

Supplementary Information

Table S1. Summary of sample size, haplotype numbers, haplotype diversity (h), nucleotide diversity (π), Tajima's D , Fu's F_s , Ramos-Onsins & Rozas R_2 tests and goodness-fit tests for cyt b sequences in each population, respectively. * $p < 0.05$; and ** $p < 0.01$.

Populations (Abbreviation)	Sample Size (n)	Haplotype Numbers	Haplotype Diversity (h)	Nucleotide Diversity (π)	Tajima's D	Fu's F_s	Ramos-Onsins & Rozas R_2	SSD	Raggedness Index
Ningde(ND)	49	16	0.798	0.002	-1.935 **	-10.989 **	0.022 **	0.001	0.041
Xiamen(XM)	37	12	0.581	0.001	-2.357 **	-9.063 **	0.036 **	0.002	0.049
Shantou(ST)	30	11	0.605	0.002	-1.958 *	-6.667 **	0.013 **	0.462	0.041
Yangjiang(YJ)	50	21	0.731	0.002	-2.482 **	-21.129 **	0.022 **	0.001	0.025
Beihai(BH)	35	14	0.717	0.002	-2.167 **	-9.125 **	0.034 **	0.006	0.032
Haikou(HK)	37	11	0.641	0.001	-1.750 *	-6.929 **	0.048 **	0.001	0.032
Sanya(SY)	28	7	0.582	0.001	-1.808 *	-4.801 **	0.067 **	0.001	0.068
Total	266	64	0.700	0.002	-2.569 **	-28.372 **	0.010 **	0.000	0.022

Table S2. Summary of sample size, haplotype numbers, haplotype diversity (h), nucleotide diversity (π), Tajima's D , Fu's F_s , Ramos-Onsins & Rozas R_2 tests and goodness-fit tests for control region (CR) sequences in each population, respectively. * $p < 0.05$; and ** $p < 0.01$.

Populations (Abbreviation)	Sample Size (n)	Haplotype Numbers	Haplotype Diversity (h)	Nucleotide Diversity (π)	Tajima's D	Fu's F_s	Ramos-Onsins & Rozas R_2	SSD	Raggedness Index
ND	49	35	0.875	0.001	-2.105 **	-26.599 **	0.035 **	0.008	0.058
XM	37	19	0.581	0.001	-1.927 *	-15.622 **	0.026 **	0.001	0.039
ST	30	24	0.977	0.003	-1.936 *	-25.882 **	0.053 **	0.009	0.059
YJ	50	26	0.900	0.002	-2.317 **	-27.100 **	0.044 **	0.008	0.089
BH	35	22	0.943	0.002	-1.460 *	-19.900 **	0.026 **	0.005	0.058
HK	37	18	0.887	0.003	-1.853 *	-12.462 **	0.019 **	0.003	0.049
SY	28	17	0.851	0.003	-1.880 *	-19.829 **	0.033 **	0.089	0.051
Total	266	112	0.916	0.003	-2.340 **	-26.782 **	0.010 **	0.001	0.044

Table S3. Matrix of pairwise of F_{ST} between 7 populations of based on cyt *b* sequences in *Cirrhimuraena chinensis*.

cyt <i>b</i>	ND	XM	ST	YJ	BH	HK	SY
ND							
XM	0.01588						
ST	0.00253	−0.00709					
YJ	0.00255	−0.00373	−0.01125				
BH	−0.00165	−0.0002	−0.01361	−0.00120			
HK	0.00950	0.00488	−0.01136	0.00169	−0.01557		
SY	0.00639	−0.01606	−0.01085	−0.00621	−0.00249	0.00348	

p values of F_{ST} (not presented here) are all greater than 0.05 and 0.01, which means all the F_{ST} values in the table above are not statistically significant under $p < 0.05$ and $p < 0.01$).

Table S4. Matrix of pairwise of F_{ST} between 7 populations of based on CR sequences in *Cirrhimuraena chinensis*.

CR	ND	XM	ST	YJ	BH	HK	SY
ND							
XM	−0.00566						
ST	−0.00126	−0.00563					
YJ	0.00349	−0.00151	0.00339				
BH	−0.00752	−0.00834	−0.01477	0.01656			
HK	0.00455	0.00390	−0.00007	0.00772	0.01090		
SY	0.00234	0.00775	−0.00075	0.00614	0.01712	0.00239	

p values of F_{ST} (not presented here) are all greater than 0.05 and 0.01, which means all the F_{ST} values in the table above are not statistically significant under $p < 0.05$ and $p < 0.01$).

