

SUPPLEMENTARY

Supplementary 1 **Number of specimens based on locations and depths represented in tables of:** (a) total number of specimens collected in sampling, (b) numbers of generated ITS-2 sequences, and (c) of numbers of generated *psbA_{ncr}* sequences obtained. FBO=Farasan Banks Offshore; FBM= Farasan Banks Midshelf; FBI= Farasan Banks Inshore; TI=Thuwal.

(a) Total number of specimens collected

LOCATIONS	SPECIMENS	DEPTHS (m)	SPECIMENS
FBO	46	0-10	63
FBM	68	10.1-20	80
FBI	47	20.1-30	54
TI	42	30.5	6
TOTAL	203		203

(b) Number of ITS2 sequences

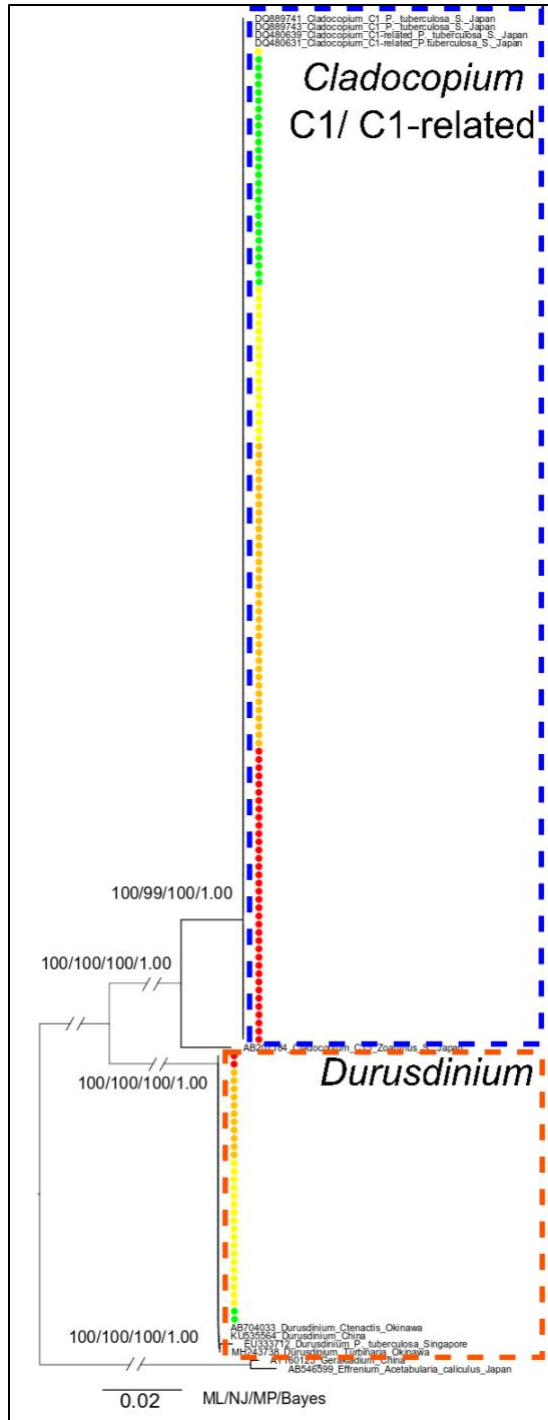
LOCATIONS	<i>Cladocopium</i>	<i>Durusdinium</i>	Total
FBO	41	2	43
FBM	54	14	68
FBI	30	16	46
TI	39	2	41
TOTAL	164	34	198

DEPTHS (m)	<i>Cladocopium</i>	<i>Durusdinium</i>	Total
0-10	50	11	61
10.1-20	57	21	78
20.1-30	51	2	53
30.5	6	0	6
TOTAL	164	34	198

