Supplementary material

Stock structure of *Lethrinus laticaudis* (Lethrinidae) across northern Australia determined using genetics, otolith microchemistry and parasite assemblage composition

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Table S1.   Summary statistics of 10 microsatellite loci for *Lethrinus laticaudis* from 304 individuals sampled from 12 locations across northern Australia (see Table 1 for location code)

n is the sample size, n_A is the number of alleles, A_R is the allelic richness, I is Shannon's Information Index, H_O is the observed heterozygosity, H_E is the expected heterozygosity, and F is the fixation index ($(H_E - H_O) \div H_E$)

Location		*Lel011*	*Lel040*	*Lel033*	*Lel012*	*Lel013*	*Lel032*	*Lel028*	*Lel027*	*Lel044*	*Lel039*
LP	n	29	30	29	18	30	28	30	29	30	29
	n_A	10	11	16	12	8	11	10	18	8	8
	A_R	3.132	8.451	10.256	5.400	5.902	9.679	7.258	12.840	5.373	3.571
	I	1.540	2.247	2.522	2.033	1.858	2.318	2.102	2.691	1.810	1.593
	H_O	0.655	0.733	0.828	0.611	0.767	0.821	0.800	0.828	0.733	0.724
	H_E	0.681	0.882	0.902	0.815	0.831	0.897	0.862	0.922	0.814	0.720
	F	0.038	0.168	0.083	0.250	0.077	0.084	0.072	0.103	0.099	–0.006
CP	n	32	32	32	27	30	32	31	32	32	31
	n_A	12	12	15	13	9	12	12	14	9	11
	A_R	4.146	5.361	11.636	7.839	5.863	7.787	6.261	11.378	5.868	3.930
	I	1.806	2.063	2.561	2.273	1.907	2.255	2.106	2.519	1.886	1.785
	H_O	0.625	0.719	0.906	0.778	0.800	0.781	0.871	0.844	0.875	0.613
	H_E	0.759	0.813	0.914	0.872	0.829	0.872	0.840	0.912	0.830	0.746
	F	0.176	0.116	0.009	0.108	0.035	0.104	–0.037	0.075	–0.055	0.178
DP	n	23	24	24	21	24	24	24	24	23	23
	n_A	8	15	17	14	7	11	11	14	8	9
	A_R	3.469	5.818	10.105	6.533	5.592	9.000	6.621	9.846	5.658	4.600
	I	1.540	2.205	2.552	2.272	1.821	2.279	2.041	2.444	1.844	1.795
	H_O	0.739	0.833	0.875	0.667	0.875	0.958	0.958	0.875	0.783	0.652
	H_E	0.712	0.828	0.901	0.847	0.821	0.889	0.849	0.898	0.823	0.783
	F	–0.039	–0.006	0.029	0.213	–0.066	–0.078	–0.129	0.026	0.049	0.167
CS	n	28	28	28	24	27	27	27	26	28	28
	n_A	9	12	19	14	9	11	11	14	7	9
	A_R	3.015	6.701	11.879	6.898	5.608	7.594	7.967	11.174	4.994	3.664
	I	1.461	2.130	2.674	2.294	1.908	2.161	2.211	2.515	1.742	1.586
	H_O	0.643	0.857	0.786	0.667	0.778	0.852	0.852	0.962	0.714	0.679
	H_E	0.668	0.851	0.916	0.855	0.822	0.868	0.874	0.911	0.800	0.727
	F	0.038	–0.007	0.142	0.220	0.053	0.019	0.026	–0.056	0.107	0.067
CV	n	30	30	30	29	30	30	30	30	30	30
	n_A	11	15	16	14	10	11	10	14	10	11
	A_R	3.896	9.677	11.250	8.327	5.590	7.895	5.788	10.465	6.207	4.147

