The Pulation Structure of the Pacific Cod (*Gadus macrocephalus* Tilesius) Based on Mitochondrial DNA Sequences

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To assess population structure and genetic diversity among the Pacific cod (*Gadus macrocephalus*), we investigated mtDNA COI gene sequences of 7 populations. Samples were obtained from Sokcho, Wolsung, Geoje, Yeosu, Geomundo and Westsout in 2008 and 2009 ($n=28$). The sequence analysis of 28 individual samples showed 8 haplotypes, ranging in sequence divergence by pairwise comparisons from 0.2 to 2.2% (1 bp–11 bp). The Ga1 haplotype was found in Wolsung, Geoje, Yeosu, Geomundo and Westsout, and was regarded as the main haplotype of Korean Pacific cod. Ga2, Ga3, Ga6 and Ga7 haplotypes were found only in Sokcho. In the PHYLIP analysis, 8 haplotypes formed two independent groups: cladeA consisted of Ga2, Ga3, Ga6 and Ga7 haplotypes, whereas cladeB contained Ga1, Ga4, Ga5 and Ga8 haplotypes. The genetic relationship between the two groups was weakly supported by bootstrap analysis (<50%). In pairwise comparisons between 6 populations other than that from Sokcho, a very high per generation migration ratio ($N_m=\infty$) and a very low level of geographic distance ($F_{ST}=-0.0123$ – (-0.0423)) were observed. The estimates of genetic distance between Sokcho and the other localities were all statistically significant ($p<0.05$, $p<0.01$, $p<0.001$), indicating a limited mtDNA-based gene flow between Sokcho and other regions. The finding of the lowest genetic diversity in the Sokcho population (nucleotide diversity=0.00589) may be a result of relatively small population size and interrupted gene flow to other localities. Consequently, the overall considerable migration of Pacific cod population in Korea caused a genetically homogeneous structure to form, although a distinct population was found in this study.

Key words : Gene flow, mtDNA, population structure, the Pacific cod

Introduction

A major concern in the field of population genetics is to understand the causes of differentiation between populations across ranges of geographic distribution. Fisheries management treats each stock as a single population, assuming little or no migration between stocks. This assumption is important to fisheries managers. Among methods for differentiating populations, biochemical genetic analyses are powerful techniques to assess the level of gene flow between, and within, populations or stocks. Genetic analyses can find useful application in taxonomic studies. Biochemical genetic analyses can also help establish the approximate timing of species divergence provided a taxonomically appropriate calibration is available, and can be useful in under-

standing phylogenetic relationships within genera and determine the stock structure of marine fishes [10].

Mitochondria carry their own DNA (mtDNA). The mitochondrial genome does not usually recombine. MtDNA provides a clonally inherited marker that traces maternal lineage. Distinct mtDNA sequences are referred to as haplotypes rather than alleles, because mtDNA is inherited as a single non-recombining unit. Due to genetically specific characteristics in mtDNA, we previously carried out population genetic structure for anchovy and octopus as commercially important species in Korea [13,18].

The Pacific cod, *Gadus macrocephalus* Tilesius, is a member of the order Gadiformes and family Gadidae. This species is a migrant fish for spawning, schooling fish and fish-feeding feeder which is associated with one of the commercially important fishery resources in Korea. In Canada, numerous techniques have been used to identify stock differences in cod and improve the management of this resource [4,12,16].

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Little has been investigated to assess the degree of diversity in a genetic population of the Pacific cod using mtDNA sequences. The aim of this study was to provide some information of population genetic structure of the Pacific cod with particular interest in its correlation within and among populations.

Materials and Methods

Specimen

The Pacific cod were obtained from 7 localities in Korea during the period of October 2008 - January 2009 (Fig. 1). We used a total of 28 individuals. The specimen in Geomundo and Westsouth (St. 6, 7) was provided by Research vessel (Tamgu 20). The cod from Wolsung and Geoje-do were purchased from a local seafood market. The samples from Sokcho and Yeosu were directly caught by fishing net. Samples were frozen at -70°C until required.

