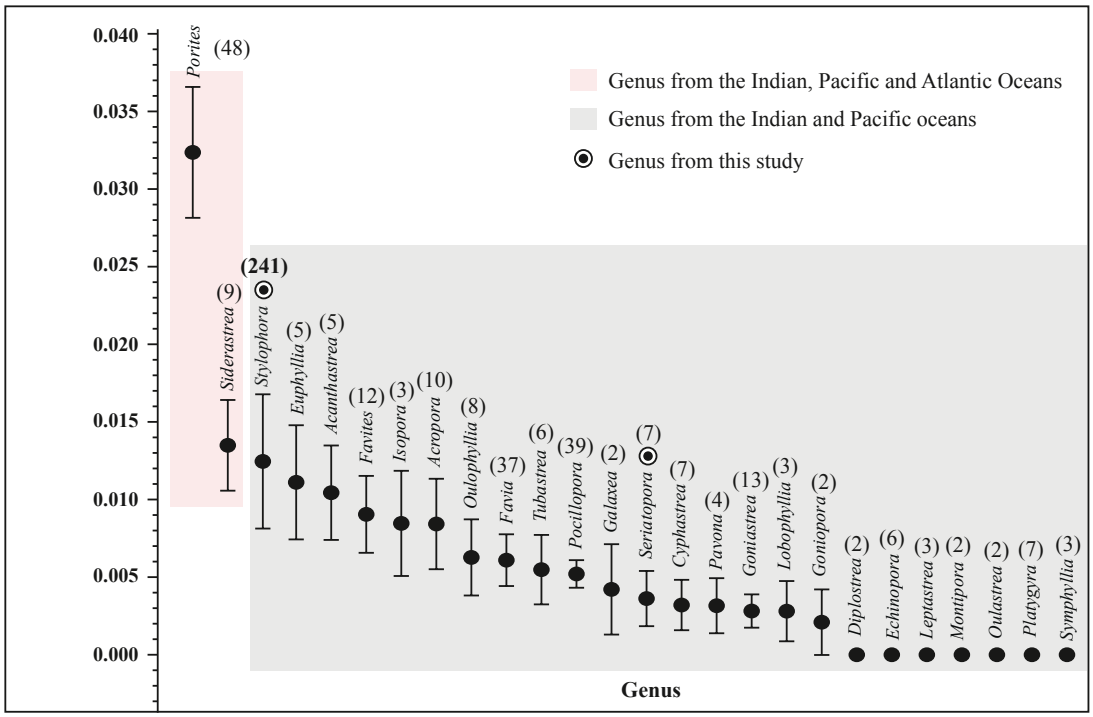

Figure S1. **Interspecific variation in COI [sequence diversity (p-distance)] for *Stylophora* samples compared with other coral groups**. Numbers in the brackets represent the number of sequences for each genus obtained from the NCBI GenBank database, except for *Stylophora* and *Seriatopora* sequences for which the samples were obtained in this study.

