Ecography

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Supplementary material

Appendix 1. Supplementary methods

Laboratory methods

Total genomic DNA was extracted from collected tissue using a salt extraction method (modified from Aljanabi and Martinez 1997). The mitochondrial control region (CR) and cytochrome *c* oxidase subunit I (COI) were amplified using CR-A and CR-E (Lee et al. 1995) and the universal fish primers (Fish F1 and Fish R1, Ward et al. 2005), respectively, following the protocols detailed in Mirams et al. (2011). Amplicons were purified using Exonuclease I and Antarctic Phosphatase following the Exo-SAP protocol (New England Biolabs) and sequenced by Macrogen (Korea) via capillary electrophoresis. Sequences were manually checked and edited in CodonCode Aligner v3.7.1.2 (CodonCode Corporation) and aligned using Se-Al v2.0a11 (Rambaut 1996). The aligned sequences were translated into amino acid sequences using the vertebrate mitochondrial code to ensure they were not of nuclear origin and the primer sequence and regions of insignificant overlap at either end of the sequences were deleted in Se-Al. All *de novo* sequences are available on GenBank (KJ779106-KJ779397, KJ779872-KJ779960).

Explanation of data integration and inclusion for analysis

The *de novo* sequences were combined with other sequences available on GenBank (Liu et al. 2008: EF420785-EF420855, Liu et al. 2010: EU366845-EU366889, Mirams et al. 2011: JF717975-JF718155, Liu et al. 2012: JF314773-JF314842, JQ418300-JQ418311). Where the sequence data from GenBank had insufficient relating information (i.e. haplotype frequency or geographic location), data were excluded from some analyses and in some cases statistics were taken from the original publication (see Supplementary material Appendix 2 for locations included in each analysis and the source of data). Where the same location was included in multiple studies, we included the location only once to avoid pseudo-replication. Potential overlapping locations (e.g. Guihou, Taiwan from Liu et al. 2012 was removed as it was unclear whether it overlapped with Maoao and Yehliu reported in Liu et al. 2010; Australia from Liu et al. 2012 was removed because it may overlap with some of the localities used herein), and locations with very small sample sizes were also removed.

Some populations of $n < 10$ from the southern periphery were kept in the dataset as their small sample sizes were indicative of naturally low densities.

All sequences from across the studies were aligned to check for overlap, sequence length consistency, and the likely influence of missing data on across study comparison of genetic diversity (π, *Hd*). Sequences across studies had few sites with missing data and were of comparable length. There was overlap across all polymorphic sites in the combined sequence dataset except two sites at the 3' end of two unique haplotypes identified in Liu et al. (2012). The sequences of Liu et al. (2008, 2010) did not overlap with these sites, whereas our *de novo* sequences overlapped, but the polymorphism was not shared with either our Pacific or Micronesian clade individuals. Given that there was substantial overlap across all sequences, we did not make any correction of genetic diversity values for differing sequence length.

To evaluate any inconsistency in our calculation of genetic diversity, we reconstructed the sequence dataset of Liu et al. (2008; using haplotypes uploaded on GenBank and the frequency data provided in their supplementary material: 71 haplotypes, 170 individuals, 343 bp) and compared our calculated values (π, *Hd*) with those reported in their original publication. Our recalculated values for the locations studied by Liu et al. (2008) were largely unchanged from their reported values. For π: two values differed from the original value by 10 and 14%; and for *Hd*: one value differed by less than 0.1%, verifying that our method of calculation was the same and therefore these summary statistics could be compared across studies (inconsistencies between values were likely due to the use of different rounding conventions).