Location		*Lel011*	*Lel040*	*Lel033*	*Lel012*	*Lel013*	*Lel032*	*Lel028*	*Lel027*	*Lel044*	*Lel039*
	I	1.781	2.473	2.542	2.358	1.915	2.179	2.002	2.455	2.001	1.787
	H_O	0.733	0.833	0.900	0.828	0.900	0.867	0.900	0.933	0.767	0.700
	H_E	0.743	0.897	0.911	0.880	0.821	0.873	0.827	0.904	0.839	0.759
	F	0.013	0.071	0.012	0.059	–0.096	0.008	–0.088	–0.032	0.086	0.078
Wa	n	27	27	27	24	26	27	27	26	26	23
	n_A	7	11	15	13	8	10	11	14	10	6
	A_R	2.928	4.214	10.962	3.959	5.681	6.451	7.010	10.903	5.474	4.744
	I	1.307	1.885	2.522	1.834	1.864	2.025	2.100	2.508	1.943	1.624
	H_O	0.556	0.741	0.963	0.750	0.731	0.815	0.815	0.885	0.769	0.783
	H_E	0.658	0.763	0.909	0.747	0.824	0.845	0.857	0.908	0.817	0.789
	F	0.156	0.029	–0.060	–0.003	0.113	0.036	0.050	0.026	0.059	0.008
RR	n	26	26	25	25	26	25	26	26	26	26
	n_A	6	14	13	10	9	10	10	14	8	8
	A_R	2.965	5.344	9.921	4.771	6.063	7.062	8.145	10.816	5.753	4.462
	I	1.248	2.146	2.403	1.825	1.932	2.103	2.174	2.483	1.862	1.702
	H_O	0.577	0.846	0.880	0.640	0.846	0.720	0.808	1.000	0.808	0.885
	H_E	0.663	0.813	0.899	0.790	0.835	0.858	0.877	0.908	0.826	0.776
	F	0.129	–0.041	0.021	0.190	–0.013	0.161	0.079	–0.102	0.022	–0.140
DH	n	23	23	24	21	24	24	24	24	24	22
	n_A	5	10	13	11	8	15	10	14	8	11
	A_R	2.587	4.165	10.195	5.313	5.647	9.366	6.436	10.766	4.220	4.400
	I	1.156	1.799	2.418	1.973	1.836	2.435	2.014	2.490	1.689	1.826
	H_O	0.696	0.739	0.833	0.810	0.875	0.917	0.917	0.917	0.750	0.818
	H_E	0.613	0.760	0.902	0.812	0.823	0.893	0.845	0.907	0.763	0.773
	F	–0.134	0.027	0.076	0.003	–0.063	–0.026	–0.085	–0.011	0.017	–0.059
CoP	n	32	33	32	31	32	33	33	33	33	31
	n_A	6	11	17	14	8	13	10	15	8	8
	A_R	2.695	3.463	11.838	5.772	5.211	9.075	4.939	10.945	5.431	4.470
	I	1.193	1.709	2.623	2.136	1.799	2.356	1.878	2.509	1.798	1.689
	H_O	0.625	0.697	0.938	0.935	0.781	0.879	0.788	0.939	0.818	0.742
	H_E	0.629	0.711	0.916	0.827	0.808	0.890	0.798	0.909	0.816	0.776
	F	0.006	0.020	–0.024	–0.132	0.033	0.012	0.012	–0.034	–0.003	0.044
VI	n	29	29	29	28	29	29	29	27	29	29
	n_A	7	11	14	14	6	13	9	13	8	6
	A_R	2.620	4.711	9.191	5.580	3.903	7.377	6.675	8.890	5.021	3.511
	I	1.217	1.910	2.393	2.130	1.510	2.210	1.980	2.327	1.784	1.424
	H_O	0.759	0.862	0.931	0.714	0.724	0.931	0.862	0.889	0.793	0.655
	H_E	0.618	0.788	0.891	0.821	0.744	0.864	0.850	0.888	0.801	0.715