DNA extraction

Total DNA was extracted from their mussel by the method of Asahida et al. [1]. Amplification and sequencing of the partial region of the mtDNA COI gene were conducted

using primer Col1cod-L (5'-CCTGCTGGAGGAGGTGATCC-3') and Cole-H (5'-CCAGAGATTAGAGGGAATCAGTG-3') [3]. PCR reactions were performed under the following conditions in 25 μl reaction volumes: 20 pmol of each primer; 0.5 mM dNTPs; 1.25 unit Taq DNA polymerase (FastStar Taq DNA polymerase, Roche); 1 $\times$ PCR reaction buffer (Roche); 5-30 ng total genomic DNA. The thermocycling profile included an initial denaturation step of 95°C for 4 min, followed by 35 cycles of 1 min at 94°C , primer annealing for 1 min at 50°C and extension for 2 min at 72°C . The final extension step was increased to 5 min. The PCR was carried out by MyCycler Thermocycle (Bio-Rad). To obtain successful DNA amplification, electrophoresis was carried out 50 min using 1 $\times$ TBE buffer in 1.5% agarose gel. The PCR product was purified using a NucleoSpin[®] Extract PCR Purification Kit by following the manufacturer's instructions. The purified DNA product was stored at -20°C until required.

Nucleotide sequence

The purified DNA was directly sequenced using an Applied Biosystem model ABI 3730XL automated sequencer and a Big Dye terminator cycle sequencing kit (Perkin-Elmer Applied Biosystems). For the sequencing reaction, 30 ng of purified PCR products, 2.5 pmol of primer, and 1 μl of Big Dye terminator were mixed and adjusted to a final volume of 7 μl with dH₂O. The reaction was run with 5% DMSO for 30 cycles of 15 sec at 95°C , 5 sec at 50°C and 4 min at 60°C . Both strands were sequenced for crosscheck.

Haplotype

Sequence data were aligned using the multiple alignment program Clustal W [22]. When homologous sequences differed by $\geq$ one nucleotide, the sequences were considered as different haplotypes. Haplotype designations (Ga1, Ga2, Ga3, and so forth) were applied to new sequences as they were discovered.

Genetic tree

Phylogenetic analysis was performed by the parsimony method incorporated in PHYLIP (Phylogeny Inference Package) ver. 3.5c [7] as a subprogram NEIGHBOR. To obtain the genetic tree, the data set was iterated 1,000 times using a subprogram SEQBOOT. Individual trees from each iterated data set were obtained using the subprogram DNAMLK with the option of Kimura's 2-parameter method

Fig. 1. Map showing the location of the Pacific cod populations investigated in this study. General locality names are as follows: 1. Sokcho, Kangwon Province; 2. Wolsung, Kyungpook Province; 3. Geoje-do, Kyungnam Province; 4. Yeosu, Chunnam Province; 5. Geomundo, Chunnam Province; 6. Westsouth; 7. Westsouth.

[15], which attempts to correct observed dissimilarities for multiple substitutions in sequences evolving with a transition bias. A consensus tree representing reliability at each branch in the tree was obtained using the subprogram CONSENSE.

Genetic distance

To investigate the magnitude and pattern of genetic diversity within localities, genetic diversity and mean number of pairwise differences among haplotypes, gene diversity, and nucleotide diversity were calculated using Arlequin ver 1.1 [21]. The mean number of differences between all pairs of haplotypes in the sample was obtained by considering the number of mutations having occurred since the divergence of any two haplotypes, and the frequency of the ones involved in the calculation. Nucleotide diversity was calculated by estimating the probability that two randomly chosen homologous sequences will be different [17]. Genetic distance (F_{ST}), coefficient of coancestry (D), and female migration rate (N_m) were estimated by subroutines in Arlequin ver 1.1 [21]. Statistical significance of the difference between pairs of localities was tested by permutations (1,000 bootstraps; Excoffier et al., 1992). Pairwise F_{ST} values were converted to the estimates of per generation female migration rate, N_m (the product of the effective population size N and female migration rate, m), using the equilibrium relationship: $F_{ST}=1/(2N_m+1)$. Although F_{ST} values do not increase linearly with divergence time, they can be linearized (assuming that migration rate is low and divergence time is relatively low) as: $D=-\log(1-F_{ST})$, where D is a coancestry coefficient that is approximately linear with divergence time [20].