Genealogical analyses

For genealogical analyses the COI dataset (cropped to 568 bp) consisted of some of our sampled populations (11 populations, 89 sequences) combined with those of Mirams et al. (2011; 4 populations, 54 sequences), Liu et al. (2012; 7 sequences), and an outgroup sequence downloaded from GenBank (*P. moluccensis*, JQ707156). The CR dataset (cropped to 336 bp) consisted of our sampled populations (21 populations, 292 sequences), those studied in Mirams et al. (2011; 4

populations, 62 sequences), and all the unique haplotypes identified in the studies of Liu et al. (2008; 71 sequences), Liu et al. (2010; 45 sequences), and Liu et al. (2012; 70 sequences). Maximum likelihood gene trees were constructed in MEGA version 6 (Tamura et al. 2013) using a General Time Reversible plus Invariant sites plus Gamma distribution (GTR+I+G) substitution model. Each analysis used a Nearest-Neighbor Interchange heuristic search. The robustness of the topologies was assessed by 1,000 bootstrap reiterations.

References

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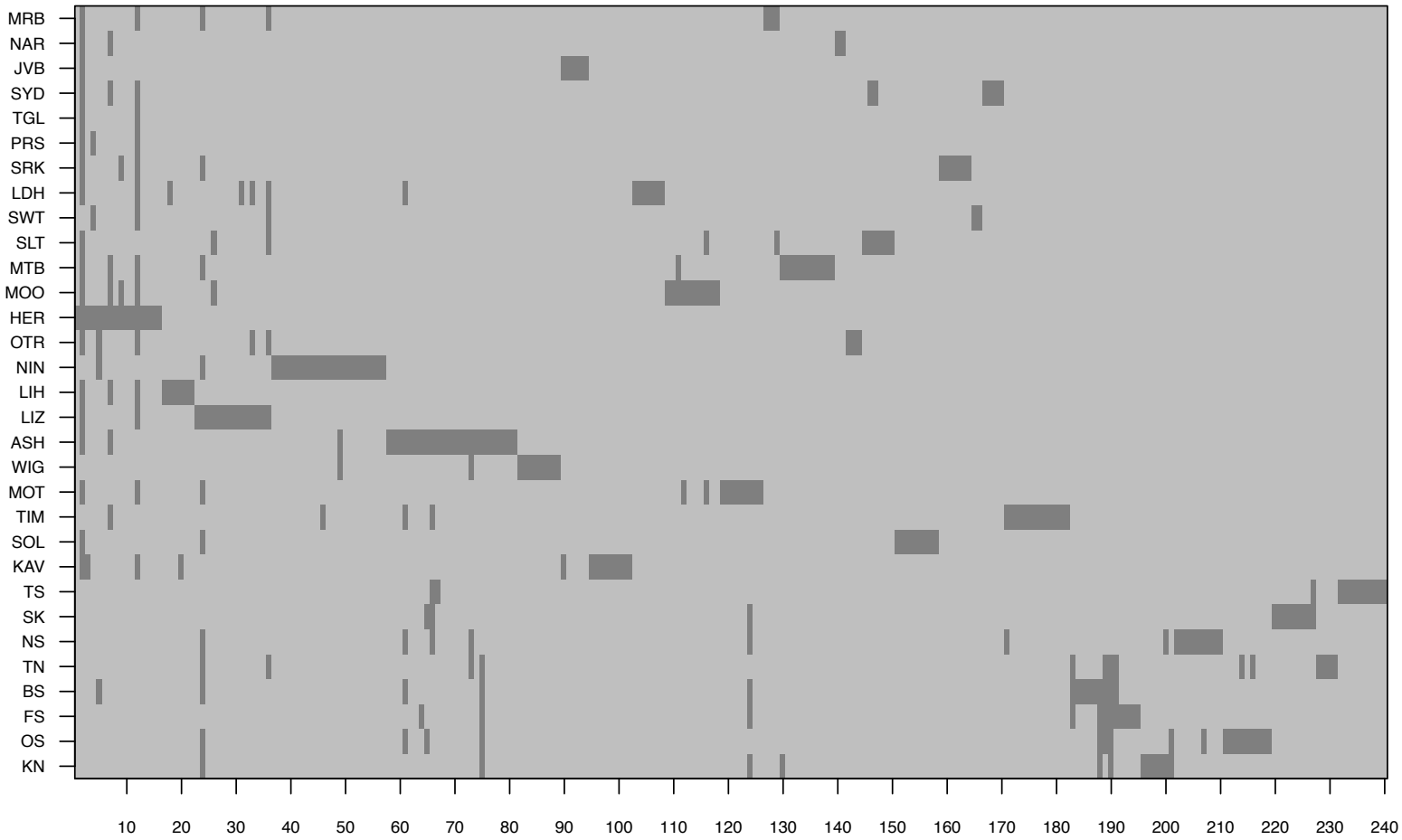
Appendix 2. Population/location data, summary of mitochondrial control region data included in each of the analyses, and source of data. Blank cells indicate where there is no data available; '-' indicate where data was omitted for the relevant analysis; '*Hd*' haplotype diversity; 'π' nucleotide diversity; 'IBD' Isolation-by-distance; 'CPH' Core–Periphery Hypothesis; 'AMOVA' Analysis of Molecular Variance; 'NP' north periphery; 'SP' south periphery; 'Pac' Pacific clade; 'Mic' Micronesian clade; 'Sym' Pacific clade and Micronesian clade; 'N core' northern sub-region of the core; 'S core' southern sub-region of the core (discussed in text).

