Supplemental Material for

Colour dimorphism in labrid fishes as an adaptation to life on coral reefs

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Other supplemental material for this manuscript includes: Tables Sl, S4 (Excel file)

1 Figures

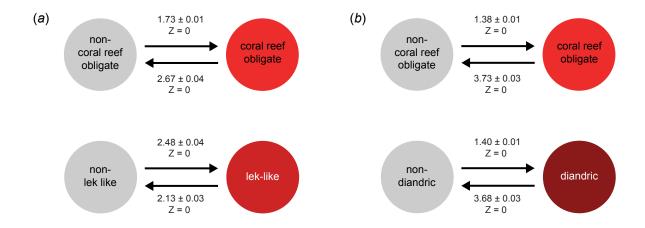


Figure S1: (*a*) Mean evolutionary transition rates (qxy \pm SE) derived from Bayesian models of discrete character evolution fit to predicted associations between coral reef exclusivity and leklike mating. (*b*) Mean evolutionary transition rates (qxy \pm SE) derived from Bayesian models of discrete character evolution fit to predicted associations between coral reef exclusivity and diandry. In both panels, Z-scores below each transition rate denote the proportion of transition rates assigned to zero – values \leq 0.05 are rarely assigned to zero and considered probable evolutionary events.

2 Tables

Table S2: Loadings from the logistic principal component analysis of the binary matrix describing colour dimorphism of labrid species.

	PC1	PC2
head	-0.372	0.466
body	-0.416	0.547
pectoral	-0.280	-0.493
pelvic	-0.301	-0.391
anal	-0.431	-0.279
dorsal	-0.476	-0.083
caudal	-0.328	0.046

Table S3: Log marginal likelihoods estimated from dependent and independent models of character evolution, and corresponding log Bayes Factors (BFs). Three independent iterations tested for correlated evolution between coral reef exclusivity and lek-like polygyny, and between coral reef exclusivity and diandric protogyny. Log Bayes Factors indicate evidence against the null hypothesis (independent model), with values < 2 indicating weak evidence, 2–5 indicating positive evidence, and > 5 indicating strong evidence.

Traits tested	Dependent model	Independent model	log Bayes Factor	
coral reef exclusive/non-coral reef exclusive				
& lek-like/non-lek-like:				
	-105.46	-102.83	-5.25	
	-105.46	-102.87	-5.18	
	-105.43	-102.88	-5.10	
coral reef exclusive/non-coral reef exclusive				
& diandric/non-diandric:				
	-100.84	-97.41	-6.85	
	-101.23	-97.24	-7.97	
	-101.14	-97.26	-7.77	

Table S5: Results of phylogenetic generalized linear models testing whether the probability of observing each colour group differs with coral reef association. Multiple starting values were specified for alpha (0.1, 0.5, and 0.9) to ensure the results returned the global maximum. Results with the maximum penalized likelihood are reported here as single values or a range of values in cases where multiple starting values returned the same maximum penalized likelihood. Significance codes are: (.) = P-values between 0.05 and 0.1; (*) = P-values between 0.01 and 0.05; and (**) = P-values less than 0.01.

	Colour group	Penalized log-likelihood	Alpha	Estimate	Standard error	Z-value	P-value	Significance code
	black/brown	-17.68	0.9533	0.4006	0.6106	0.6561	0.5117	
initial	white	-21.75	0.9678	-0.7656	0.5277	-1.4508	0.1468	
	yellow	-51.80	0.4694-0.5041	0.0064-0.0143	0.3099-0.3102	0.0206-0.0462	0.9631-0.9836	
phase	red/orange	-50.86	0.1553-0.1596	0.0414-0.0553	0.3214-0.3220	0.1287-0.1718	0.8636-0.8976	
	blue/green	-56.61	0.1715-0.1738	0.2828-0.2933	0.3046-0.3049	0.9285-0.9618	0.3361-0.3531	
	black/brown	-29.73	0.0744-0.0749	-0.80050.7874	0.4470-0.4532	-1.76641.7499	0.0773-0.0801	
terminal	white	-48.42	0.3631	-1.0448	0.3377	-3.0936	0.0020	**
	yellow	-50.09	0.1367-0.1446	0.4351-0.4503	0.3305-0.3317	1.3127-1.3577	0.1746-0.1893	
phase	red/orange	-37.99	0.2427-0.2501	0.8129-0.8393	0.4171-0.4173	1.9489-2.0114	0.0443-0.0513	*
	blue/green	-29.90	0.0135-0.0136	0.9550-0.9642	0.3744-0.3773	2.5503-2.5552	0.0106-0.0108	*