Location		*Lel011*	*Lel040*	*Lel033*	*Lel012*	*Lel013*	*Lel032*	*Lel028*	*Lel027*	*Lel044*	*Lel039*
	F	−0.227	−0.094	−0.045	0.130	0.026	−0.077	−0.014	−0.002	0.010	0.084
HB	n	12	12	11	12	10	12	12	11	12	12
	n_A	5	4	9	7	5	7	11	10	5	7
	A_R	2.420	2.420	6.541	3.600	3.390	4.966	6.261	8.963	3.692	4.235
	I	1.133	1.072	2.021	1.536	1.349	1.759	2.102	2.240	1.418	1.653
	H_O	0.583	0.500	0.909	0.500	0.700	0.833	0.917	0.909	0.917	0.917
	H_E	0.587	0.587	0.847	0.722	0.705	0.799	0.840	0.888	0.729	0.764
	F	0.006	0.148	−0.073	0.308	0.007	−0.043	−0.091	−0.023	−0.257	−0.200
SC	n	9	9	8	9	9	9	9	9	9	9
	n_A	4	6	8	6	5	9	7	12	5	6
	A_R	3.057	3.176	5.565	4.050	3.000	6.480	3.857	9.000	2.531	3.951
	I	1.223	1.377	1.890	1.538	1.301	2.029	1.629	2.351	1.164	1.542
	H_O	0.889	0.556	0.875	0.556	0.778	1.000	0.889	0.889	0.778	0.778
	H_E	0.673	0.685	0.820	0.753	0.667	0.846	0.741	0.889	0.605	0.747
	F	−0.321	0.189	−0.067	0.262	−0.167	−0.182	−0.200	0.000	−0.286	−0.041
All locations	n	300	303	299	269	297	300	302	297	302	293
	n_A	16	21	24	24	14	17	18	21	14	16
	A_R	3.206	5.862	13.170	6.757	6.023	9.453	7.716	12.815	5.592	4.455
	I	1.577	2.263	2.742	2.370	1.942	2.415	2.226	2.648	1.900	1.822
	H_O	0.663	0.766	0.886	0.732	0.801	0.857	0.858	0.906	0.788	0.730
	H_E	0.688	0.829	0.924	0.852	0.834	0.894	0.870	0.922	0.821	0.776
	F	0.036	0.077	0.041	0.140	0.039	0.042	0.015	0.018	0.040	0.058

Table S2. **Mean concentrations of element : ^{43}Ca ratios from the near core and margin of *Lethrinus laticaudis* otoliths collected from 13 locations across northern Australia**

Mn data are not presented for the otolith margin because measurements were generally below detection limits

Location	Li:Ca	Mg:Ca	Mn:Ca	Cu:Ca	Sr:Ca	Ba:Ca
Near core						
Locker Point	0.59657	0.03258	0.30711	0.03752	0.50799	0.59169
Cape Preston	0.60339	0.03880	0.31884	0.03897	0.51557	0.55524
Dampier Peninsula	0.56804	0.03439	0.21931	0.04013	0.51963	0.60075
Camden Sound	0.62068	0.03705	0.34115	0.04289	0.51815	0.65674
Cape Voltaire	0.60595	0.03549	0.36830	0.05034	0.51992	0.67203
Wadeye	0.66468	0.04024	0.49941	0.06123	0.50503	0.66699
Roche Reef	0.66905	0.04067	0.49575	0.05327	0.49857	0.66567
Darwin Harbour	0.65711	0.04028	0.45413	0.04676	0.50736	0.69810
Coburg Peninsula	0.63451	0.03758	0.40964	0.04785	0.49836	0.58151
Vanderlin Islands	0.65843	0.05071	0.58931	0.04620	0.51226	0.70818
Halifax Bay	0.61151	0.03297	0.59989	0.04360	0.51361	0.59588
Sunshine Coast	0.63981	0.03197	0.54945	0.04106	0.47495	0.50343
Moreton Bay	0.68527	0.04006	0.50135	0.05295	0.48461	0.60363
Margin						
Locker Point	0.39906	0.01061	<LOD	0.02636	0.62620	0.63843
Cape Preston	0.44393	0.01331	<LOD	0.02820	0.60710	0.74291
Dampier Peninsula	0.46168	0.01600	<LOD	0.02498	0.60120	0.91130
Camden Sound	0.48318	0.01607	<LOD	0.03086	0.58845	0.70090
Cape Voltaire	0.45976	0.01253	<LOD	0.03309	0.63425	0.82913
Wadeye	0.42843	0.01115	<LOD	0.04069	0.68103	0.73175
Roche Reef	0.53802	0.02458	<LOD	0.03411	0.55718	0.67397
Darwin Harbour	0.55079	0.02405	<LOD	0.02734	0.55422	0.54346
Coburg Peninsula	0.44138	0.01368	<LOD	0.03650	0.61432	0.69180
Vanderlin Islands	0.40217	0.01054	<LOD	0.03166	0.63209	0.79726
Halifax Bay	0.47105	0.00920	<LOD	0.03870	0.64461	0.61327
Sunshine Coast	0.46464	0.00872	<LOD	0.02534	0.57536	0.56780
Moreton Bay	0.48365	0.01416	<LOD	0.02725	0.52527	0.48720

