

Genetic variation in two starfish, *Acanthaster planci* and *Echinaster luzonicus*, from Okinawa

Norimasa MATSUOKA

*Division of Molecular Evolution, Faculty of Agriculture & Life Science,
Hirosaki University, Hirosaki 036-8561, Japan*

(Received for publication September 7, 2005)

Introduction

Since the technique of enzyme electrophoresis was introduced into population genetic studies, many workers have reported the levels of genetic variation observed in various groups of organisms. However, biochemical surveys of genetic variation in marine invertebrates have been limited when compared with those in other animals such as insects or mammals.

The present author has been studying the molecular phylogeny of echinoids and asteroids of echinoderms (*eg.* Matsuoka, 1987; Matsuoka and Hatanaka, 1991; Matsuoka and Suzuki, 1989; Matsuoka *et al.*, 1994). In addition to the serial biochemical systematics of echinoderms, I reported on the population genetic studies of echinoderms which survey the genetic variation within populations by using allozyme analysis. Such studies would provide basic information to clarify the maintenance mechanism of genetic variation within populations of echinoderms. Echinoderms are in some respects well suited for population genetic studies. Many species are abundant and form large dense populations which can be sampled extensively without disturbing their natural population densities. Furthermore, as many species have broad geographical distribution, we can study the difference in the extent of genetic variation among local populations of one species and the population genetic factors that produce the differences. Fortunately, the seas around Japan are diversified in biogeochemical conditions and the marine fauna, and have been well known to be a rich yield for marine invertebrates. In particular, the echinoderm fauna is very abundant and in echinoids the number of endemic species and genera from the Japanese waters are greatest in the world (Shigei, 1974). Therefore, we have good conditions for undertaking the studies to clarify the genetic structure of natural populations of echinoderms.

Though the asteroids and echinoids have been used extensively as experimental animals in the fields of developmental biology and biochemistry, the population genetic study is much backward when compared with other experimental animals such as insects (*Drosophila*) and mammals. Recently, the molecular phylogenetic study indicated that the echinoderms are closely related to vertebrates (Miyata, 1994). Namely, the echinoderms are on the key position in the animal evolution. As the population genetic study is closely related to the evolution, it would provide valuable information for elucidation of evolution to examine how much genetic variation has accumulated within echinoderm populations by using allozyme analysis. In the present population genetic studies, the author chose the two starfish species, *Acanthaster planci* of the family Acanthasteridae and *Echinaster luzonicus* of the family Echinasteridae as target species. These two starfish are found in shallow water of subtropical seas of Ryukyu Islands (Okinawa) in Japan. It is famous

that *A. planci* is the poisonous starfish and destroys the coral reef by eating the polyps of corals. On the other hand, *E. luzonicus* shows extensive intraspecific variation in body color.

In this paper, I report on the results of allozyme study designed to estimate the degree of genetic variation and genetic differentiation in the two starfish, *Acanthaster planci* and *Echinaster luzonicus* from Ryukyu Islands (Okinawa) in southern Japan, and compare the data with those of other echinoderms reported previously. Further, I would like to discuss about the maintenance mechanism of protein polymorphism in echinoderms.

Materials and Methods

The two starfish species, *Acanthaster planci* and *Echinoaster luzonicus* were collected from the coasts of Seragaki in Onnamura of Okinawa Pref. by scuba diving and snorkeling. Immediately after collection, the pyloric caeca were cut off from living specimens and frozen in dry ice. They were then transported to my laboratory of Hirosaki University, where they were stored at -40 until being analysed. The number of individuals used in allozyme analysis was three for *A. planci* and 12 for *E. luzonicus*. As *A. planci* is poisonous and dangerous starfish, it was much difficult to collect by scuba diving and snorkeling, and thus the number of specimens was small. Allozyme analysis was performed on 7.5 % polyacrylamide gel by the method described in Matsuoka and Hatanaka (1991). About 0.2g pyloric caeca was individually homogenized with 3 vols. of 20mM phosphate buffer containing 0.1M KCl and 1mM EDTA (pH 7.0) by using Potter-Elvehjem type homogenizer in an ice water bath. The tissue extract was centrifuged at 10,000 rpm at 5 min and the clear supernatant was used for enzyme electrophoresis. Electrode buffer was Glycine-tris buffer, pH 8.3. After electrophoresis, the following 11 different enzymes was analyzed: malate dehydrogenase (MDH), nothing dehydrogenase (NDH), xanthine dehydrogenase (XDH), glucose-6-phosphate isomerase (GPI), hexokinase (HK), superoxide dismutase (SOD), aspartate aminotransferase (AAT), alkaline phosphatase (ALK), peroxidase (PO), esterase (EST) and leucine amino peptidase (LAP). Allozyme analysis was conducted as described in Matsuoka and Hatanaka (1991).