(c) Number of *psbA_{ncr}* sequences

LOCATIONS	Pt-1-a	Pt-1-b	Pt-3-a	Pt-3-b	Pt-1-c	Pt-1-d	Total	No.	SWDI	Evenness
FBO	4	1	25	3	1	0	34	5	0.900	0.559
FBM	5	3	8	20	1	0	37	5	1.235	0.768
FBI	2	11	0	2	2	3	20	5	1.304	0.810
TI	3	0	0	32	0	0	35	2	0.293	0.422
TOTAL	14	15	33	57	4	3	126			

DEPTHS (m)	Pt-1-a	Pt-1-b	Pt-3-a	Pt-3-b	Pt-1-c	Pt-1-d	Total	No.	SWDI	Evenness
0-10	4	5	4	20	3	3	39	6	1.468	0.819
10.1-20	5	7	11	19	1	0	43	5	1.343	0.834
20.1-30	3	2	18	15	0	0	38	4	1.076	0.776
30.5	2	1	0	3	0	0	6	3	1.011	0.921
TOTAL	14	15	33	57	4	3	126			



Supplementary 2 **Phylogeny of Symbiodiniaceae from *Palythoa tuberculosa* at Farasan Banks and Thuwal.** Maximum Likelihood (ML) tree of the internal transcribed spacer 2 of ribosomal DNA (ITS-2) of nuclear ribosomal DNA of Symbiodiniaceae with reference sequences from Reimer et al. (2017a). Coloured dots on the tree represent each specimen found at FBO (red), FBM (orange) and FBI (yellow), and TI (green). Values at the branches represent ML, neighbor joining (NJ) and maximum parsimony (MP) bootstrap supports, and Bayesian inference (Bayes) posterior probability, respectively. Dotted boxes in the figure represent genera of Symbiodiniaceae. FBO=Farasan Banks Offshore; FBM= Farasan Banks Midshelf; FBI= Farasan Banks Inshore; TI=Thuwal.

Supplementary 3 **Genetic difference among lineages in this study (Pt-1-a, Pt-1-b, Pt-1-c, Pt-1-d, Pt-3-a, Pt-3-b)**. Two tables represent the (a) within-group genetic difference with mean and standard deviation (StDev), and (b) pairwise genetic differences between groups with mean (bottom black) and standard deviation (top, grey).

(a) Within group genetic difference

GROUP	GROUPS	MEAN	StDev
Specimens	Pt-1-a	0.040	0.010
	Pt-1-b	0.000	0.000
	Pt-1-c	0.028	0.011
	Pt-1-d	0.000	0.000
	Pt-3-a	0.001	0.001
	Pt-3-b	0.008	0.002

(b) Pairwise genetic differences between groups

	Pt-1-a	Pt-1-b	Pt-1-c	Pt-1-d	Pt-3-a	Pt-3-b
Pt-1-a		0.029	0.025	0.044	0.05	0.05
Pt-1-b	0.089		0.027	0.03	0.046	0.045
Pt-1-c	0.079	0.070		0.043	0.048	0.047
Pt-1-d	0.180	0.082	0.160		0.057	0.056
Pt-3-a	0.213	0.161	0.195	0.233		0.015
Pt-3-b	0.208	0.159	0.192	0.232	0.027	

Supplementary 4 **Analysis of the Molecular Analysis (AMOVA) for *Cladocopium psbA_{ncr}***. Two statistical comparisons were conducted based on populations sorted by (a) locations and (b) depths (meter).

(a) LOCATIONS

Source	df	SS	MS	Est. Var.	%	PhiPT	P
Among Pops	3	878.571	292.857	9.007	40%	0.401	<0.001
Within Pops	122	1641.738	13.457	13.457	60%		
Total	125	2520.310		22.464	100%		

(b) DEPTHS

Source	df	SS	MS	Est. Var.	%	PhiPT	P
Among Pops	3	135.674	45.225	0.880	4%	0.043	0.038
Within Pops	122	2384.636	19.546	19.546	96%		
Total	125	2520.310		20.427	100%		