Table S3.   Results of the multivariate analysis of variance (MANOVA) investigating the spatial variability in otolith near core and margin microchemistry and parasite assemblage of *Lethrinus laticaudis*: overall (all locations, independent of region) and by region

d.f. is the degree of freedom; asterisks indicate significance at: ***, $P < 0.001$

Source	Source (error d.f.)			Pillai's Trace			F		
	Near Core	Margin	Parasite	Near core	Margin	Parasite	Near core	Margin	Parasite
Overall	72 (1896)	60 (1580)	288 (3792)	0.947	1.466	3.615	4.936***	10.925***	5.676***
WA	24 (560)	20 (564)	68 (548)	0.548	0.650	1.746	3.706***	5.474***	6.240***
NT	24 (540)	20 (544)	44 (536)	0.368	1.151	1.946	2.281***	10.994***	11.536***
Qld	12 (66)	10 (68)	34 (44)	0.918	1.035	1.738	4.668***	7.295***	8.572***

Table S4. Jack-knife reclassification success for the near core and margin otolith microchemistry results for *Lethrinus laticaudis* sampled from the three jurisdictional management units

Data are presented as the percentage of fish captured from locations (rows) that are classified by discriminant functions into the various locations (columns) for analysis within each region. Bold values indicate successful reclassification to the location of origin

Location	LP	CP	DP	CS	CV	Wa	RR	DH	CoP	VI	HB	SC	MB
Near core													
Locker Point	**47**	17	17	13	7								
Cape Preston	23	**27**	33	7	10								
Dampier Peninsula	0	29	**61**	4	7								
Camden Sound	21	17	10	**24**	28								
Cape Voltaire	13	20	7	10	**50**								
Wadeye						**20**	10	13	33	23			
Roche Reef						36	**4**	16	36	8			
Darwin Harbour						13	4	**17**	42	25			
Coburg Peninsula						12	9	6	**58**	15			
Vanderlin Islands						10	0	13	20	**57**			
Halifax Bay											**86**	0	14
Sunshine Coast											7	**57**	36
Moreton Bay											17	42	**42**
Margin													
Locker Point													
Cape Preston	**63**	20	0	3	13								
Dampier Peninsula	33	**17**	13	23	13								
Camden Sound	0	18	**46**	21	14								
Cape Voltaire	0	21	14	**59**	7								
Wadeye	10	17	7	13	**53**								
Roche Reef						**57**	7	0	17	20			
Darwin Harbour						0	**52**	36	12	0			
Coburg Peninsula						0	17	**79**	4	0			
Vanderlin Islands						9	6	0	**58**	27			
Halifax Bay						17	0	0	33	**50**			
Sunshine Coast											**86**	14	0
Moreton Bay											7	**79**	14
											0	42	**58**

Table S5.   Parasites found infecting *Lethrinus laticaudis* sampled from 13 locations across northern Australia that were used in analyses

Data are presented as mean abundance with prevalence in parentheses. Data presented are untransformed