Genetic structure

Hierarchical genetic relationships among populations and sets of populations were assessed by the Holsinger and Mason-Gamer (H-MG) method [11]. In addition to the hierarchical structure among populations, these statistics enabled us to test the statistical significance of the genetic differentiation detected at each hierarchical level (10,000 bootstraps). The degree of hierarchical subdivision between specified sets of localities was examined with the AMOVA (Analysis of Molecular Variance) program [6] incorporated in Arlequin ver 1.1 [21]. This analysis provided correlation of DNA haplotype diversity at different levels of hierarchical subdivision in the form of three variance components: between regions; within regions; and within localities. This

study enabled us to determine changes in allocation of the components of variance, depending upon different geographic grouping schemes. Data set enabled us to calculate nucleotide diversity within localities [17].

Results

mtDNA analysis

The primer pair Co1fcod-L and Cole-H was successful in amplifying the cod genomic DNA, and a PCR product of the expected size (495 bp) is shown (Fig. 2). A total of 8 haplotypes (Ga1-Ga8) was obtained from the partial sequences of COI gene of 35 individuals of the cod collected from 7 localities including offshore waters (Westsouth, St. 6, 7). Sequence alignment revealed 24 variable nucleotides: 16 A $\rightleftharpoons$ T transversion, 8 G $\rightleftharpoons$ C transversion (Fig. 3). 13 among 24 variable nucleotides were at the first and second places of codons, 11 were 5th, 6th, 7th and 8th places.

DNA divergence

A pairwise comparison between pairs of haplotypes is performed to determine the divergence and relationships among haplotypes (Table 2). The sequence divergence among the 8 haplotypes by pairwise comparisons, ranged from 0.2-2.2% (1 bp-11 bp). The largest sequence divergence of 2.0% was observed when haplotypes Ga7 from Sokcho were compared to the Ga8 from Geojeodo, Geomundo and Westsouth (St. 7). In addition, a pairwise comparison between Ga2, Ga3 and Ga4 from Sokcho and the other hap-

Fig. 2. PCR product of mtDNA COI gene in examined species of the Pacific cod. M, size marker (100 bp); 1. Geomundo.

Fig. 3. Sequence alignment of 8 haplotypes obtained from 495 bp of mtDNA COI gene sequences. An asterisk represents an identical sequence on vertical lines. Only positions that differ from haplotype Ga1 are indicated.

lotypes Ga1, Ga5 and Ga8 from Wolsung, Geojeodo, Yeosu, Geomundo and Westsouth showed a somewhat higher sequence divergence. Within locality, highly sequence divergence was found in Sokcho, where the maximum sequence divergence among 4 haplotypes was 2.0% (9 bp).

Relative frequency of haplotypes

Geographic distribution and relative frequency of haplotypes are shown in Table 1 and Table 3, respectively. Among 8 haplotypes, four haplotypes (Ga2, Ga3, Ga6 and

Ga7) were found only in Sokcho, haplotype Ga4 was in Wolsung, Yeosu, Geomundo and Westsouth (St. 6, 7), haplotype Ga5 was observed in Geojeodo, Yeosu and Westsouth (St. 6), and haplotype Ga8 was found in Geojeodo, Geomundo and Westsouth (St. 7). Interestingly, haplotype Ga1 was common in all of the sampling sites except for Sokcho. Wolsung showed the highest relative frequency of the haplotype Ga1 than any other regions. Sokcho obtained 4 different haplotypes among 4 individuals, indicating local restriction in most haplotypes from Sokcho. Local populations in Wolsung, Geojeodo, Yeosu, Geomundo and Westsouth show no regional limitations in most haplotypes and far-reaching co-existence with each other.