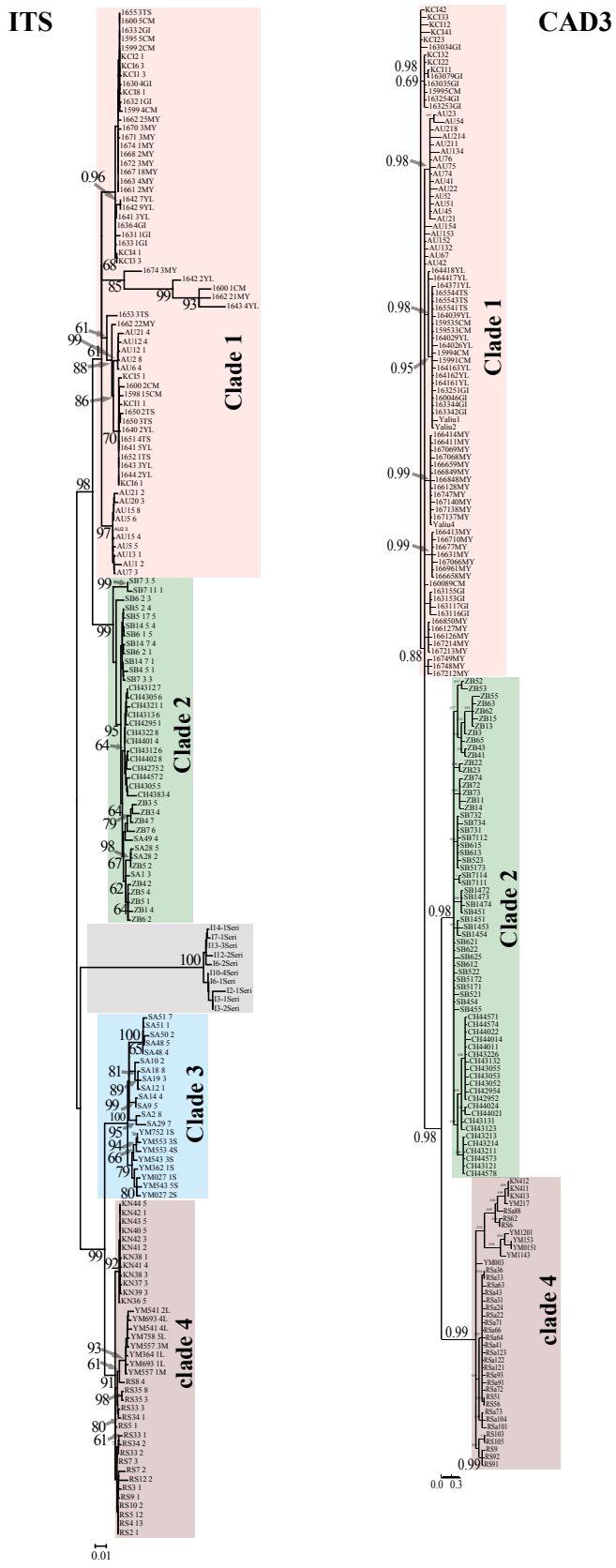

Figure S2. Phylogenetic analysis of ITS (whole ITS1 and ITS2 corresponding to 1138bp) and CAD3 (corresponding to 500bp) sequences of *Stylophora* samples. The absence of clade 3 and *Seriatoproa* groups in CAD3 phylogenetic tree was due to non-amplification of the corresponding samples. Bootstrap values are based on ML/Baysian analysis.

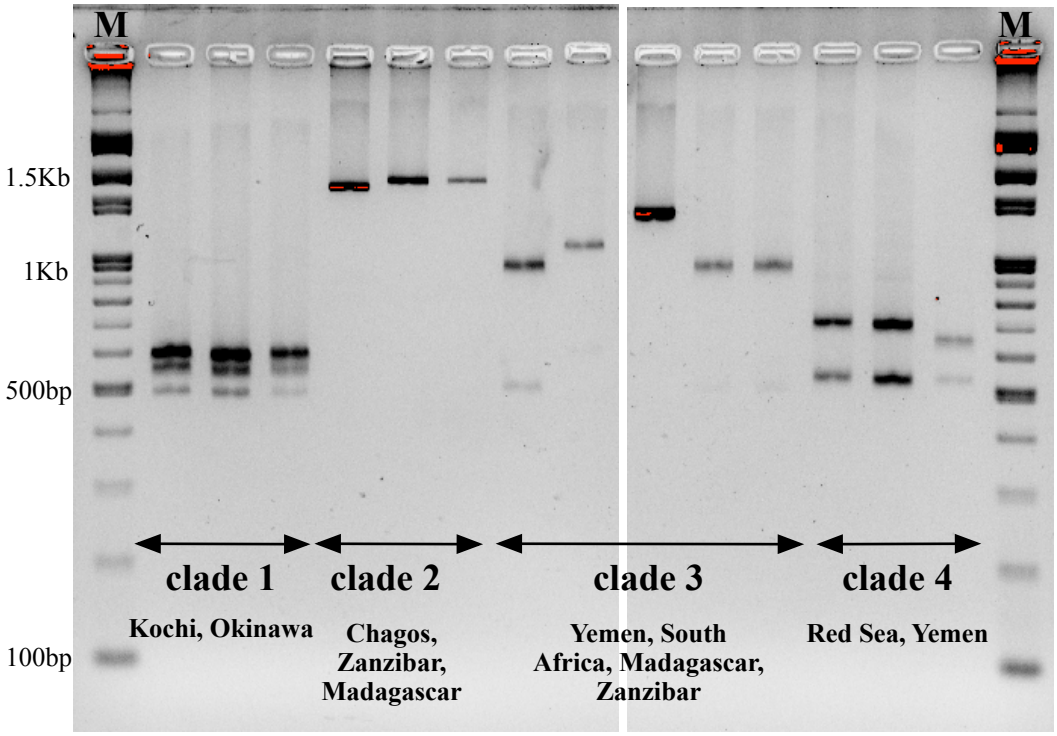

Figure S3. Representative tRNAW pattern for clade 1, clade 2, clade 3 and clade 4 of *Stylophora* sp. obtained by restriction enzyme (RSAI) digestion of PCR products.