Results and Discussion

Thirty five genetic loci were detected from the allozyme variation observed in 11 enzymes. Of 35 loci scored, the following nine loci were polymorphic (*Mdh-2*, *Hk*, *Po-3*, *Po-4*, *Est-1*, *Est-3*, *Est-6*, *Lap-1* and *Lap-6*). From the allele frequencies data in 35 genetic loci, the author calculated the extent of genetic variation within populations of the two starfish. The results are summarized in Table 1. As shown in this table, the number of alleles per locus (*A*) was 1.13 and 1.26, the proportion of polymorphic loci (*P*) 12.5 % and

Table 1. Genetic variation and genetic differentiation in two starfish species, *Acanthaster planci* and *Echinaster luzonicus* from Ryukyu Islands

Parameter	<i>Ap</i>	<i>El</i>
No. of enzymes analysed	11	11
No. of genetic loci scored	35	35
No. of alleles per locus (<i>A</i>)	1.13	1.26
Proportion of polymorphic loci (<i>P</i> %))	12.5	22.9
Expected average heterozygosity (<i>H</i> %))	6.1	9.3
Genetic identity (<i>I</i>)	0.417	
Genetic distance (<i>D</i>)	0.875	

Ap : *A. planci*, *El* : *E. luzonicus*

Table 2. Genetic variation in various starfish populations

Species	Average heterozygosity(H)	Source
(1) Shallow water echinoderms		
Class Asteroidea		
<i>Asterina pectinifera</i>	2.9	a
<i>Asterina batheri</i>	8.7	a
<i>Asterina coronata japonica</i>	3.3	a
<i>Asterina pseudoexigua pacifica</i>	3.8	a
<i>Asterina minor</i>	0	a
<i>Asterias forbesi</i>	4.1	b
<i>Asterias vulgaris</i>	2.3	b
<i>Asterias amurensis</i>	7.6	c
<i>Coscinasterias acutispina</i>	8.5	c
<i>Aphelasterias japonica</i>	6.4	c
<i>Plazaster borealis</i>	5.9	c
* <i>Acanthaster planci</i>	6.1	present study
* <i>Echinaster luzonicus</i>	9.3	present study
(2) Deep-sea echinoderms		
Class Asteroidea		
<i>Distolasterias nippon</i>	16.7	d
<i>Myxoderma sacculatum ectenes</i>	14.4	e
<i>Pteraster jordanii</i>	10.1	e
<i>Diplopteraster multiples</i>	10.8	e
<i>Nearchaster aciculosus</i>	19.5	e
Class Ophiuroidea		
<i>Ophiomusium lymani</i>	17.0	f
Class Echinoidea		
<i>Prionocidaris baculosa</i>	14.0	g
<i>Asthenosoma ijimai</i>	22.4	h
<i>Asthenosoma ijimai R.</i>	27.7	h

a=Matsuoka (1981) , b=Schopf and Murphy (1973) , c=Matsuoka *et al.* (1994) ,
d=Matsuoka *et al.* (1993) , e=Ayala *et al.* (1975) , f=Ayala and Valentine (1974) ,
g=Matsuoka and Inamor (1999) , h=Matsuoka *et al.* (2004)

22.9 % , and the expected average heterozygosity per locus (H) 6.1 % and 9.3 % for *A. planci* and *E. luzonicus*, respectively.

In parallel with the molecular phylogenetic studies of echinoderms, I have reported on the extent of genetic variation within populations of various echinoderm species. It is valuable to compare the extent of genetic variation in two starfish species studied here with those observed in other echinoderm populations. Table 2 summarizes the values of the average heterozygosity per locus (H) in various echinoderms reported previously and those of the two starfish, *A. planci* and *E. luzonicus* in this study. The echinoderm species shown in this table are divided into two large groups: one is those living in shallow water and the other those in deep-sea water. Table 2 indicates that the asteroids from shallow water have the lower genetic variability than the echinoderms from deep-sea. The average heterozygosity per locus ($H=6.1$ %, 9.3 %) in the two starfish examined in this study were comparable to H values of other echinoderm species living in shallow water as well as the two asteroids, but considerably lower than those of echinoderms from deep-sea. In addition to asteroids, we reported the genetic variation within various echinoids from Japanese waters (Matsuoka, 1987; Matsuoka and Suzuki, 1989; Matsuoka, 1989). According to it, all of 13 species belonging to four different families of the order Echinoida and four species of the order Diadematoida from shallow water showed the low genetic variability. For example, *Toxopneustes pileolus* of the family Toxopneustidae was $H=0.9$ %, *Strongylocentrotus nudus* of the Strongylocentrotidae $H=2.6$ %, *Echinometra mathaei* of the Echinometridae $H=1.5$ %, and *Diadema setosum* of the Diadematidae $H=3.5$ %. Similar results have also been observed in some marine invertebrates other than echinoderms (Valentine and Ayala, 1978).