Table S5. AMOVA results for testing genetic subdivision between populations of using cyt *b* fragment among geographic district.

cyt <i>b</i>	Sum of Squares	Percentage of Variation	Fixation Indices	Significance Tests
Groups: Taiwan strait (ND)(XM, ST, YJ, BH, HK, SY)				
Among groups	2.178	0.18	$\Phi_{CT} = 0.00182$	$p = 0.571$
Among populations within groups	9.447	0.11	$\Phi_{SC} = 0.00115$	$p = 0.235$
Within populations	469.925	99.70	$\Phi_{ST} = 0.00297$	$p = 0.271$
Groups: Pearl River (ND, XM, ST) (YJ, BH, HK, SY)				
Among groups	1.438	−0.26	$\Phi_{CT} = −0.00283$	$p = 0.917$
Among populations within groups	10.187	0.33	$\Phi_{SC} = 0.00324$	$p = 0.161$
Within populations	469.925	99.93	$\Phi_{ST} = 0.00042$	$p = 0.236$
Groups: Leizhou Peninsula (ND, XM, ST, YJ, HK, SY) (BH)				
Among groups	2.010	0.09	$\Phi_{CT} = −0.00259$	$p = 0.696$
Among populations within groups	9.614	0.16	$\Phi_{SC} = 0.00328$	$p = 0.220$
Within populations	469.925	99.76	$\Phi_{ST} = 0.00070$	$p = 0.242$
Groups: Qiongzhou Strait (ND, XM, ST, YJ, BH) (HK, SY)				
Among groups	2.170	0.16	$\Phi_{CT} = 0.00159$	$p = 0.288$
Among populations within groups	9.454	0.11	$\Phi_{SC} = 0.00110$	$p = 0.359$
Within populations	469.925	99.73	$\Phi_{ST} = 0.00269$	$p = 0.281$

Table S6. AMOVA results for testing genetic subdivision between populations of using CR fragment among geographic district.

CR	Sum of Squares	Percentage of Variation	Fixation Indices	Significance Tests
Groups: Taiwan strait (ND)(XM,ST,YJ,BH,HK,SY)				
Among groups	2.178	0.18	$\Phi_{CT} = 0.00182$	$p = 0.573$
Among populations within groups	9.447	0.11	$\Phi_{SC} = 0.00115$	$p = 0.275$
Within populations	469.925	99.70	$\Phi_{ST} = 0.00297$	$p = 0.269$
Groups: Pearl River (ND,XM,ST)(YJ,BH,HK,SY)				
Among groups	1.463	-0.28	$\Phi_{CT} = -0.00283$	$p = 0.897$
Among populations within groups	10.161	0.33	$\Phi_{SC} = 0.00324$	$p = 0.152$
Within populations	469.925	99.96	$\Phi_{ST} = 0.00042$	$p = 0.284$
Groups: Leizhou Peninsula (ND,XM,ST,YJ,HK,SY)(BH)				
Among groups	2.010	0.09	$\Phi_{CT} = 0.00085$	$p = 0.710$
Among populations within groups	9.614	0.16	$\Phi_{SC} = 0.00156$	$p = 0.229$
Within populations	469.925	99.76	$\Phi_{ST} = 0.00242$	$p = 0.271$
Groups: Qiongzhou Strait (ND,XM,ST,YJ,BH)(HK,SY)				
Among groups	2.010	0.16	$\Phi_{CT} = 0.00085$	$p = 0.713$
Among populations within groups	9.614	0.09	$\Phi_{SC} = 0.00156$	$p = 0.270$
Within populations	469.925	99.76	$\Phi_{ST} = 0.00242$	$p = 0.260$

Figure S1. Median-joining network of *Cirrhimuraena chinensis* Kaup for concatenated sequences (cyt *b* + CR) using software NETWORK.