Area in body	Location	LP	CP	DP	CS	CV	Wa	RR	DH	CoP	VI	HB	SC	MB
Parasite type	Sample Size	34	35	28	29	29	30	29	24	33	30	14	14	12
Gills and pharyngeal teeth														
Copepoda	*Hatschekia gracilis*	1.21 (61.8)	1.89 (62.9)	20.07 (100)	4.07 (89.7)	3.97 (93.1)	6.47 (93.3)	7.59 (93.1)	0.33 (16.7)	0.09 (9.1)	16.33 (96.7)		3.86 (78.6)	3.75 (91.7)
	Sagum vespertilio		0.06 (2.9)										0.50 (28.6)	
Isopoda	Adult					0.03 (3.4)	0.10 (10.0)							
Monogenea	*Haliotrema* sp.	24.32 (97.1)	27.54 (100)	9.36 (46.4)	4.24 (31.0)	10.28 (89.7)	15.70 (93.3)	0.76 (20.7)	1.50 (54.2)	22.30 (87.9)	8.63 (46.7)	5.07 (85.7)	0.50 (21.4)	7.50 (58.3)
	Diplectanidae sp.	24.88 (97.1)	12.29 (94.3)	4.93 (50.0)	2.52 (27.6)	6.07 (48.3)	13.53 (96.7)	0.03 (3.4)		12.61 (84.8)	17.93 (73.3)	1.29 (14.3)	2.86 (14.3)	
	Encotyllabe sp.	0.21 (17.6)	0.17 (11.4)	2.32 (71.4)		1.07 (58.6)						2.07 (71.4)	0.07 (7.1)	
Body cavity, mesenteries and tissues														
Cestoda	*Pseudogilquinia* sp.	1.24 (38.2)	4.40 (37.1)	6.57 (53.6)	0.86 (31.0)	0.79 (24.1)	0.80 (36.7)		0.04 (4.2)	0.03 (3.0)		1.00 (21.4)	0.21 (21.4)	
	Paratobothrium sp.		0.03 (2.9)	0.04 (3.6)									1.14 (28.6)	
	Nybelinia sp. 1	0.50 (8.8)	1.09 (31.4)	0.89 (21.4)		0.10 (10.3)	0.07 (6.7)	0.03 (3.4)	0.17 (12.5)		0.50 (33.3)		0.43 (14.3)	
	Nybelinia sp. 2		0.34 (17.1)	0.18 (10.7)		0.28 (27.6)	0.03 (3.3)				0.03 (3.3)			
	Nybelinia sp. 5											0.14 (14.3)	2.43 (71.4)	
	Nybelinia sp. 6					0.07 (3.4)							0.57 (14.3)	
	Nybelinia sp. 7	0.65 (8.8)	0.34 (14.3)											
	Callitetrarhynchus sp.		0.03 (2.9)			0.14 (10.3)	0.03 (3.3)							
	Proteocephalidae spp.	0.09 (8.8)	2.51 (22.9)			2.59 (27.6)	0.03 (3.3)	0.17 (3.4)		0.33 (9.1)				

Area in body	Location	LP	CP	DP	CS	CV	Wa	RR	DH	CoP	VI	HB	SC	MB
Digenea	Didymozoidae ex stomach wall	0.35 (32.4)	0.09 (5.7)	0.29 (286)		0.38 (24.1)	0.20 (13.3)			0.21 (21.2)	0.10 (10.0)	0.29 (14.3)		
Nematoda	Anisakidae spp.	0.97 (55.9)	3.17 (74.3)	3.71 (50.0)	0.24 (17.2)	2.17 (65.5)	3.63 (56.7)	0.21 (13.8)	0.04 (4.2)	0.15 (12.1)	0.23 (23.3)	4.00 (78.6)	9.07 (71.4)	0.42 (8.3)
Acanthocephala	*Corynosoma* sp.												0.14 (14.3)	
	Serrasentis sagitiffer		0.06 (5.7)								0.03 (3.3)		0.36 (35.7)	
Intestinal canal														
Digenea	Acanthocolpidae sp.	0.03 (2.9)	0.11 (11.4)		0.14 (6.9)	0.14 (10.3)							0.21 (7.1)	0.25 (25.0)
	Fairfaxia sp.	0.12 (8.8)	0.17 (11.4)	0.04 (3.6)	0.03 (3.4)				0.14 (3.4)		0.03 (3.3)			
	Hemiuridae sp.	0.50 (14.7)	0.46 (22.9)	0.07 (7.1)		0.07 (6.9)	0.40 (23.3)						0.93 (50.0)	0.42 (8.3)
	Bucephalidae sp.	0.03 (2.9)		0.11 (10.7)		0.03 (3.4)				0.03 (3.0)	0.20 (20.0)	0.07 (7.1)		
Nematoda	*Cucullanus laurotravassosi*		0.23 (20.0)	0.64 (42.9)					0.13 (12.5)	0.12 (6.1)	0.57 (30.0)	0.50 (35.7)		

