

Supplementary Information

Genetic Diversity and Connectivity of *Ocypode ceratophthalmus* in the East and South China Seas and Its implications for conservation

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Table S1. Current status of genetic connectivity between populations in the East China Sea and populations in the South China Sea. The Web of science and CNKI were used to search the published papers. ((genetic OR gene) AND (" East China Sea" AND "South China Sea ")) were used as search keywords for English articles, and ("East China Sea", "South China Sea" and "genetic") (in Chinese) were used as search keywords for Chinese articles. The search deadline was December 29, 2022. Only articles in which the studies species had sampling sites in the East China Sea and the South China Sea were retained. A case was considered to have significant genetic differentiation if there was at least one significant value of the fixation index (F_{ST}) between populations in the East China Sea and populations in the South China Sea.

ID	Species	Genetic marker	Genetic differentiation	Number of populations	Reference
1	<i>Pampus chinensis</i>	COI	Yes	6	Population genetic structure and genetic diversity of Chinese pomfret at the coast of the East China Sea and the South China Sea
2	<i>Pagrus major</i>	SSR	Yes	2	Genetic Structure of Red Sea Bream (<i>Pagrus major</i>) Population off Japan and the Southwest Pacific, Using Microsatellite DNA Markers
3	<i>Eleutheronema tetradactylum</i>	Cytb	Yes	4	Low mtDNA <i>Cytb</i> diversity and shallow population structure of <i>Eleutheronema tetradactylum</i> in the East China Sea and the South China Sea
4	<i>Thamnaconus hypargyreus</i>	D-Loop	No	5	Shallow mitochondrial phylogeographical pattern and high levels of genetic connectivity of <i>Thamnaconus hypargyreus</i> in the South China Sea and the East China Sea
5	<i>Eleutheronema rhadinum</i>	COI	No	2	Genetic diversity and population structure of <i>Eleutheronema rhadinum</i> in the East and South China Seas revealed in mitochondrial COI sequences
6	<i>Nibea albiflora</i>	COI	No	3	Genetic diversity and population structure of <i>Nibea albiflora</i> in the

7	<i>Epinephelus akaara</i>	D-Loop	Yes	6	China Sea revealed by mitochondrial COI sequences Genetic population structuring and demographic history of red spotted grouper (<i>Epinephelus akaara</i>) in South and East China Sea
8	<i>Scomber japonicus</i>	SSR	Yes	6	Microsatellite analysis reveals the population structure and migration patterns of <i>Scomber japonicus</i> (Scombridae) with continuous distribution in the East and South China Seas
9	<i>Chelon haematocheilus</i>	D-Loop	Yes	3	Pleistocene isolation in the North-western Pacific marginal seas and limited dispersal in a marine fish, <i>Chelon haematocheilus</i> (Temminck & Schlegel, 1845)
10	<i>Eriocheir sensu stricto</i>	AFLP	Yes	7	Genome scan of the mitten crab <i>Eriocheir sensu stricto</i> in East Asia: Population differentiation, hybridization and adaptive speciation
11	<i>Portunus sanguinolentus</i>	D-Loop	Yes	6	Phylogeography and Genetic Structure of the Swimming Crabs <i>Portunus sanguinolentus</i> (Herbst, 1783) in East Asia
12	<i>Scylla paramamosain</i>	COI+16S rDNA	Yes	10	Late Pleistocene population expansion of <i>Scylla paramamosain</i> along the coast of China: A population dynamic response to the Last Interglacial sea level highstand
13	<i>Liza affinis</i>	SSR	Yes	8	Population Genetic Structure of <i>Liza affinis</i> (Eastern Keelback Mullet), Reveals High Gene Flow Inferred from Microsatellite Analysis
14	<i>Periophthalmus modestus</i>	ND5	No	5	Biogeographical role of the Kuroshio Current in the amphibious mudskipper <i>Periophthalmus modestus</i> indicated by mitochondrial DNA data
15	<i>Platypleura hilpa</i>	COI+COII+Cytb	Yes	24	Phylogeography of the cicada <i>Platypleura hilpa</i> in subtropical and tropical East Asia based on mitochondrial and nuclear genes and microsatellite markers
16	<i>Atrina pectinata</i>	COI	No	10	Population genetic structure of the pen shell <i>Atrina pectinata</i> sensu lato (Bivalvia: Pinnidae) throughout East Asia
17	<i>Siphonaria japonica</i>	COI	No	5	Causations of phylogeographic barrier of some rocky shore species along the Chinese coastline
18	<i>Siphonaria japonica</i>	ITS	No	5	Causations of phylogeographic barrier of some rocky shore species along the Chinese coastline