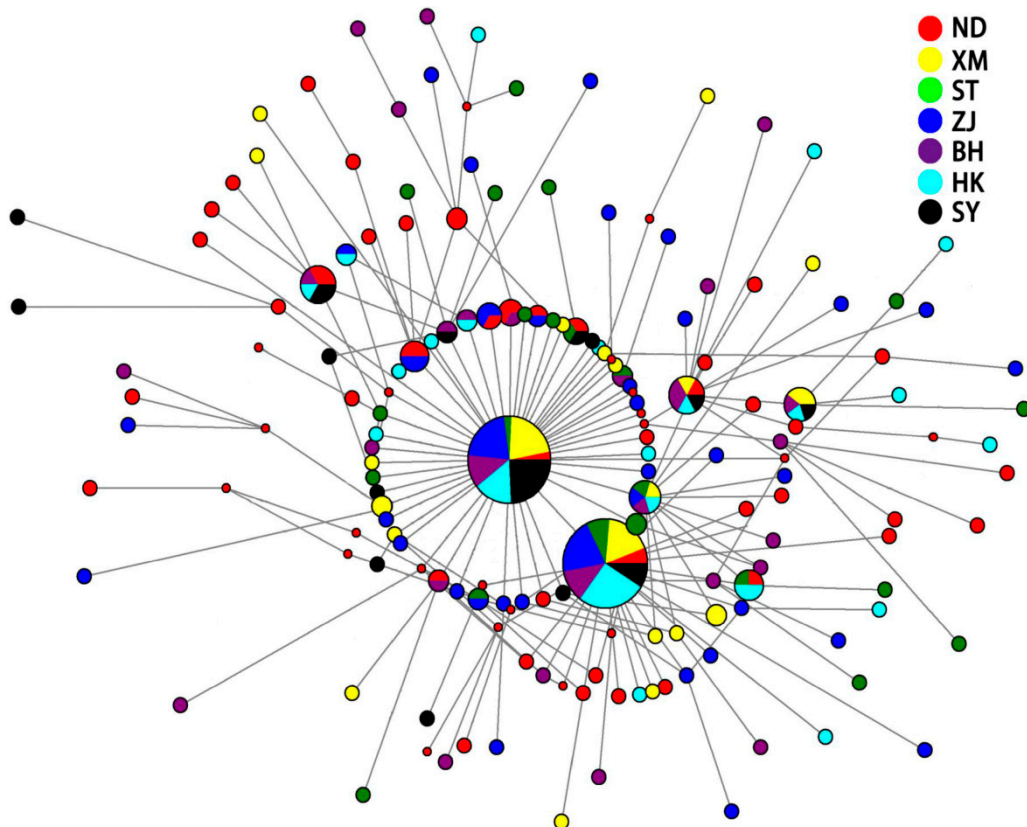


Figure S2. Median-joining network of *Cirrhimuraena chinensis* Kaup for concatenated sequences (cyt *b* + CR) using software TCS.