Table S6: The relationship between minimum, maximum and midpoint depth and the magnitude of colour dimorphism. Positive estimates reflect the expected relationship between depth and dichromatism such that as depth increases, dichromatism decreases.

	Estimate	SE	Adjusted R ²	t-value	P-value	Pagel's λ	95% CI
Minimum	0.281	0.227	0.030	1.241	0.218	0.228	0.018-0.602
Midpoint	0.036	0.064	0.021	0.558	0.578	0.187	0.006-0.553
Maximum	0.015	0.035	0.020	0.436	0.664	0.183	0.005-0.549

Table S7: Results of phylogenetic generalized linear models testing whether the probability of each body and fin region being colour-dimorphic varies with coral reef association. Multiple starting values were specified for alpha (0.1, 0.5, and 0.9) to ensure the results returned the global maximum. Results with the maximum penalized likelihood are reported here as single values or a range of values in cases where multiple starting values returned the same maximum penalized likelihood. Significance codes are: (.) = P-values between 0.05 and 0.1; (*) = P-values between 0.01 and 0.05; and (**) = P-values less than 0.01.

Body/fin region	Penalized log-likelihood	Alpha	Estimate	Standard error	Z-value	P-value	Significance code
head	-53.99	0.1575625	0.7312	0.32271	2.2659	0.02346	*
body	-52.21	0.1424935	0.757	0.32848	2.3045	0.02119	*
pectoral fin	-49.37	0.081-0.082	0.5872-0.5875	0.3433-0.3436	1.7093-1.7113	0.0870-0.0874	
pelvic fin	-44.38	0.080-0.081	0.7967-0.8022	0.3559-0.3565	2.2352-2.2539	0.0242-0.0254	*
anal fin	-54.37	0.128	0.5563-0.5659	0.3164-0.3168	1.7583-1.7866	0.0740-0.0787	
dorsal fin	-54.47	0.164-0.166	0.5919-0.5934	0.3169-0.3170	1.8672-1.8721	0.0612-0.0619	
caudal fin	-52.54	0.126-0.129	0.7504-0.7513	0.3313-0.3316	2.2629-2.2677	0.0234-0.0236	*

3 Captions for Tables S1, S4

Table S1: Trait data, colour dimorphism, and colour data by species. For colour dimorphism, '0' indicates colour similarity and '1' indicates colour difference between initial and terminal phase fish. The 'Proportion colour dimorphic' column summarises colour dimorphism data by indicating the proportion of body regions that were scored colour dimorphic relative to the total number of body regions considered. For colour group expression, '0' indicates absence and '1' indicates expression of the colour group by initial or terminal phase fish. (separate file)

Table S4: Evolutionary models best-fit to colour dimorphism as predicted separately by habitat association, mating system and sex allocation. Models with ΔAICc values less than two were considered to have comparable support (Comp. model). Regime specific parameters are denoted as: (N) non-coral reef; (A) coral reef associated; (E) coral reef exclusive; (P) promiscuous; (H) harem polygyny; (L) lek-like polygyny; (G) gonochorous; (M) monandric protogyny; and (D) diandric protogyny. 95% confidence intervals for all-best-fit model parameters were generated by parametric bootstrapping. Statistical power to identify the correct model, or class of model (i.e. single-peak versus multi-peak) was estimated with simulations. (separate file)