

Table S1. Haplotype distribution of *Ascidella aspersa* inferred from 80 COI sequences in Korea population. Each column represents the sampling location, and the rows refer to the 14 haplotypes.

	Incheon (IC)	Bieung (BU)	Wando (WD)	Yeosu (YS)	Tongyeong (TY)	Ulsan (US)	Yangpo (YP)	Jukbyeon (JB)	Donghae (DH)	Sokcho (SC)
Hap_1	5	3	0	2	0	1	0	0	1	2
Hap_2	0	1	0	0	0	0	0	0	0	0
Hap_3	2	3	4	3	5	4	2	4	4	2
Hap_4	0	1	0	0	0	0	0	0	0	0
Hap_5	1	1	0	0	0	1	1	1	0	1
Hap_6	1	0	0	0	0	0	0	0	1	0
Hap_7	0	0	0	0	1	0	0	1	1	0
Hap_8	1	0	0	1	0	0	3	0	0	0
Hap_9	0	0	0	0	1	0	2	2	0	3
Hap_10	0	0	0	0	1	0	0	0	0	0
Hap_11	0	0	1	1	0	1	0	0	0	0
Hap_12	0	0	1	0	0	0	0	0	0	0
Hap_13	0	0	1	0	0	0	0	0	0	0
Hap_14	0	0	0	1	0	0	0	0	0	0

Table S2. Results of mt-COI analysis of molecular variance (AMOVA) for *Ascidrella aspersa* along the coast of Korea and global population.

	Source of variation	d.f.	Sum of squares	Variance components	Percentage of variation
Korean population	Among populations	2	1.653	0.01752	4.39
	Within populations	77	29.359	0.38129	95.61
	Total	79	31.012	0.39881	
		Fst = 0.04394 p-values = 0.09271 ± 0.01575			
Global population	Among populations	8	46.852	0.38665 Va	27.69
	Within populations	145	146.380	1.00952 Vb	72.31
	Total	153	193.232	1.39617	
		Fst = 0.27694 p-values = 0.00098			

Table S3. The pairwise genetic distances (K2P) mt-COI results between Korean populations.

	Incheon (IC)	Bieung (BU)	Wando (WD)	Yeosu (YS)	Tongyeong (TY)	Ulsan (US)	Yangpo (YP)	Jukbyeon (JB)	Donghae (DH)	Sokcho (SC)
Incheon (IC)	0.00000									
Bieung (BU)	-0.05412	0.00000								
Wando (WD)	0.24345	0.08510	0.00000							
Tongyeong (TY)	0.18203	0.08040	0.00689	0.00000						
Yeosu (YS)	0.04171	-0.01011	0.01299	-0.10353	0.00000					
Donghae (DH)	0.08069	-0.03432	-0.03927	0.00805	-0.04313	0.00000				
Jukbyeon (JB)	0.10561	-0.01094	-0.08571	0.03827	-0.01261	-0.08108	0.00000			
Ulsan (US)	0.02314	-0.02612	0.02433	-0.09979	-0.14324	-0.03949	-0.01818	0.00000		
Yangpo (YP)	0.17392	0.07377	-0.02463	0.02057	0.00100	0.00297	-0.04464	0.02056	0.00000	
Sokcho (SC)	0.00789	-0.02598	0.07692	0.12583	0.02430	0.03743	-0.05357	0.00533	0.05751	0.00000

Table S4. Haplotype distribution of *Ascidrella aspersa* inferred from 154 mt-COI sequences in the global population. Each column represents the sampling location, and the rows refer to the 21 haplotypes in global population.

	KOREA (KO)	CANADA (CA)	ENGLAND (EN)	FRANCE (FR)	INDIA (IN)	JAPAN (JA)	SPAIN (SP)	SWEDEN (SW)	USA (US)
Hap_1	23	1	2	0	0	1	0	1	2
Hap_2	36	0	8	1	0	4	6	0	8
Hap_3	1	0	0	1	0	2	7	0	0
Hap_4	2	0	0	0	0	0	1	0	0
Hap_5	0	0	1	0	0	0	0	0	0
Hap_6	0	0	1	0	0	0	0	0	0
Hap_7	0	0	0	1	0	0	0	0	0
Hap_8	6	0	0	0	0	0	0	0	0
Hap_9	0	0	0	0	1	1	0	0	0
Hap_10	9	0	0	0	0	0	3	1	0
Hap_11	1	0	0	0	0	0	0	0	0
Hap_12	1	0	0	0	0	0	0	0	0
Hap_13	0	0	0	0	0	0	3	0	0
Hap_14	0	0	0	0	0	0	6	0	0
Hap_15	0	0	0	0	0	0	1	0	0
Hap_16	0	0	0	0	0	0	4	0	0
Hap_17	0	0	0	0	0	0	1	0	0
Hap_18	0	0	0	0	0	0	1	0	0
Hap_19	0	0	0	0	0	0	1	0	0
Hap_20	0	0	0	0	0	0	1	0	0
Hap_21	3	0	0	0	0	0	0	0	0

Table S5. The pairwise genetic distances (K2P) mt-COI results between Global populations.

	Korea (KO)	Canada (CA)	England (EN)	France (FR)	India (IN)	Japan (JA)	Spain (SP)	Sweden (SW)	USA (US)
Korea (KO)	0.00000								
Canada (CA)	-0.21246	0.00000							
England (EN)	-0.00419	0.29244	0.00000						
France (FR)	0.00011	0.00132	0.17892	0.00000					
India (IN)	0.92672	1.00000	0.96693	0.93738	0.00000				
Japan (JA)	-0.00759	0.23100	0.04821	-0.13067	0.96054	0.00000			
Spain (SP)	0.14438	0.10233	0.19557	-0.04963	0.93267	0.03478	0.00000		
Sweden (SW)	-0.12073	-1.00000	0.21460	-0.07085	0.96777	0.05595	0.01982	0.00000	
USA (US)	0.00411	0.55556	-0.06552	0.22517	0.97791	0.05169	0.18201	0.40688	0.00000

Table S6. Haplotype distribution of *Ascidella aspersa* inferred from 124 18S-rDNA sequences in the global population. Each column represents the sampling location, and the rows refer to the 5 haplotypes in global population.

Haplotype	Korea (KO)	England (EN)	Japan (JA)	Spain (SP)	Sweden (SW)
Hap 1	81	10	8	21	2
Hap 2	0	0	0	1	0
Hap 3	0	1	0	0	0
Hap 4	0	1	0	0	0
Hap 5	2	0	0	0	0

Table S7. Results of 18S-rDNA analysis of molecular variance (AMOVA) for *Ascidella aspersa* along the coast of Korea and global population.

Source of variation	d.f	Sum of squares	Variance components	Percentage variation
Among populations	2	0.065	0.00033 Va	1.39
Within populations	124	2.921	0.02356 Vb	98.61
Total	126	2.986	0.02389	
Fixation Index	Fst: 0.01390 p-value = 0.06940 ± 0.00772			

Table S8. The pairwise genetic distances (K2P) among populations 18S-rDNA results between Global populations.

	Korea (KO)	England (EN)	Japan (JA)	Spain (SP)	Sweden (SW)
Korea (KO)	-				
England (EN)	-0.0000000221				
Japan (JA)	0.0000000000	-0.0000000221			
Spain (SP)	0.0000000000	0.0000000055	0.0000000000		
Sweden (SW)	0.0000000000	-0.0000000221	0.0000000000	0.0000000000	-