PHYLP analysis

Phylogenetic analysis was performed to infer the genetic relationships among haplotypes using PHYLP. Because analyses run through several transitions: transversion weightings of 1:0, 1:1, 1:10 and 1:20 did not affect the topology of the genetic tree, only the results obtained by unordered analysis are shown (Fig. 4). 8 haplotypes were subdivided into two independent groups (termed clade A and clade B). One group (clade A) consisting of haplotypes Ga2, Ga3, Ga6 and Ga7 formed a monophyletic group, which was weakly supported by bootstrap analysis (>55% of frequency). The other group (clade B) consisted of haplotypes Ga1, Ga4, Ga5 and Ga8, of which the overall sequence divergence was moderate (see Table 2, 1-2 nucleotides difference, 0.2-0.4%) and very strongly supported by bootstrap analysis (100%). These four haplotypes (Ga2, Ga3, Ga6 and Ga7) and clade B were somewhat weakly supported by bootstrap analysis (<50%) which the bootstrap values at the nodes supporting each clade were 53%, 61% in the method of parsimony and maximum likelihood incorporated in PHYLP, respectively. The haplotypes Ga2, Ga3, Ga6 and Ga7 found in Sokcho formed a relatively weak monophyletic group, separated from clade B in PHYLP analysis.

Nucleotide diversity

Within-locality genetic diversity genetic diversity is estimated at the level of maximum sequence divergence (Table 4). Sokcho showed the lowest estimates of maximum sequence divergence of 0.2% and nucleotide diversity of 0.00589 compared with other localities. Maximum sequence divergence and nucleotide diversity, ranging from 1.2-1.6 and 0.01109-0.01245, respectively, were extremely low in

Table 1. Sampling regions, animal numbers and mitochondrial COI gene haplotypes

Collection locality (no. of individuals)	Collection date	Animal number	COI haplotype
1. Sokcho, Kangwon Province (4)	2008. 11. 14	CO101	Ga2
		CO102	Ga3
		CO103	Ga6
		CO104	Ga7
2. Wolsung, Kyungpook Province (4)	2008. 11.21	CO105	Ga1
		CO106	Ga4
		CO107	Ga1
		CO108	Ga1
3. Geojedo, Kyungnam Province (4)	2008. 12. 18	CO109	Ga8
		CO110	Ga1
		CO111	Ga5
		CO112	Ga1
4. Yeosu, Chunnam Province (4)	2008. 12. 22	CO113	Ga4
		CO114	Ga5
		CO115	Ga1
		CO116	Ga1
5. Geomundo, Chunnam Province (4)	2008. 10. 3	CO117	Ga1
		CO118	Ga8
		CO119	Ga1
		CO120	Ga4
6. Westsouth (4)	2008. 10. 14	CO121	Ga4
		CO122	Ga5
		CO123	Ga5
		CO124	Ga1
7. Westsouth (4)	2009. 1. 14	CO125	Ga8
		CO126	Ga1
		CO127	Ga4
		CO128	Ga1

Table 2. Pairwise comparisons among 8 haplotypes obtained from the partial sequences of mitochondrial COI gene

	Ga1	Ga2	Ga3	Ga4	Ga5	Ga6	Ga7	Ga8
Ga1	—	0	0	0	0	0.010	0.020	0
Ga2	4	—	0.014	0	0.010	0	0	0
Ga3	3	7	—	0	0	0	0	0.010
Ga4	1	6	8	—	0	0	0	0
Ga5	1	5	9	1	—	0	0	0
Ga6	5	8	8	6	7	—	0	0
Ga7	10	9	7	9	8	8	—	0
Ga8	2	6	5	1	2	6	11	—

Table 3. Relative frequencies of mitochondrial COI gene haplotypes through the populations

Haplotype	Sokcho (4)	Wolsung (4)	Geojedo (4)	Yeosu (4)	Geomundo (4)	Westsouth St. 6(4)	Westsouth St. 7 (4)
Ga1	0	0.75	0.50	0.50	0.50	0.25	0.50
Ga2	0.25	0	0	0	0	0	0
Ga3	0.25	0	0	0	0	0	0
Ga4	0	0.25	0	0.25	0.25	0.25	0.25
Ga5	0	0	0.25	0.25	0	0.50	0
Ga6	0.25	0	0	0	0	0	0
Ga7	0.25	0	0	0	0	0	0
Ga8	0	0	0.25	0	0.25	0	0.25

Numbers in parentheses indicate sample size of each population.

