Population structure in the *Pocillopora damicornis* cryptic species complex along Ningaloo Reef, Western Australia

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A key characteristic influencing the recovery potential of coral reefs to environmental perturbations is the level of connectivity between adjacent reefs by the dispersal of larvae. Here we report on the population structure of *P. damicornis* along the Ningaloo Reef Marine Park using a panel of microsatellite markers and a mitochondrial gene marker (ORF).

Cryptic Species Complex

Three morphologically cryptic mitochondrial lineages in *P. damicornis* were found to co-occur on a single reef system.

These findings add to the mounting global evidence showing a large discrepancy between morphology and genetics within this genus of widely-distributed habitat-forming corals (Pinzon et al. 2013; Souter et al. 2009).

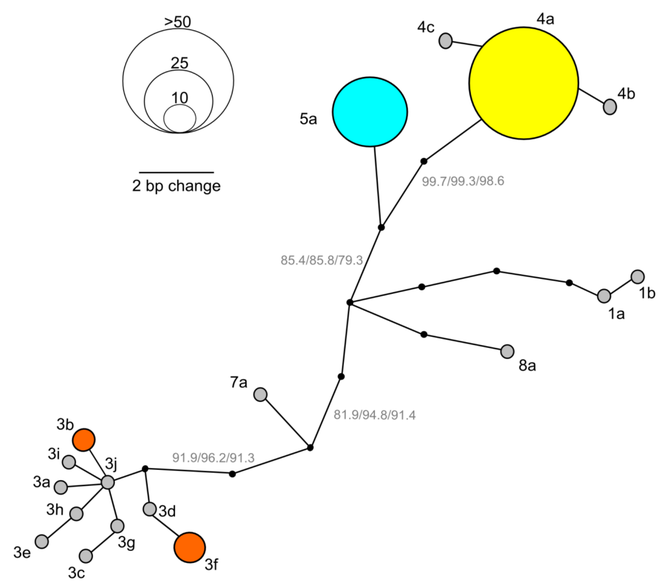

Figure 2 Unrooted maximum parsimony tree redrawn to incorporate published sequence data on all Open Reading Frame haplotypes recovered from unique MLGs of *Pocillopora damicornis*. Coloured circles indicate haplotypes detected in this study. Numbers adjacent to branches are bootstrap values based on 10,000 replicate parsimony, neighbour joining, and likelihood analyses, respectively.

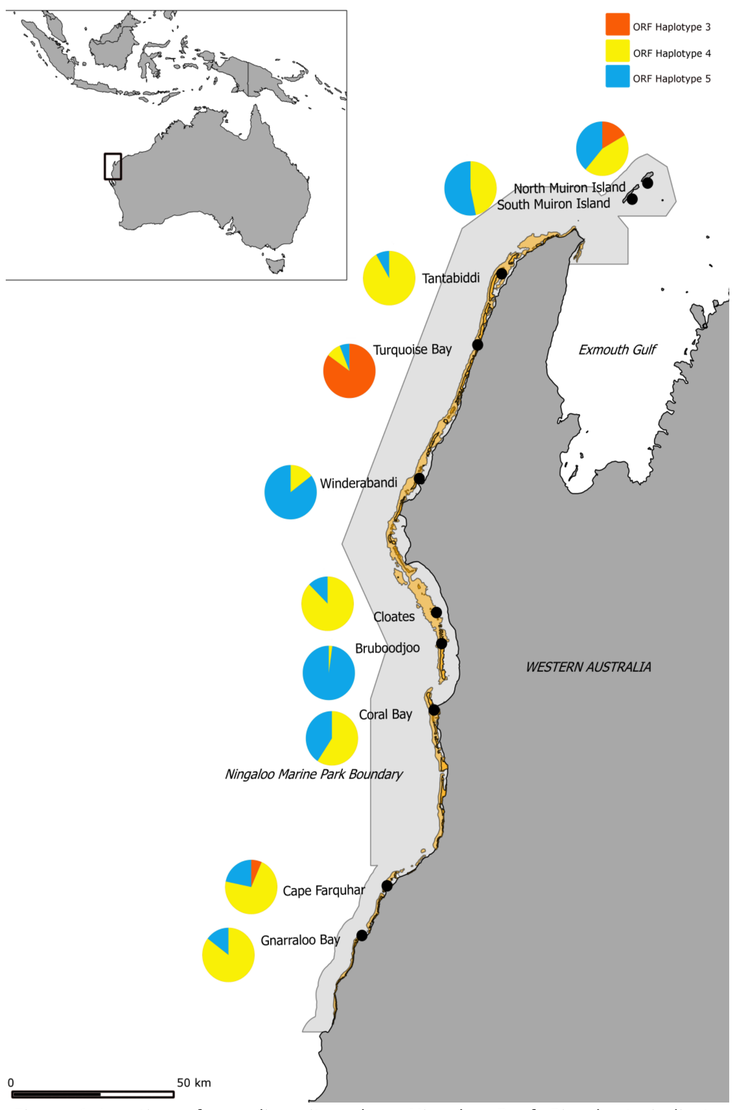

Figure 1 Location of sampling sites along Ningaloo Reef. Pie charts indicate frequency of the three mitochondrial Open Reading Frame haplotypes recovered across the marine park: Types 3, 4 and 5.