Code	Location	Latitude, longitude	Range position	Clade affinity	*n*	*Hd*	π	Φ_{ST} based IBD analyses testing CPH	AMOVAs; multisite *β*-diversity analyses	IBD analyses of *β*-diversity; nestedness analyses	Source
KN	Kominato, Japan	35.04°N, 140.07°E	NP	Pac	20	0.8895	0.0076	NP	NP	northern transect	Liu et al. 2008
OS	Okinoshima Is., Japan	34.09°N, 130.04°E	NP	Pac	29	0.9335	0.0101	NP	NP	northern transect	Liu et al. 2008
FS	Funakoshi, Japan	33.02°N, 132.16°E	NP	Pac	15	0.9619	0.0099	NP	NP	northern transect	Liu et al. 2008
BS	Bohnotsu, Japan	31.09°N, 131.09°E	NP	Pac	23	0.9368	0.0085	NP	NP	northern transect	Liu et al. 2008
TN	Tanegashima Is., Japan	30.43°N, 130.59°E	NP	Pac	26	0.9385	0.0102	NP	NP	northern transect	Liu et al. 2008
NS	Nakanoshima, Japan	29.30°N, 129.31°E	NP	Pac	22	0.9610	0.0121	NP	NP	northern transect	Liu et al. 2008
SK	Sesoko Is., Japan	26.23°N, 127.31°E	NP	Pac	16	0.9083	0.0114	NP	NP	northern transect	Liu et al. 2008
MA	Maoao, Taiwan	25.21°N, 121.73°E	Core	Pac	25	0.9430	0.0100	N core			Liu et al. 2010
YL	Yehliu, Taiwan	25.10°N, 122.07°E	Core	Pac	26	0.9480	0.0130	N core			Liu et al. 2010
CW	Chinwan Outer Bay, Taiwan	23.47°N, 119.62°E	Core	Pac	23	0.9530	0.0080	N core			Liu et al. 2010
TS	Tiaoshi, Taiwan	21.57°N, 120.46°E	Core	Pac	19	0.8713	0.0079	N core	Core	northern transect	Liu et al. 2008
HN	Hainan Is., China	18.64°N, 110.67°E	Core	Pac	16	0.9500	0.0140	N core			Liu et al. 2010
KW	Kwajalein Atoll, Marshall Is.	9.21°N, 167.47°E	Core	Mic	10	0.6667	0.0028				Liu et al. 2012
KOR	Koror, Palau	8.17°N, 134.66°E	Core	Mic	14	0.6813	0.0033				Liu et al. 2012

