

Table. S1. Repeat motifs and primers of 10 microsatellites of *E. awoara*.

Locus	Primer (5'-3')	Repeat motif	Tm/°C
Qsby-9	F: AAGTATGGCAGCGACACC R: TGTAAAACGACGGCCAGTCCA CAACCACAGCAAAGC	(TATC) ₉ (T GTC) ₇	53.9
Qsby-11	F: GGTGGATAGATGGGTTAGG R: TGTAAAACGACGGCCAGTCAT TCGTGATAGCAAGTGT	(TAGA) ₂₇	48.3
Qsby-24	F: TGTAAAACGACGGCCAGTCAA TTTGAGTCTGTGCTGC R: GTTTGTGTTGTTTGTAGGCT	(GATA) ₈	49.7
Qsby-26	F: TGTAAAACGACGGCCAGTCTC CTGATGCTGCCAAC R: GCCACCACTATAAAGGTCTG	(TCTA) ₁₇	51.6
Qsby-30	F: TGTAAAACGACGGCCAGTACA TGACAAACCTGGACT R: CGATTGGTAGACAGCGACA	(TCTA) ₂₂	50.1
Qsby-60	F: ACAGATGATGAACCACCCA R: TGTAAAACGACGGCCAGTATG CTAATTCCGCCCTA	(TGTC) ₅ A G(GATA) ₄ ...(TCAT) ₅	51.1
Qsby-65	F: TGTAAAACGACGGCCAGTTAT GCCAAGATGACAACAGC R: TGTAAAACGACGGCCAGTCAG ACAGAGAGAGAACACAATG	(CTAT) ₂₇	49.9
Qsby-70	F: GGTGTAATGTAGTTCAAGCAA G R: TGTAAAACGACGGCCAGTAGC AGAATCCCAAAAAGC	(CTAT) ₂₉	49.1
Qsby-71	F: TGTAAAACGACGGCCAGTTGG TGTGTTCAAGTGCTCA R: GTCCTGCTAGTTGTCCTGTT	(TATC) ₁₅ (C ATC) ₄ (TATC) ₂	51.8
Qsby-72	F: CCTGTCCATCACCCCTTGT R:TGTAAAACGACGGCCAGTCCTT TGTCAAGTGCTTG	(TAGA) ₁₅	49.4

Table. S2. The distribution information of the shared haplotypes of mitochondrial COI, Cyt b and ND2 sequence (Hap01–Hap82).

Haplotype	MB	MN	DYW	BBW
Hap01	1			
Hap02	1			
Hap03	1			
Hap04	1			
Hap05	1			

Hap06	1			
Hap07	2	4	3	
Hap08	1	1		
Hap09	1			
Hap10	1			
Hap11	1			
Hap12	1			
Hap13	2	5	4	2
Hap14	1			
Hap15	1			
Hap16	1			
Hap17	1			
Hap18	1			
Hap19	1			
Hap20	1			
Hap21	1			
Hap22	1		1	
Hap23	2	2	1	4
Hap24	1			
Hap25	1			
Hap26	1			
Hap27	1			
Hap28	1			
Hap29	1			
Hap30			2	
Hap31			1	
Hap32			1	
Hap33			1	
Hap34			1	
Hap35		2	1	
Hap36			1	
Hap37			1	
Hap38			1	
Hap39			1	
Hap40			1	
Hap41		1	2	
Hap42			1	
Hap43			1	
Hap44			1	
Hap45			1	
Hap46			1	
Hap47			1	
Hap48			1	
Hap49		1	1	

Hap50		1		
Hap51		1		
Hap52		1		
Hap53			1	
Hap54			1	
Hap55			1	
Hap56			3	
Hap57			1	
Hap58			1	
Hap59			1	
Hap60			1	
Hap61			1	
Hap62		1		
Hap63		1		
Hap64		1		
Hap65		1		
Hap66		1		
Hap67		1		
Hap68		1		
Hap69		1		
Hap70		1		
Hap71		1		
Hap72		1		
Hap73		1		
Hap74		1		
Hap75		1		
Hap76		1		
Hap77		1		
Hap78		1		
Hap79		1		
Hap80		1		
Hap81		1		
Hap82	1			
Total	33	36	34	17

Table. S3. The distribution information of the shared haplotypes of RyR3 sequence (Hap01–Hap82).

Haplotype	MB	MN	DYW	BBW
Hap01	60	57	61	25
Hap02	3	6	2	1
Hap03	1	3	1	5
Hap04		3	2	1
Hap05			1	
Hap06		3	1	
Hap07	1			1

Hap08				1
Hap09		1		
Total	66	72	68	34

Table. S4. Matrix of pairwise F_{ST} among four populations based on RyR3 gene.

	MB	MN	DYW	BBW
MB				
MN	0.00339			
DYW	-0.00151	0.00038		
BBW	0.03120	0.02256	0.04604**	

*P<0.05, **P<0.01, ***P<0.001 for indices of population differentiation, F_{ST} .

Table. S5. Characteristics and genetic diversity indices for ten microsatellite loci in *Epinephelus awoara*.