Table S6.   Jack-knife reclassification success for the parasite assemblage of *Lethrinus laticaudis* sampled from the three jurisdictional management units

Data are presented as the percentage of fish captured from locations (rows) that are classified by discriminant functions into the various locations (columns)

for analysis within each region. Bold values indicate successful reclassification to the location of origin

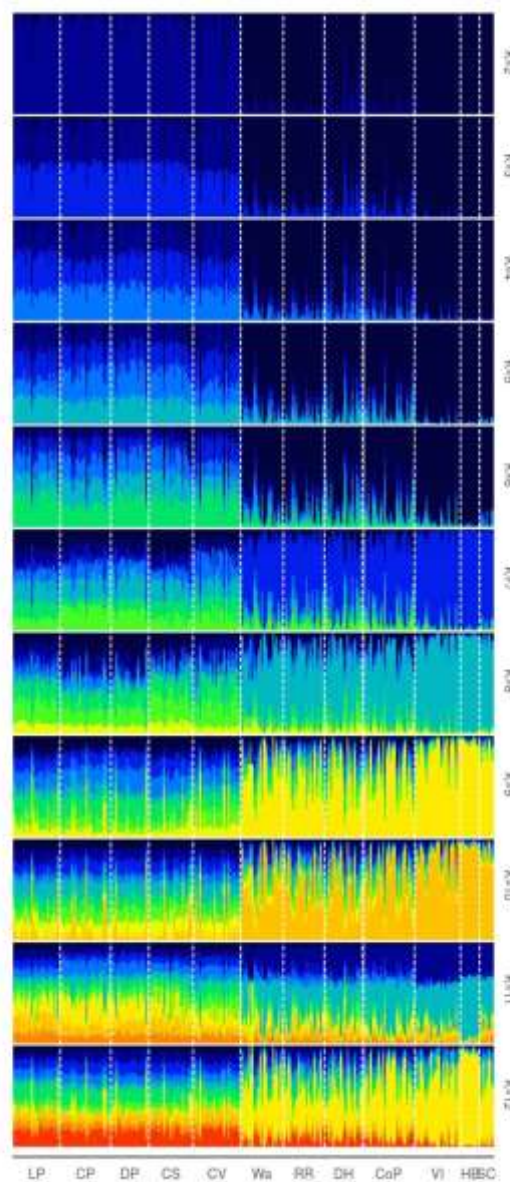| Group	LP	CP	DP	CS	CV	Wa	RR	DH	CoP	VI	HB	SC	MB
Locker Point	**68**	26	0	6	0								
Cape Preston	40	**46**	0	3	11								
Dampier Peninsula	0	0	**64**	21	14								
Camden Sound	7	0	0	**93**	0								
Cape Voltaire	3.5	14	3.5	24	**55**								
Wadeye						**67**	3	0	17	13			
Roche Reef						0	**79**	21	0	0			
Darwin Harbour						0	8	**92**	0	0			
Coburg Peninsula						0	0	18	**82**	0			
Vanderlin Islands						3	20	3	0	**74**			
Halifax Bay											**79**	7	14
Sunshine Coast											7	**79**	14
Moreton Bay											0	0	**100**

Fig. S1. Results from the Bayesian model-based clustering of microsatellite data from *Lethrinus laticaudis* using the software STRUCTURE. Each vertical line represents an individual and the posterior probability proportions of its genotype assigned to the different genetic clusters. The number of genetic clusters shown ranges from $k = 2$ to $k = 9$; each plot represents one tested k. Individuals are plotted in order along the sampling gradient from west to east. Population information was used as a prior in the analysis.