CH	Chuuk Atoll	7.30°N, 151.53°E	Core	Mic	11	0.7455	0.0034				Liu et al. 2012
MO	Mortlock Is., Chuuk State	5.50°N, 153.83°E	Core	Mic	7	0.7143	0.0025				Liu et al. 2012
TW	Two Fat Thom, Brunei	5.25°N, 115.07°E	Core	Pac	8	1.0000	0.0149				Liu et al. 2012
KA	Kawe Is., Indonesia	0.17°N, 130.05°E	Core	Sym	7	1.0000	0.0489				Liu et al. 2012
WA	Waigeo Is., Indonesia	0.42°S, 131.30°E	Core	Sym	6	0.7333	0.0115				Liu et al. 2012
KO	Kofiau Is., Indonesia	1.14°S, 129.93°E	Core	Sym	10	0.6667	0.0261				Liu et al. 2012
BO	Boo Kecil, Indonesia	2.12°S, 130.88°E	Core	Pac	3	1.0000	0.0098				Liu et al. 2012
CE	Cenderawasih Bay, Indonesia	2.44°S, 135.32°E	Core	Mic	13	0.1538	0.0005				Liu et al. 2012
KAV	Kavieng, Papua New Guinea	2.57°S, 150.78°E	Core	Pac	17	0.9485	0.0108	-	Core	-	this study
SOL	New Georgia, Solomon Islands	8.17°S, 157.41°E	Core	Pac	16	0.8250	0.0071	-	Core	-	this study
TIM_{Sym}	North Coast, Timor L'este	8.30°S, 126.42°E	Core	Sym	40	0.8564	0.0401	-	-	-	this study
TIM_{Pac}	North Coast, Timor L'este	8.30°S, 126.42°E	Core	Pac	19	0.9649	0.0206	-	Core	-	this study
MOT	Motupore Is., Papua New Guinea	9.44°S, 147.24°E	Core	Pac	15	0.9714	0.0110	-	Core	-	this study
WIG	Wigram Is., Australia	11.15°S, 136.59°E	Core	Pac	16	0.8917	0.0094	-	Core	-	this study
ASH	Ashmore Reef, Australia	12.24°S, 123.13°E	Core	Pac	32	0.9839	0.0147	-	Core	-	this study
LIZ	Lizard Is., Australia	14.69°S, 145.49°E	Core	Pac	22	0.9481	0.0137	S core	Core	-	Mirams et al. 2011, this study
FI	Fiji	16.73°S, 177.67°E	Core	Pac	3	1.0000	0.0254				Liu et al. 2012
LIH	Lihou Reef, Australia	17.62°S, 151.53°E	Core	Pac	11	0.9636	0.0091	S core	Core	southern transect	Mirams et al. 2011
NIN	Ningaloo Reef, Australia	21.73°S, 113.98°E	Core	Pac	24	0.9964	0.0151	-	Core	-	Mirams et al. 2011, this study
OTR	One Tree Is., Australia	23.42°S, 151.90°E	Core	Pac	12	0.8485	0.0085	S core	Core	southern transect	this study
HER	Heron Is., Australia	23.49°S, 151.93°E	Core	Pac	20	0.9474	0.0088	S core	Core	southern transect	Mirams et al. 2011
MOO	Mooloolaba, Australia	26.64°S, 153.12°E	SP	Pac	19	0.9591	0.0133	SP	SP	southern transect	this study
MTB	Moreton Bay, Australia	27.19°S, 153.25°E	SP	Pac	23	0.9170	0.0113	SP	SP	southern transect	this study
SLT	Solitary Is., Australia	30.30°S, 153.16°E	SP	Pac	14	0.9341	0.0106	SP	SP	southern transect	this study
SWT	South West Rocks, Australia	30.88°S, 153.06°E	SP	Pac	5	1.0000	0.0107	SP	SP	southern transect	this study

LDH	Lord Howe Is., Australia	31.52°S, 159.07°E	SP	Pac	18	0.9281	0.0115	SP	SP	southern transect	this study
SRK	Seal Rocks, Australia	32.42°S, 152.57°E	SP	Pac	12	0.9697	0.0096	SP	SP	southern transect	this study
PRS	Port Stephens, Australia	32.68°S, 152.19°E	SP	Pac	3	1.0000	0.0060	SP	SP	southern transect	this study
TGL	Terrigal, Australia	33.43°S, 151.47°E	SP	Pac	5	0.4000	0.0024	SP	SP	southern transect	this study
SYD	Sydney, Australia	33.88°S, 151.30°E	SP	Pac	10	0.9778	0.0103	SP	SP	southern transect	this study
JVB	Jervis Bay, Australia	35.11°S, 150.78°E	SP	Pac	6	1.0000	0.0142	SP	SP	southern transect	this study
NAR	Narooma, Australia	36.20°S, 150.14°E	SP	Pac	4	1.0000	0.0080	SP	SP	southern transect	this study
MRB	Merimbula, Australia	36.88°S, 149.95°E	SP	Pac	10	0.9111	0.0084	SP	SP	southern transect	this study