	N _a	A _R	H _O	H _E	F _{ST}	F _{IT}	F _{IS}
Qsby-9	23	14.221	0.907	0.909	0.016	-0.015	-0.031
Qsby-11	34	16.059	0.653	0.934	0.026	0.288	0.269
Qsby-24	19	12.242	0.907	0.890	0.038	0.009	-0.030
Qsby-26	27	15.328	0.890	0.939	0.019	0.044	0.026
Qsby-30	32	16.660	0.695	0.948	0.025	0.272	0.254
Qsby-60	22	12.862	0.881	0.879	0.015	-0.020	-0.036
Qsby-65	40	18.762	0.898	0.953	0.017	0.044	0.027
Qsby-70	34	17.855	0.924	0.951	0.023	0.031	0.008
Qsby-71	23	14.393	0.890	0.922	0.025	0.022	-0.003
Qsby-72	18	11.647	0.805	0.916	0.037	0.108	0.074
Mean	27	15.003	0.845	0.924	0.024	0.078	0.056

^aNumber of alleles.

^bMean allelic richness with standard deviation.

^cMean observed heterozygosity with standard deviation.

^dMean expected heterozygosity with standard deviation.

Table. S6. Bottleneck results for four populations based on Wilcoxon's signed-rank test.

Model	Wilcoxon	Population			
		MB	MN	BBW	DYW
IAM	P (one-tail for H excess)	0.0005	0.0010	0.0161	0.0015
TPM	P (one-tail for H excess)	0.1377	0.0161	0.5391	0.3477
SMM	P (one-tail for H excess)	0.8838	0.7842	0.9878	0.9473
Allele frequency distribution		L-shaped			

Values in boldface type are significant at p<0.05. IAM: infinite allele model; TPM: two-phase mutation model; SMM: stepwise mutation model.

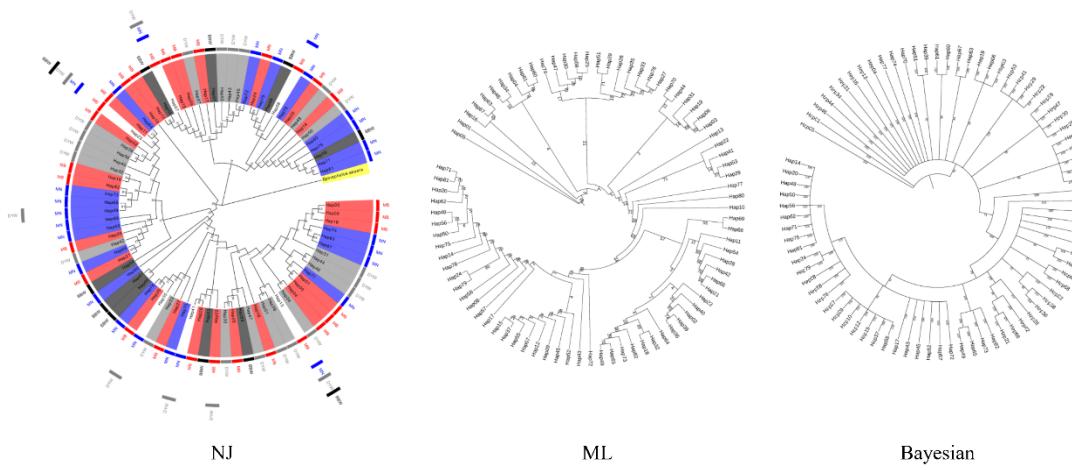


Figure S1. Phylogenetic trees reconstructed from mitochondrial sequences of COI Cyt b and ND2 gene in *Epinephelus awoara*. The values above the branches are bootstrap values for the NJ, ML, and BI analyses.

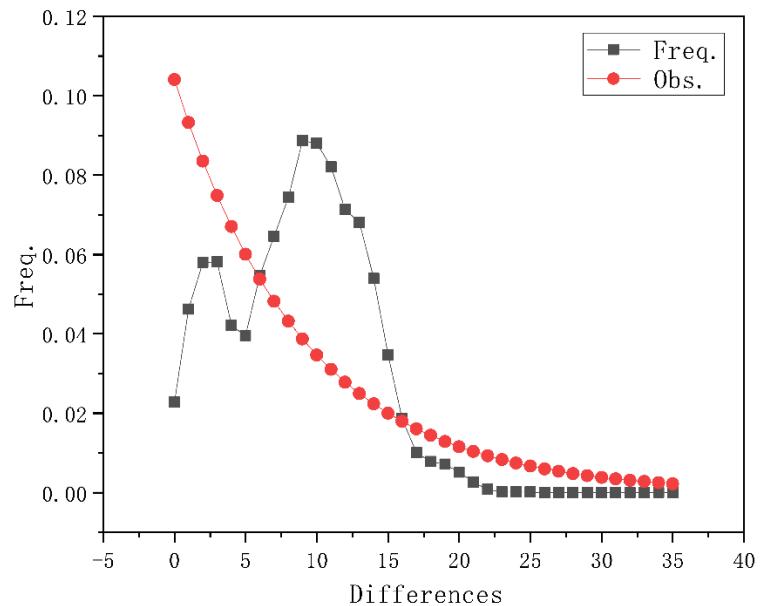


Figure S2. Mismatch distribution plot from mitochondrial sequences of COI Cyt b and ND2 gene in *Epinephelus awoara*.