Clonal Diversity

62 % of colonies sampled were of asexual origin. This is consistent with previous reports of *P. damicornis* from this region that show asexual reproduction through brooding is the dominant reproductive mode (Whitaker 2006).

While asexual reproduction appeared to be favoured when data from all lineages were pooled, Types 4 and 5 displayed patterns consistent with that of predominantly sexual reproduction

Table1 Estimates of clonal diversity at each site. *N* = number of samples; N_G = number of multilocus genotypes; N_G/N = genotypic richness; *G* = genotypic diversity

	ORF 3				ORF 4				ORF 5			
Site	**N**	**N_G**	**N_G /N**	**G**	**N**	**N_G**	**N_G /N**	**G**	**N**	**N_G**	**N_G /N**	**G**
NM	6	6	1.00	1.00	16	10	0.63	0.94	14	11	0.79	0.96
SM	--	--	--	--	14	11	0.79	0.96	16	5	0.31	0.75
TBD	--	--	--	--	22	10	0.45	0.90	2	2	1.00	1.00
TRQ	28	1	0.04	0.00	3	2	0.67	0.67	2	2	1.00	1.00
WNB	--	--	--	--	6	3	0.50	0.60	35	6	0.17	0.77
CLO	--	--	--	--	28	18	0.64	0.96	4	4	1.00	1.00
BBJ	--	--	--	--	1	1	1.00	1.00	46	5	0.11	0.31
CB	--	--	--	--	16	14	0.88	0.97	12	3	0.25	0.62
FQ	3	3	1.00	1.00	35	22	0.63	0.97	9	4	0.44	0.58
GNB	--	--	--	--	29	6	0.21	0.73	1	1	1.00	1.00
Pooled	37	10	0.27	0.43	170	94	0.55	0.99	141	94	0.67	0.85

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Connectivity and Dispersal

Populations of Type 4 *P. damicornis* appear to display high levels of connectivity between adjacent reefs.

Significant shared genetic structure was observed at distances up to 80 km, with positive spatial structure extending up to 200 km when distance classes were pooled.

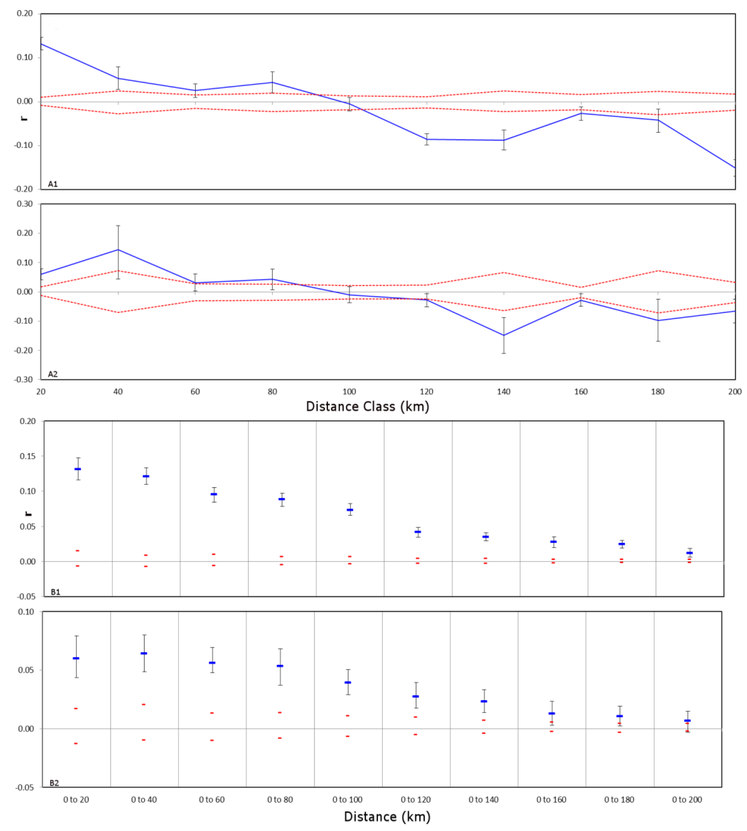

Figure 3 Spatial autocorrelation analyses of Open Reading Frame Type 4 colonies of *Pocillopora damicornis* from the Ningaloo Reef Marine Park. The permuted 95% confidence intervals (dashed lines) and bootstrap error bars are shown. A) Single correlogram plot for all individuals (1) and for unique MLG only (2); B) Multiple distance class plot for all individuals (1) and for unique MLG only (2)

Hybridization

All hybrids originated from the Muiron Islands. We propose that heightened exposure to thermal stress has led to the breakdown of boundaries between lineages and hybridization in this region.

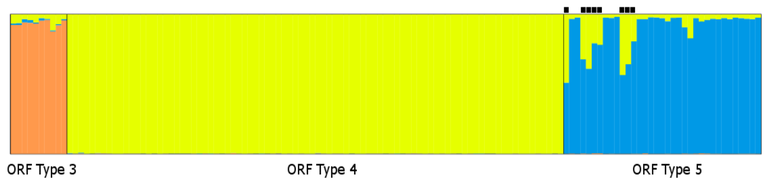

Figure 4 Results from STRUCTURE analysis testing for admixture between lineages (K = 3). Individuals were grouped according to mitochondrial Open Reading Frame lineage (3, 4 and 5). Individuals identified as F_1 hybrids using NEWHYBRIDS are indicated with dots.

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