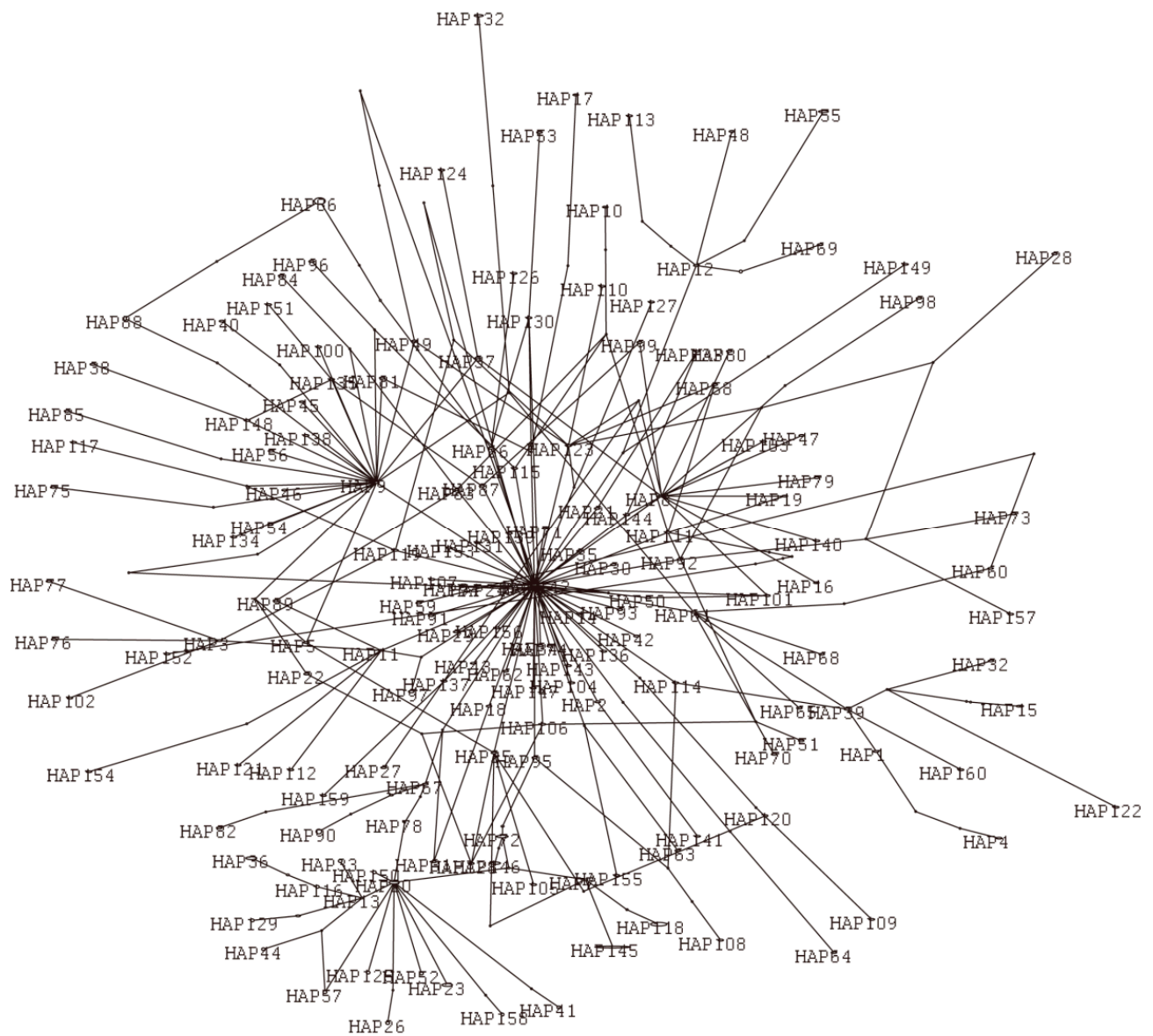


Figure S3. Bayesian Skyline Plots of the effective sizes through time for *Cirrhimuraena chinensis* Kaup based on cyt *b* fragment. The upper and lower limits of light blue trend represent the 95% confidence intervals of highest posterior densities (HPD) analysis.

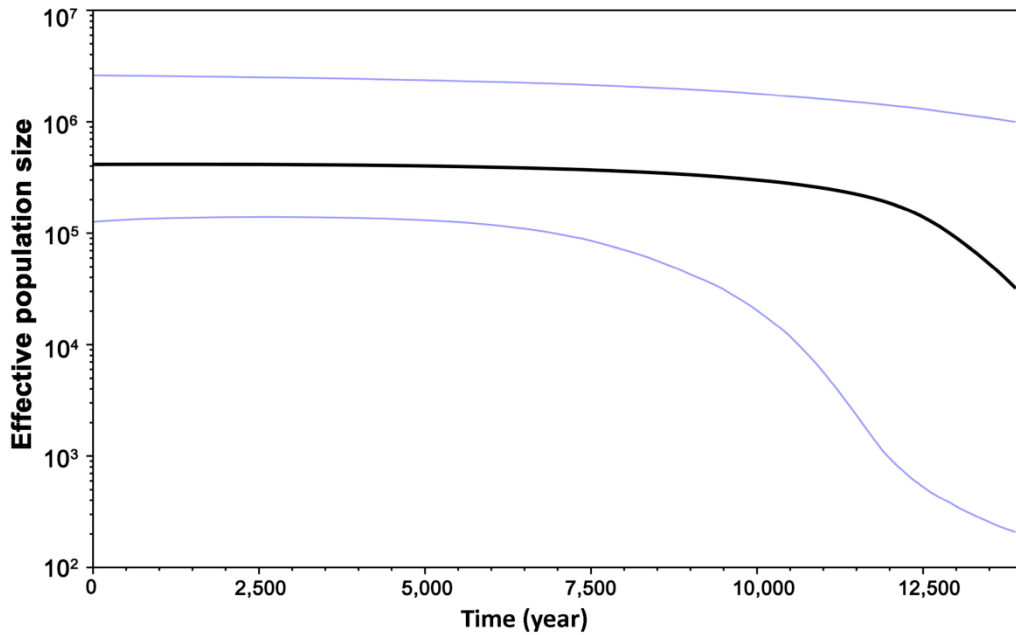


Figure S4. Bayesian Skyline Plots of the effective sizes through time for *Cirrhimuraena chinensis* Kaup based on cyt *b* fragment. The upper and lower limits of light blue trend represent the 95% confidence intervals of HPD analysis.