Fig. 4. PHYLIP analysis inferred from nucleotide sequences of the Pacific cod mtDNA mtDNA COI gene. The phylogenetic tree was obtained using subprogram NEIGHBOR incorporated in PHYLIP with the option of Kimura's 2-parameter method (1980). The tree was rooted using *Trisopterus luscus* (GenBank No. EF609486). The numbers shown on branches, which represent bootstrap values for 1,000 replications, were obtained by using the subprogram CONSENSE.

Wolsung, Geojeodo, Yeosu, Geomundo and Westsouth (St. 6, 7).

Geographic distance

The genetic distance (F_{ST}), coancestry (D) and per-generation migration rates (N_m) are shown in Table 5. The greatest genetic distance ($F_{ST}=0.5127$) was found in a comparison between Sokcho and Yeosu. In particular, the greatest distance ($F_{ST}=0.4329$) was found in a comparison between the geographically closest localities, Sokcho and Wolsung. Pairwise comparisons of populations in Sokcho and the other localities were also similar to genetic distance in Sokcho and Yeosu, ranging from 0.3295 to 0.4458. A test of the statistical significance of pairwise F_{ST} estimates determined that the Sokcho population is significantly differentiated from other populations. The increase in genetic isolation was not observed in proportion to the increase in geographical

Table 4. Within-locality diversity estimates

Locality	No.	Number of haplotypes	Maximum sequence divergence (%)	Nucleotide diversity
Sokcho	4	4	0.2	0.00589
Wolsung	4	2	1.6	0.01245
Geojeodo	4	3	1.5	0.01197
Yeosu	5	3	1.4	0.01205
Geomundo	4	3	1.3	0.01189
Westsouth (St. 6)	4	3	1.5	0.01224
Westsouth (St. 7)	4	3	1.2	0.01109

Table 5. Mitochondrial COI gene sequence data of genetic distance (F_{ST}), coancestry coefficients (D) and per generation female migration rate (N_m) of each locality

Locality	Sokcho	Wolsung	Geojeodo	Yeosu	Geomundo	Westsouth (St. 6)	Westsouth (St. 7)
Sokcho	—						
Wolsung	$F_{ST} = 0.4329^*$ $D = 0.3923$ $N_m = 9.83$	—					
Geojeodo	$F_{ST} = 0.4458^{**}$ $D = 0.2567$ $N_m = 2.34$	$F_{ST} = -0.0157$ $D = 0.0000$ $N_m = \text{infinite}$	—				
Yeosu	$F_{ST} = 0.5127^{**}$ $D = 0.4253$ $N_m = 5.34$	$F_{ST} = -0.0432$ $D = 0.0000$ $N_m = \text{infinite}$	$F_{ST} = -0.0357$ $D = 0.0000$ $N_m = \text{infinite}$	—			
Geomundo	$F_{ST} = 0.3599^*$ $D = 0.3957$ $N_m = 9.66$	$F_{ST} = -0.0256$ $D = 0.0000$ $N_m = \text{infinite}$	$F_{ST} = -0.0264$ $D = 0.0000$ $N_m = \text{infinite}$	$F_{ST} = -0.0221$ $D = 0.0000$ $N_m = \text{infinite}$	—		
Westsouth (St. 6)	$F_{ST} = 0.3295^{**}$ $D = 0.3863$ $N_m = 13.52$	$F_{ST} = -0.0137$ $D = 0.0000$ $N_m = \text{infinite}$	$F_{ST} = -0.0367$ $D = 0.0000$ $N_m = \text{infinite}$	$F_{ST} = -0.0309$ $D = 0.0000$ $N_m = \text{infinite}$	$F_{ST} = -0.0123$ $D = 0.0000$ $N_m = \text{infinite}$	—	
Westsouth (St. 7)	$F_{ST} = 0.4562^*$ $D = 0.4156$ $N_m = 8.93$	$F_{ST} = -0.0197$ $D = 0.0000$ $N_m = \text{infinite}$	$F_{ST} = -0.0225$ $D = 0.0000$ $N_m = \text{infinite}$	$F_{ST} = -0.0321$ $D = 0.0000$ $N_m = \text{infinite}$	$F_{ST} = -0.0203$ $D = 0.0000$ $N_m = \text{infinite}$	$F_{ST} = -0.0275$ $D = 0.0000$ $N_m = \text{infinite}$	—

