

Supplementary Tables

Table S1. The eight species for the phylogenetic analysis. Species annotated with an asterisk is outgroup.

Family	Species	GenBank accession number
Trichodontidae	<i>Arctoscopus japonicus</i>	AP003090
Cyclopteridae	<i>Aptocyclus ventricosus</i>	AP004443
Liparidae	<i>Liparis tessellatus</i>	MN88063
Agonidae	<i>Hemitripterus villosus</i>	MN316630
Cottidae	<i>Cottus amblystomopsis</i>	KY563345
Psychrolutidae	<i>Dasycottus setiger</i>	MW420925
Hexagrammidae	<i>Hexagrammos otakii</i>	KR362879
Gasterosteidae	<i>Gasterosteus aculeatus</i> *	MH205729

Table S2. The evidence for estimating divergence times includes the fossil record and lower-bound constraint parameters used in the estimation. Less reliable records were incorporated into the analysis as soft-bound. The dagger symbol in the table indicates that the species is extinct.

Fossil record	Fossil age (Ma)	Constraint parameter	Reference
† <i>Diaphantes tilesii</i>	11.6–5.3 Ma	L (5.33, 1e-300)	Nazarkin and Voskoboinikova (2000)
† <i>Lirosceles elegans</i>	11.6–7.2 Ma	L (7.22, 1e-300)	Jordan (1925)
†Hexagrammidae indet.	16.0–11.6 Ma	L (11.6, 0.025)	Ono and Uyeno (1985)
†Gasterosteidae indet.	23.0–20.4 Ma	L (20.44, 0.025)	Nazarkin and Malyshkina (2012)

Table S3. Uniform prior distributions of the parameters included in the ABC analysis. N_{SH} , N_{WJ} , and N_{ANC} represent the effective population sizes of the SH group, the WJ group, and the ancestral population, respectively. t_0 , t_1 , and t_2 denote the times of demographic events, while r indicates the admixture proportion.

Parameter	Minimum	Maximum
N_{SH}	1,000	1,000,000
N_{WJ}	10,000	10,000,000
N_{ANC}	100	1,000,000
t_0	10	7,600
t_1	10	7,600
t_2	7,600	20,000
r	0.0001	0.999

Table S4. Summary statistics of mitochondrial (mt) DNA and microsatellite DNA loci. h and π are haplotype diversity and nucleotide diversity for mtDNA. n_a , n_e , H_o and H_e indicate the number of alleles, the effective number of alleles (Kimura and Crow, 1964), observed heterozygosity, and expected heterozygosity, respectively.

Sample population	mtDNA			10 microsatellite loci			
	No. haplotypes	h	π (%)	n_a	n_e	H_o	H_e
Akkeshi (AK)	22	0.952	0.773	12.9	7.848	0.783	0.791
Muroran (MR)	19	0.952	0.638	12.1	7.517	0.760	0.776
Abashiri (AS)	23	0.983	0.825	14.9	8.590	0.787	0.806
Atsuta (AT)	23	0.979	0.681	12.0	6.632	0.730	0.716
Hachimori (HM)	17	0.945	0.381	13.6	7.779	0.760	0.788
Funagawa (FG)	21	0.963	0.449	12.5	7.287	0.783	0.778
Wakasa (WS)	26	0.984	0.523	14.5	8.238	0.777	0.773
Oki (OK)	23	0.959	0.491	13.3	7.662	0.737	0.749
Mishima (MS)	27	0.991	0.926	14.8	8.386	0.773	0.767

Table S5. Comparison of partitioning schemes for maximum likelihood tree estimations.

Data set	Partitioning scheme	Mean bootstrap value	Log-likelihood	AIC	Number of parameters
1 _N 2 _N 3 _N	Genes and codon positions	66.8	-46245.513	93283.027	396
1 _N 2 _N 3 _N	Codon positions	76.4	-47049.323	94170.646	36
1 _N 2 _N 3 _{RY}	Genes and codon positions	72.4	-29520.525	59679.049	319
1 _N 2 _N 3 _{RY}	Codon positions	75.6	-30247.942	60553.884	29
1 _N 2 _N	Genes and codon positions	59.0	-18148.366	36824.732	264
1 _N 2 _N	Codon positions	59.8	-18738.033	37524.065	24

Table S6. Estimated parameters for the best demographic scenario (scenario 6) and associated 95% confidence intervals defined by the 0.025 and 0.975 quantiles of the posterior distribution.