19	<i>Macrobrachium nipponense</i>	COI+16S rRNA	Yes	6	Phylogeography and genetic structure of the oriental river prawn <i>Macrobrachium nipponense</i> (Crustacea: Decapoda: Palaemonidae) in East Asia
20	<i>Cyclina sinensis</i>	COI	Yes	9	Phylogeography of Bivalve <i>Cyclina sinensis</i> : Testing the Historical Glaciations and Changjiang River Outflow Hypotheses in Northwestern Pacific
21	<i>Cyclina sinensis</i>	ITS-1	Yes	9	Phylogeography of Bivalve <i>Cyclina sinensis</i> : Testing the Historical Glaciations and Changjiang River Outflow Hypotheses in Northwestern Pacific
22	<i>Tachypleus tridentatus</i>	AT-rich region	Yes	8	Phylogeography, Demographic History, and Reserves Network of Horseshoe Crab, <i>Tachypleus tridentatus</i> , in the South and East China Sea-boards
23	<i>Penaeus japonicus</i>	COI	Yes	5	Molecular population structure of the kuruma shrimp <i>Penaeus japonicus</i> species complex in western Pacific
24	<i>Penaeus japonicus</i>	D-Loop	Yes	5	Molecular population structure of the kuruma shrimp <i>Penaeus japonicus</i> species complex in western Pacific
25	<i>Penaeus japonicus</i>	SSR	No	5	Molecular population structure of the kuruma shrimp <i>Penaeus japonicus</i> species complex in western Pacific
26	<i>Eleutheronema rhadinum</i>	COI	Yes	4	Population genetic characteristics of <i>Eleutheronema rhadinum</i> and <i>Eleutheronema tetradactylus</i> in China (in Chinese)
27	<i>Eleutheronema rhadinum</i>	D-Loop	Yes	4	Population genetic characteristics of <i>Eleutheronema rhadinum</i> and <i>Eleutheronema tetradactylus</i> in China (in Chinese)
28	<i>Arcotheres sinensis</i>	COI	Yes	4	Morphological variation and population genetic structure of the crab <i>Arcotheres sinensis</i> from coastal China (in Chinese)
29	<i>Parasesarma affinis</i>	COI	No	12	Studies on molecular phylogeny of sesarmid crabs from the coast of China and molecular phylogeography of two mangrove crabs (in Chinese)
30	<i>Octopus ovulum</i>	Cyt b	No	4	Analysis of genetic diversity and structure of octopuses (in Chinese)
31	<i>Sthenoteuthis oualaniensis</i>	Cytb	Yes	2	Genetic structure of <i>Sthenoteuthis oualaniensis</i> population in the north-west Pacific ocean (in Chinese)
32	<i>Pagrus major</i>	D-Loop	Yes	9	Genetic diversity of 3 sparid species in coastal waters of China based on

						mitochondrial control region sequences (in Chinese)
33	<i>Acanthopagrus schlegeli</i>	D-Loop	Yes	11		Genetic diversity of 3 sparid species in coastal waters of China based on mitochondrial control region sequences (in Chinese)
34	<i>Rhabdosargus sarba</i>	D-Loop	Yes	6		Genetic diversity of 3 sparid species in coastal waters of China based on mitochondrial control region sequences (in Chinese)
35	<i>Ilisha elongata</i>	D-Loop	Yes	8		Population genetics of the <i>Ilisha elongata</i> (Clupeiformes: Pristigasteridae) along the Northwestern Pacific coast and the development of SNP marker for <i>Ilisha elongata</i> and <i>coilia nusus</i> (in Chinese)
36	<i>Oratosquilla oratoria</i>	ND5+COI+COB	Yes	6		Phylogeography of Manatosquilla shrimp populations and molecular phylogeny of Sternoporus in the coastal mouth of China (in Chinese)
37	<i>Pampus chinensis</i>	D-Loop	No	2		Studies on Morphology and genetics of Pampus species (in Chinese)
38	<i>Pampus minor</i>	D-Loop	Yes	2		Studies on Morphology and genetics of Pampus species (in Chinese)
39	<i>Cyclina sinensis</i>	COI	Yes	9		Phylogeography of four marine bivalves along China' coastline, with views into the evolutionary processes and mechanisms (in Chinese)
40	<i>Tegillarca granosa</i>	COI	Yes	9		Phylogeography of four marine bivalves along China' coastline, with views into the evolutionary processes and mechanisms (in Chinese)
41	<i>Scomber japonicus</i>	D-Loop	No	5		Molecular phylogeography of two scomber species in Northwestern Pacific (in Chinese)
42	<i>Scomber japonicus</i>	SSR	Yes	5		Molecular phylogeography of two scomber species in Northwestern Pacific (in Chinese)
43	<i>Konosirus punctatus</i>	D-Loop+COI	Yes	3		Population genetic structure and molecular phylogeography of <i>Konosirus punctatus</i> and <i>Sardinella zunasi</i> (in Chinese)
44	<i>Konosirus punctatus</i>	AFLP	Yes	3		Causations of phylogeographic barrier of some rocky shore species along the Chinese coastline
45	<i>Konosirus punctatus</i>	ISSR	Yes	2		Causations of phylogeographic barrier of some rocky shore species along the Chinese coastline