* $p < 0.05$, ** $p < 0.01$.

distance. Pairwise comparisons of coefficients of coancestry (0-1, where $D=0$ is identical, shared ancestry) ranging from 0.2567 to 0.4253, were also consistent with the F_{ST} estimates. In the analysis of per generation migration rate (N_m), overall lower estimates of N_m (2.34-13.52) were obtained from between Sokcho and the other six regions. Except for Sokcho, pairwise comparisons of each population had an infinite estimate of N_m . Thus, Wolsung, Geojeodo, Yeosu and Westsouth (St. 6, 7) populations have a fairly high estimate of N_m and still suggest high gene flow among populations of the Pacific cod over geographical barriers.

Hierarchical population genetic structure

In the Holsinger and Mason-Gamer analysis, the resulting dendrogram grouped Sokcho and the other six localities (significant genetic distance between them) and set Sokcho population apart ($p=0.0000$) from the other six localities (Fig. 5). The six localities were grouped together with a neighboring one and their genetic distance was negative. It is understood that the Pacific cod occurred in those waters appears to form a large and close genetic group covering a wide geographic area. The hierarchical partition of genetic variance and fixation index (Φ) of each hierarchical level is shown in Table 6. This analysis was performed based on the HM-G result, so the localities were grouped into two primary geographic regions (Sokcho as a single region and Wolsung/Geojeodo/Yeosu/Geomundo/Westsouth as another region). In the analysis, variance component of between regions was 52.32% and the estimate was statistically significant ($p<0.001$) and fixation index ($\Phi=0.521$; $p<0.001$). This result suggests that there is maximized heterogeneity in between regions, and the result is consistent with that obtained

Fig. 5. Hierarchical genetic relationship among localities analyzed using the Holsinger and Mason-Gamer Method (1996). The value at each node is the genetic distance (d) between two daughter nodes and the p value is the significance of differentiation based on 10,000 random re-sampling.

Table 6. Hierarchical analysis of variance

Source of variation	(W+G+Y+Ge+W1+W2) + S			
	d.f.	%	Φ	p
Between regions	3	52.32	0.521	***
Among localities within regions	9	7.05	0.059	*
Within localities	42	49.56	0.537	**

W, Wolsung; G, Geojeodo; Y, Yeosu; Ge, Geomundo; W1, Westsouth (St. 6); W2, Westsouth (St. 7); S, Sokcho; d.f., degree of freedom; %, percentage of variation; Φ , fixation index; p , significant of percentage variation and fixation indices estimated from permutation tests (1,000 permutations); * $p<0.05$; ** $p<0.01$; *** $p<0.001$.

from F_{ST} analysis (Table 5).

Discussion

Our two general goals were to make an initial assessment of the genetic structure and levels of gene flows in the Pacific cod populations and to characterize the genetic diversity of population. Using DNA sequencing in mitochondrial COI gene, we found evidence of genetic differences between geographically separated populations of the Pacific cod. The Sokcho population is to be strongly divergent. Gene flow is insufficient to have kept this regional group from diverging.