Parameter	Median	0.025	0.975
N_{SH}	197,000	47,800	588,000
N_{WJ}	3,890,000	765,000	9,730,000
N_{ANC}	29,600	1,310	85,500
t_0	164	25	5,525
t_1	13,925	6,175	18,675
t_2	49,250	23,300	139,000
r	0.0186	0.000270	0.380

Supplementary Figures

The fossil records corresponding to the calibration points

1. †*Diaphantes tilesii* 11.6-5.3 Ma
2. †*Lirosceles elegans* 11.6-7.2 Ma
3. †*Hexagrammidae* indet. 16.0-11.6 Ma
4. †*Gasterosteridae* indet. 23.0-20.4 Ma

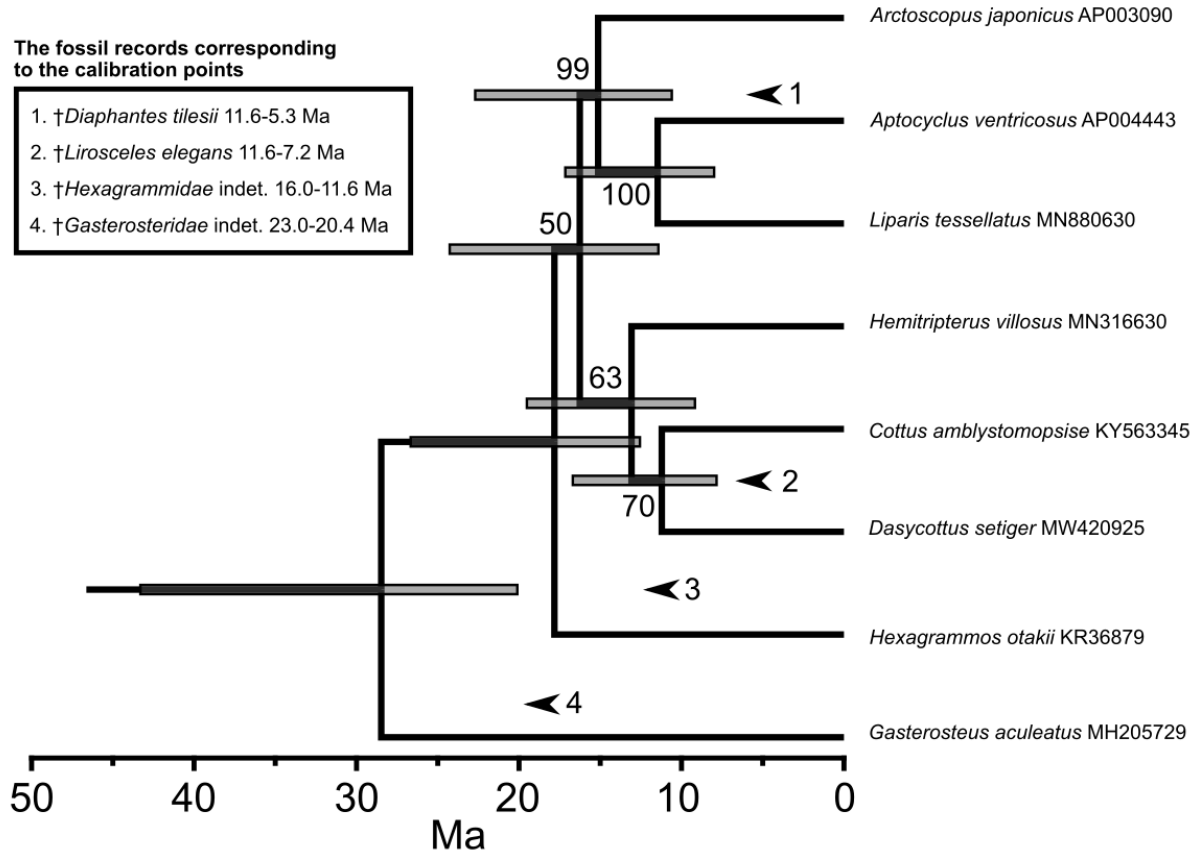


Fig. S1. Time-calibrated mitochondrial genomic tree for representative species of Suborder Cottoidei.