Table S2. The information of carapace width, carapace length, abdomen width, abdomen length, weight and gender.

Population	Carapace width (cm)	Carapace length (cm)	Abdomen width (cm)	Abdomen length (cm)	Weight (g)	Female: Male
MA	2.04 ± 0.36	1.71 ± 0.34	0.67 ± 0.24	1.41 ± 0.32	5.41 ± 2.25	5:10
CW	3.09 ± 0.34	2.64 ± 0.23	1.44 ± 0.47	2.31 ± 0.26	16.59 ± 5.40	17:7
DT	3.23 ± 0.35	2.72 ± 0.37	1.38 ± 0.55	2.44 ± 0.37	18.06 ± 6.17	14:6
DZG	1.99 ± 0.29	1.72 ± 0.27	0.65 ± 0.21	1.40 ± 0.29	5.28 ± 2.51	7:14
MZD	2.94 ± 0.20	2.47 ± 0.21	1.16 ± 0.38	2.18 ± 0.19	13.38 ± 2.66	9:7
QA	2.94 ± 0.26	2.44 ± 0.24	1.22 ± 0.49	2.11 ± 0.23	15.01 ± 3.54	15:7
NJLD	3.11 ± 0.40	2.65 ± 0.36	1.42 ± 0.49	2.39 ± 0.47	16.15 ± 6.95	8:2
PT	2.95 ± 0.35	2.45 ± 0.30	1.19 ± 0.51	2.14 ± 0.31	13.68 ± 4.54	10:8
ZJS	3.40 ± 0.29	2.86 ± 0.35	1.48 ± 0.51	2.57 ± 0.34	22.82 ± 7.11	9:5
DH	3.07 ± 0.27	2.49 ± 0.25	1.10 ± 0.61	2.27 ± 0.30	14.43 ± 4.56	7:8
SYH	2.21 ± 0.32	1.93 ± 0.26	0.81 ± 0.36	1.67 ± 0.31	5.54 ± 2.50	5:10
XM	3.06 ± 0.32	2.58 ± 0.28	1.31 ± 0.47	2.26 ± 0.33	16.65 ± 5.72	13:5
FYLD					16.07 ± 3.32	7:8
HA					13.42 ± 2.33	8:7
JH					14.03 ± 2.41	2:3

Table S3. Pairwise F_{ST} values between populations based on *COI* sequences. All pairwise F_{ST} values between populations were not statistically significant ($p > 0.05$).

	JH	PT	ZJS	SYH	MA	HA	XM	CW	DT	FYLD	DH	DZG	MZD	QA	NJLD
JH	0.0000														
PT	0.0054	0.0000													
ZJS	-0.0370	-0.0328	0.0000												
SYH	-0.0134	0.0025	-0.0124	0.0000											
MA	-0.0147	0.0070	-0.0273	0.0177	0.0000										
HA	-0.0412	0.0068	-0.0308	-0.0116	-0.0129	0.0000									
XM	0.0358	0.0138	0.0162	0.0602	-0.0003	0.0321	0.0000								
CW	-0.0039	0.0040	-0.0249	0.0433	-0.0315	-0.0018	0.0107	0.0000							
DT	-0.0232	0.0094	-0.0290	0.0170	-0.0327	-0.0054	0.0087	-0.0133	0.0000						
FYLD	-0.0131	0.0076	-0.0170	0.0329	-0.0163	0.0124	0.0229	-0.0123	-0.0091	0.0000					
DH	0.0065	0.0115	-0.0168	0.0234	-0.0402	0.0063	-0.0213	-0.0149	-0.0269	0.0066	0.0000				
DZG	-0.0190	-0.0106	-0.0353	0.0105	-0.0076	-0.0047	0.0507	-0.0134	0.0007	-0.0247	0.0239	0.0000			
MZD	-0.0275	0.0062	-0.0212	0.0109	0.0065	-0.0182	0.0526	0.0025	0.0038	-0.0188	0.0345	-0.0201	0.0000		
QA	-0.0240	-0.0034	-0.0400	0.0119	-0.0230	-0.0146	0.0261	-0.0192	-0.0310	-0.0066	-0.0131	-0.0143	-0.0122	0.0000	
NJLD	-0.0116	-0.0456	-0.0406	-0.0130	0.0033	-0.0087	0.0181	-0.0013	0.0041	-0.0245	0.0152	-0.0393	-0.0359	-0.0111	0.0000