The genetics of marine populations, with pelagic larval development, has often been characterized by low genetic variation among populations, a pattern driven by high dispersal capabilities and large scale oceanic mixing [19]. A characteristic example can be found in the anchovy (*Engraulis japonicus*) from Korean waters [14,15,18], a species that has a fairly limited pelagic larval phase, in which similar genetic composition is found among populations. Although the genetic patterns found in the Pacific cod populations probably typify many marine species, the growing attention being paid to the conservation of marine stock has resulted in a renewed emphasis on better understanding of larval dispersal and gene flow. The current DNA sequencing evidence supporting the occurrence of the significant local retention of larvae is now being recognized as an important influencing factor in the population dynamics of this species.

Overall, the high estimate of gene flow among populations may be associated with actual long distance migrations of the Pacific cod. It is assumed that a small number of migrants may be sufficient to homogenized genetic differentiation through genetic drift. Although the number of samples available was relatively small, the distribution of

mtDNA haplotypes between the populations, in the Sokcho and the other localities, was suggestive of geographic subdivision, as reflected in the Φ_{ST} value of 52.32%. This regional differentiation was found to be statistically significant at the $p < 0.001$ level, for Φ_{ST} statistics. The observed differentiation between populations suggests a long-term exchange of only a few females per generation ($N_m < 9$) despite the absence of obvious geographic barriers. Some researchers have suggested that genetic distinct populations are attributed to geographic heterogeneity: oceanographic discontinuity [2], freshwater discharge [23] and different reproduction [9]. Limited migration events caused by geographic and physical barriers are sufficient to provide the existence of temporally or spatially isolated populations over time. The occurrence of the genetic differentiation can be explained. First, heterogeneous environments such as geographic scale and hydrographic restriction are limited to effective gene flow or dispersal between populations. Second, long-distance dispersal by adults have a local retention

For a population to maintain a high level of genetic diversity, the maintenance of a large and stable population is an essential factor [8]. A larger population will tend to have a higher probability of sustaining a higher level of genetic diversity. The Sokcho population, which was assigned the lowest genetic diversity estimate, appears to have a relatively small population size. In this role, the Sokcho population may have a restricted migration of adults that sustain a smaller population as compared with other populations that potentially interconnected to one another. Consequently, this study provides evidence that the Sokcho stock should be considered as an independent management unit.

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초록 : 미토콘드리아 유전자 염기서열 분석에 의한 대구 계군 분석

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본 연구는 2008년에서 2009년 동안 속초, 월성, 거제도, 여수, 거문도, 서남해역에서 채집된 대구어미를 대상으로 유전적 집단구조를 조사했다. 시험에 사용된 28 마리 중에서 8 종류의 haplotype이 발견되었다. 상호 유전자 비교시 0.2-2.2% 범위에서 유전자 변이율을 볼 수 있었다. Ga1 haplotype은 월성, 거제도, 여수, 거문도, 서남해역에서 모두 발견된 haplotype으로 우리나라 대구의 가장 대표적인 haplotype인 것으로 추측된다. 그러나 Ga2, Ga3, Ga6, Ga7 haplotype은 속초에서만 나타났다. 또한 유전자 상호관계 분석에서도 속초에서 나타난 haplotype은 독립적인 개체군을 형성하고 있으면 다른 haplotype과의 유연 성립율은 50% 이하로 나타났다. 속초를 제외한 나머지 지역의 지역적 유전거리는 -0.0123에서 -0.0423이면 유전적 이동률은 거의 무한대로 보여 동일한 집단을 형성하고 있는 것으로 보였다. 그러나 속초와는 현저한 유전적 거리를 나타내고 있고, 속초의 유전적 다양성이 가장 낮게 나타나서 속초의 대구 개체군은 소형임과 아울러 다른 지역군의 유전적 이동이 거의 차단된 것으로 보인다. 따라서 우리나라에서 어획되는 대구 계군은 속초를 제외하고 활발한 유전적 이동으로 동일한 유전적 집단을 형성하고 있는 것으로 보인다.