Appendix 3. Matrix of haplotype presence–absence based on the mitochondrial control region organized according to latitude (south to north): dark gray = haplotype presence; light gray = haplotype absence. For location codes refer to Supplementary material Appendix 2.



Appendix 4. Full acknowledgements and permit information

All fish sampling was undertaken with the authority of The University of Queensland and University of Technology Sydney animal ethics committees (Approvals: SIB/817/08/ARC; UTS/RNSH 0706-030A). Sampling in Timor-L'este was supported by the Coral Triangle Support Partnership and the Ministério da Aquicultura e Pescas, Direcção Nacional de Pescas e Aquicultura (authorised by A. Fernandes, L. Fontes, J. Freitas; guia de marssa: 502/DNPA/VIII/10 and 452/DNPA/VII/11). Export of samples was authorised by the Departmento de Quarentena das Pescas (export permit: 162/FQ006/EXP./DNQB/VII/2011). Sampling in the Solomon Islands was via the Australian Government's Pacific Strategy Assistance Program and with the assistance of the Roviana Conservation Foundation (Solomon Islands Government Ministry of Education and Human Resource Development and Ministry of Fisheries and Marine Resources research permit to S. Albert). Sampling in Papua New Guinea was in coordination with the National Research Institute, the Department of Foreign Affairs and Immigration (Research Visa: 10350008304) and the Department of Environment and Conservation (Permit to Export Wildlife: 011318). All tissue samples were imported with an Australian Quarantine Inspection Service Permit to Import Quarantine Material (IP10017966). Authority to sample at Ashmore Reef was provided by the Australian Government Department of Sustainability, Environment, Water, Population and Communities (Access to Biological Resources in a Commonwealth Area for Non-Commercial Purposes permit: AU-COM2010068) and with logistic support from Australian Customs and Border control. Sampling in the Coral Sea was supported by the Marine Division of the Australian Government Department of Sustainability, Environment, Water, Population and Communities (Access to Biological Resources in a Commonwealth Area for Non-Commercial Purposes permit: AU-COM2008042). Authority to sample at Wigram Island was provided by the Northern Territory Government Department of Resources (Special Permit Number: 2007-2008/S17/2696). Sampling at Ningaloo Reef was under the authority of the Western Australia Department of Environment and Conservation (License to take Fauna for Scientific Purposes: SF007126, SF006619; Authority to enter calm land/or waters: CE002227, CE002627). We are grateful to the staff of the Australian

Museum Lizard Island Research Station and Heron Island Research Station for their facilities and support, and to the Great Barrier Reef Marine Park Authority and Queensland Parks and Wildlife Marine Parks for their permission to conduct this research (permits: G08/26733.1, G08/28114.1, G09/31678.1, G10/33597.1, G11/34452.1, G11/34640.1). All collections within Queensland and New South Wales were conducted with the permission of the Queensland or New South Wales Government Department of Primary Industries (QLD General Fisheries Permit: 118636, 150981; NSW permit: F94/696, F86/556A). We especially thank J. D. Aguirre, J. Aini (Ailan Awareness), S. Albert, K. Davis, M. Jimuru, J. Keyse, J. Kinch (National Fisheries College, Papua New Guinea), W. Lovell (Freeflow Dive, Dili), I. McLeod, A. Mirams, S. Penny, R. Pinto (and the Coral Triangle Support Partnership, Dili), T. Sinclair-Taylor, A. Turner, P. Waldie, Stephen, Lavud, and Takenda for logistical support and field assistance; G. David for laboratory assistance; and H. Possingham and J. D. Aguirre for providing helpful comments on the manuscript.