Table S4. Pairwise F_{ST} values between populations based on *D-Loop* sequences. The genetic differentiation between the remaining populations showed insignificant differences ($p > 0.05$), except for the significant differences between MZD and FYLD, and between MZD and HA populations ($p < 0.05$).

	MA	DT	FYLD	MZD	NJLD	PT	ZJS	HA	XM	CW	QA	DH	JH	DZG	SYH
MA	0.0000														
DT	-0.0417	0.0000													
FYLD	-0.0651	0.0139	0.0000												
MZD	0.0519	0.0704	0.1889	0.0000											
NJLD	-0.0482	-0.0933	0.0172	0.0110	0.0000										
PT	-0.0359	-0.0330	0.0906	-0.0284	-0.0688	0.0000									
ZJS	-0.0547	-0.0290	0.0259	-0.0155	0.0625	-0.0260	0.0000								
HA	-0.0436	0.0488	-0.0716	0.2675	0.0552	0.1571	0.0640	0.0000							
XM	-0.0214	-0.0298	0.0490	-0.0477	-0.0699	-0.0451	-0.0571	0.1024	0.0000						
CW	-0.0692	-0.0684	-0.0479	0.1071	-0.0672	0.0219	-0.0161	-0.0460	-0.0023	0.0000					
QA	-0.0325	-0.0591	0.0200	0.1287	-0.0213	0.0129	-0.0107	0.0286	0.0295	-0.0397	0.0000				
DH	-0.0974	0.0121	-0.0628	0.0725	-0.0135	0.0386	-0.0619	-0.0286	-0.0013	-0.0386	-0.0489	0.0000			
JH	-0.0838	-0.0327	0.0351	-0.0541	-0.0918	-0.0910	-0.0514	0.0603	-0.0425	-0.0276	-0.0102	-0.0480	0.0000		
DZG	-0.0988	-0.0797	-0.0705	0.1537	-0.0397	0.0451	-0.0386	-0.0709	-0.0012	-0.1128	-0.0739	-0.0602	-0.0143	0.0000	
SYH	-0.0247	-0.0422	0.1111	-0.0545	-0.0350	-0.0737	-0.0524	0.1410	-0.0512	0.0292	0.0384	0.0330	-0.0536	0.0198	0.0000

Table S5. The effective population sizes for each population based on *COI* and *D-Loop* sequences.

Population	<i>COI</i>	<i>D-Loop</i>
MA	82784000	127069000
ZJS	84495000	79514000
HA	40708000	60300000
DT	90766000	103192000
NJLD	41633000	106242000
FYLD	2477000	108329000
PT	88047000	119829000
MZD	2060000	15060000
CW	100252000	142173000
XM	11573000	102886000
QA	115895000	132202000
DH	80819000	130186000
JH	39004000	115484000
DZG	34860000	98923000
SYH	40811000	4266000

