Supplementary Table 1. Hierarchical structure analyses of molecular variance for polkadot skate (*Dipturus chinensis*) sampled during 2010–2017 from 6 populations around Japan in the East China Sea, Sea of Japan, and Pacific Ocean, based on the mitochondrial cytochrome *b* gene (931 base pairs) and 4 microsatellite loci. Isls.=Islands.

Groupings[a]	Source of variation	Sum of squares	Variance components	Φ or R statistics	Percentage of variation
Mitochondrial cytochrome *b* gene					
All 6 populations	Among populations	703.56	8.6712	Φ_{ST}=0.8976 (*P*<0.001)	89.76
	Within populations	205.78	0.9893		10.24
2 groups					
1. Clade A (Danjo Isls.–Goto Isls.–Kyoto–Niigata)	Among groups	640.39	8.3197	Φ_{CT}=0.8529 (*P*=0.068)	85.29
	Among populations within groups	68.93	0.4588	Φ_{SC}=0.3199 (*P*<0.001)	4.70
2. Clade B (Kochi–Aomori)	Within populations	200.01	0.9757	Φ_{ST}=0.9000 (*P*<0.001)	10.00
3 groups					
1. Clade A (Danjo Isls.–Goto Isls.–Kyoto–Niigata)	Among groups	703.56	8.6555	Φ_{CT}=0.8964 (*P*=0.064)	89.64
2. Clade B1 (Kochi)	Among populations within groups	5.76	0.0242	Φ_{SC}=0.0242 (*P*=0.072)	0.25
3. Clade B2 (Aomori)	Within populations	200.01	0.9757	Φ_{ST}=0.8990 (*P*<0.001)	10.11
Microsatellite loci					
All 6 populations	Among populations	39.13	0.2251	R_{ST}=0.1409 (*P*<0.001)	14.09
	Within populations	572.25	1.3723		85.91
2 groups					
1. Clade A (Danjo Isls.–Goto Isls.–Kyoto–Niigata)	Among groups	24.94	0.1351	R_{CT}=0.0868 (*P*=0.067)	8.68
	Among populations within groups	21.27	0.0561	R_{SC}=0.0394 (*P*<0.001)	3.60

Groupings[a]	Source of variation	Sum of squares	Variance components	Φ or R statistics	Percentage of variation
2. Clade B (Kochi–Aomori)	Within populations	565.18	1.3652	R_{ST}=0.1228 (P<0.001)	87.72
3 groups					
1. Clade A (Danjo Isls.–Goto Isls.–Kyoto–Niigata)	Among groups	39.13	0.2167	R_{CT}=0.1359 (P=0.066)	13.59
2. Clade B1 (Kochi)	Among populations within groups	7.08	0.0128	R_{SC}=0.0093 (P<0.05)	0.80
3. Clade B2 (Aomori)	Within populations	565.18	1.3652	R_{ST}=0.1439 (P<0.001)	85.61

[a] Partitioning of genetic variability among the geographic populations of Japan was performed by hierarchical AMOVA, which grouped them into alterative structures by maximizing Φ_{CT} or R_{CT} values