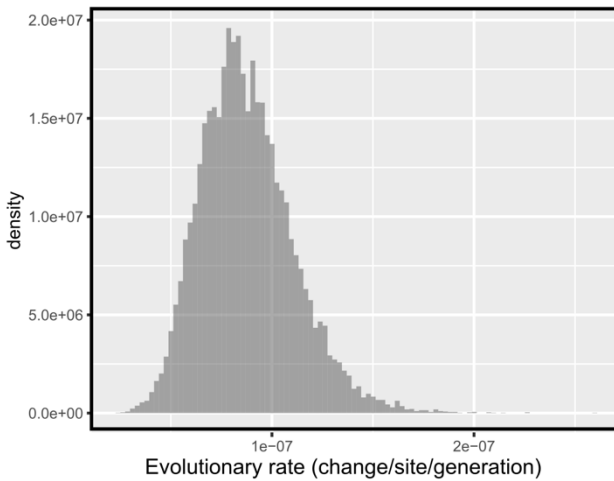


Fig. S2. Posterior distribution of the molecular evolutionary rate for the mitochondrial DNA Cytochrome *b* gene region.

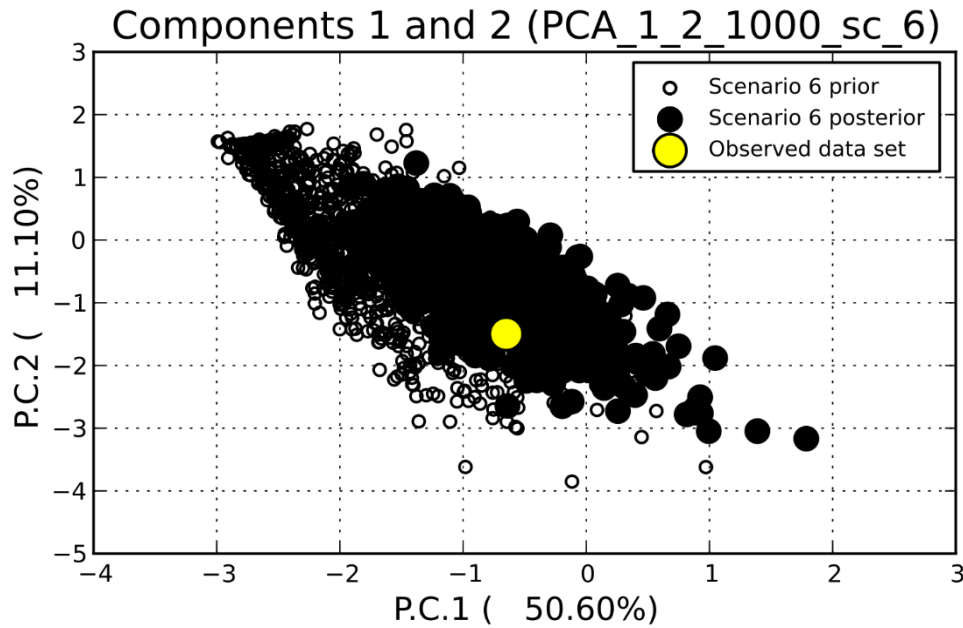


Fig. S3. Model evaluation outcomes for the best scenario (Scenario 6), indicating a principal component analysis of summary statistics from the observed dataset, datasets generated based on parameter priors, and datasets from the posterior predictive distribution. A suitable model fit is indicated when the datasets derived from prior parameters cover a wide region on the graph, and the observed dataset is positioned within a compact cluster of posterior datasets.

LITERATURE CITED

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