Phylogeography of the neon damselfish *Pomacentrus coelestis* indicates a cryptic species and different species origins in the West Pacific Ocean

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Supplement. Phylogenetic analyses with concatenated COI and control region sequences.

A subset of cytochrome *c* oxidase subunit I (COI) sequences was analyzed. The genetic divergence between taxa is shown in Table S1, and a neighbor-joining (NJ) tree with bootstrap and credibility values is shown in Fig. S1. Methodological details and results are provided in the following section, and Table S2 gives bidirectional migration rates.

In total, 600 bp of partial mitochondrial COI was amplified from a subset of 4 haplotype groups (see Fig. 2 in the main text) and the closely related species *Pomacentrus auriventris* (6 individuals). Five individuals were chosen from each clade, except the orange clade, for which only 2 individuals were used. The COI sequences were submitted to GenBank (accession numbers JQ418300 to JQ418311). Pairwise Kimura 2-parameter distances (K2P) were estimated between taxa, including the Micronesian group (orange, white, and black haplotypes), Pacific group (blue haplotypes), and *P. auriventris*, with MEGA 5 (Tamura et al. 2011). The optimal substitution model was HKY plus Gamma, and the Gamma value was 0.1468. The phylogenetic tree was constructed by NJ and Bayesian inference methods with sequences of concatenated COI and the control region and used *P. moluccensis* as the outgroup.

Table S1. Kimura 2-parameter genetic distance of cytochrome *c* oxidase subunit I between the Pacific clade, Micronesian clade, and *Pomacentrus auriventris*

Group	Pacific clade	Micronesian clade	*P. auriventris*
Pacific clade	-		
Micronesian clade	0.040	-	
P. auriventris	0.015	0.050	-

Table S2. Migration estimates and 95% confidence values as estimated by MIGRATE (Beerli & Felsenstein 2001)

| Migration	2.5%	25.0%	75.0%	97.5%	Mean
Cenderawasih Bay to Micronesia	0	70	310	560	327
South Pacific to Micronesia	0	0	125	430	163.2
West Pacific to Micronesia	45	155	345	765	359.3
Raja Ampat to Micronesia	0	0	55	205	77
Micronesia to Cenderawasih Bay	220	545	825	1000	549.9
South Pacific to Cenderawasih Bay	0	0	55	470	211.7
West Pacific to Cenderawasih Bay	0	0	65	620	284.1
Raja Ampat to Cenderawasih Bay	0	0	180	350	362.2
Micronesia to South Pacific	0	0	40	335	145.8
Cenderawasih Bay to South Pacific	0	10	125	345	141.9
West Pacific to South Pacific	385	865	985	1000	706.9
Raja Ampat to South Pacific	0	0	40	200	62
Micronesia to West Pacific	0	0	70	180	75.5
Cenderawasih Bay to West Pacific	0	0	35	120	41.1
South Pacific to West Pacific	50	90	185	710	376
Raja Ampat to West Pacific	300	605	835	940	639.5
Micronesia to Raja Ampat	120	260	515	790	469.3
Cenderawasih Bay to Raja Ampat	375	570	805	1000	655.9
South Pacific to Raja Ampat	0	0	60	525	203
West Pacific to Raja Ampat	40	70	285	820	344.1
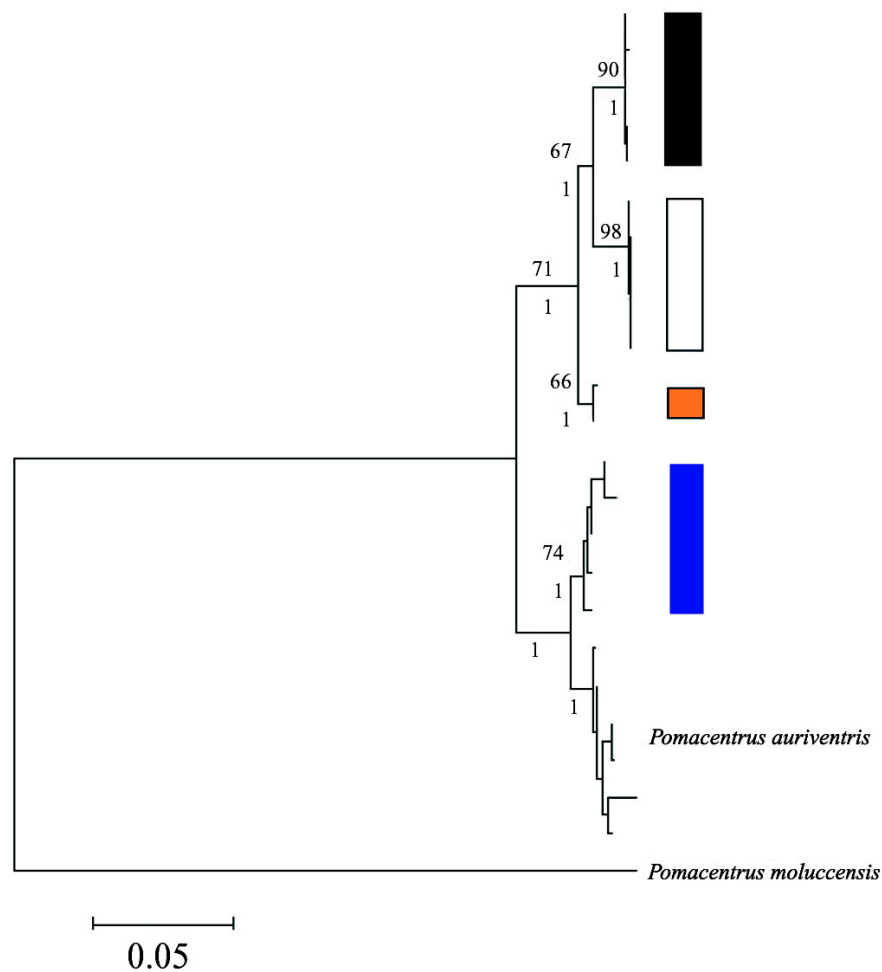
Fig. S1. *Pomacentrus coelestis*. Neighbor-joining phylogenic tree based on the concatenated mtDNA control region and cytochrome *c* oxidase subunit I. Numbers above nodes represent support based on 1000 bootstrap replicates, and numbers below nodes represent clade credibility values from Bayesian analysis. The scale bar represents 0.05 nucleotide changes. The color bar indicates 4 clades corresponding to the blue, orange, white, and black clades shown in Fig. 2 of the main text

LITERATURE CITED

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Tamura K, Peterson D, Peterson N, Stecher G, Nei M, Kumar S (2011) MEGA5: Molecular evolutionary genetics analysis using maximum likelihood, evolutionary distance, and maximum parsimony methods. Mol Biol Evol 28:2731–2739