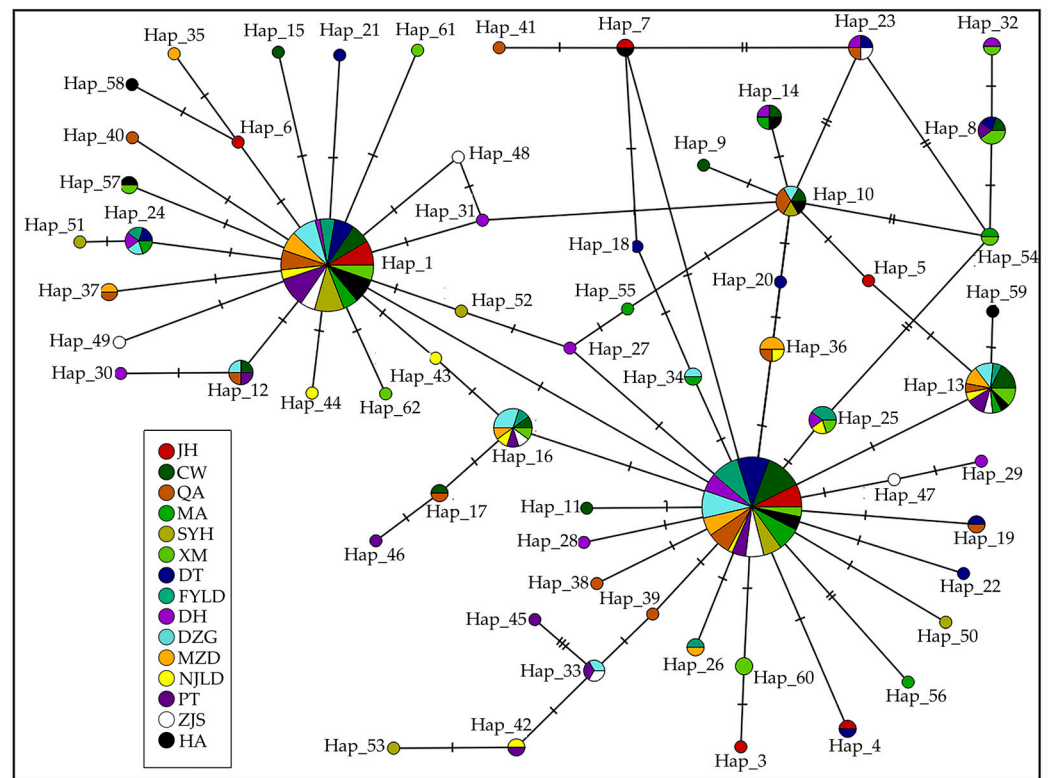


Figure S1. The minimum spanning network based on *COI* sequences.

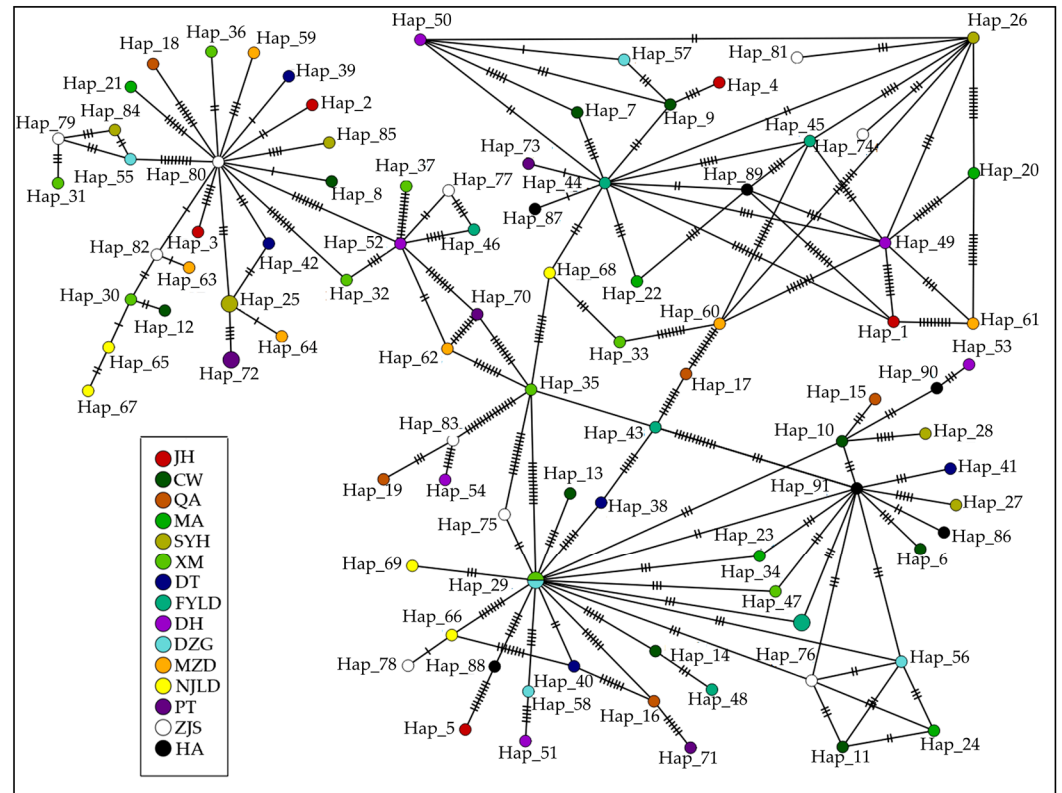


Figure S2. The minimum spanning network based on *D-Loop* sequences.