To explain the difference of genetic variation in marine invertebrate populations from different

environments, several predictions were proposed until now. Ayala and Valentine (1974) suggested that marine invertebrates from trophically stable environment such as deep-sea water generally show higher genetic variation than those from trophically unstable environment such as shallow water in temperate latitudes. Namely, populations in trophically unstable environment would be selected, and the population size becomes smaller and the founder effect begins to act for the population. The founder effect decreases the extent of genetic variability in population. Their prediction is based on the natural selection theory, but it can also be explained by the neutral theory. Kimura (1983) stated in his neutral theory that most mutations at molecular level are selectively neutral and most of the remainings mildly deleterious. Therefore, the latter mildly deleterious genes would be selected in unstable environment such as shallow water in temperate latitudes. On the other hand, in more stable environment such as deep-sea water, some of such mildly deleterious genes can function and may be maintained in populations. As a result, the extent of genetic variation in marine invertebrates from unstable environment such as shallow water would become lower than that from stable environment such as deep-sea water. The prediction of Ayala and Valentine (1974) seems not to be contradictory to the neutral theory of Kimura (1983).

From the extensive allozyme studies in various organisms, several workers noted that small populations have lower heterozygosity than large populations. For example, Selander *et al.* (1971) reported that the Santa Rosa Island (off the Gulf Coast of the Florida panhandle) population of *Peromyscus polionotus* of which the population size is known to be of the order of 12,000, showed much lower heterozygosity ($H=1.8\%$) than the Florida population ($H=8.6\%$). The cave populations (200-500 individuals) of the characid fish *Astyanax mexicanus* in Mexico also showed a very low heterozygosity when compared with the nearby surface population (Awise and Selander, 1972). One of the most extreme examples of low heterozygosity is that of the cheetah, the fastest running land animal of the carinivores. The population size of the species has been estimated to be from 1,500 to 25,000. O'Brien *et al.* (1985) examined 52 electrophoretic loci for 55 individuals, and they discovered that the cheetah has no genetic variability. It is interesting to see that this highly evolved animal species has little genetic variability. Nei (1983) and Nei and Graur (1984) examined the relationship between average heterozygosity and population size for 77 different species. As a result, they found a positive correlation between heterozygosity and population size. Putting these data together, I would like to propose that the difference in the extent of genetic variation between invertebrates from shallow water and those from deep-sea is closely related to their population size. Namely, it would be well expected that the population size of invertebrates from deep-sea is much larger than that from shallow water, and thus marine invertebrates of the large population size from deep-sea can maintain higher genetic variability than those of the small population size from shallow water.

As evident from Table 2, several workers reported until now that deep-sea echinoderms have higher genetic variation than shallow water species: The starfish, *Distolasterias nipon* from deep-sea of Mutsu Bay in Aomori Pref. of northern Japan showed considerably high genetic variation ($H=17\%$) (Matsuoka *et al.*, 1993). Additionally, the primitive echinoid, *Prionocidaris baculosa*, of the order Cidaroida from deep-sea had high genetic variation ($H=14.0\%$) (Matsuoka and Inamori, 1999). Ayala *et al.* (1975) reported that all of four starfish species from deep-sea water showed high genetic variation ($H=10-20\%$). Further, Ayala and Valentine (1974) found that the ophiuroid, *Ophiomusium lymani* from deep-sea also showed the high genetic variation ($H=17\%$). More recently, we reported the allozyme study demonstrating that the echinothurioid, *Asthenosoma iijimai*, from Japanese waters consists of two distinct species: one is *A. iijimai* from Sagami Bay in Honsyu and the other *A. iijimai* R. from Rykyu Islands (Okinawa) (Matsuoka *et al.*, 2004). The two echinothurioids, *A. iijimai* and *A. iijimai* R. are deep-sea species and both of them showed the high genetic variation (Table 2).

With respect to the difference of genetic variation in echinoderms from shallow water and deep-sea,

Table 3. Genetic identities(*I*)and genetic distances(*D*)between different genera of asteroids

Pairs	<i>I</i>	<i>D</i>
<i>A. amurensis</i> vs <i>Ap. japonica</i>	0.475	0.744
<i>A. amurensis</i> vs <i>C. acutispina</i>	0.434	0.835
<i>A. amurensis</i> vs <i>D. nipon</i>	0.484	0.726
<i>A. amurensis</i> vs <i>P. borealis</i>	0.598	0.514
<i>Ap. japonica</i> vs <i>C. acutispina</i>	0.433	0.837
<i>Ap. japonica</i> vs <i>D. nipon</i>	0.506	0.681
<i>Ap. japonica</i> vs <i>P. borealis</i>	0.397	0.924
<i>C. acutispina</i> vs <i>D. nipon</i>	0.401	0.914
<i>C. acutispina</i> vs <i>P. borealis</i>	0.370	0.994
<i>D. nipon</i> vs <i>P. borealis</i>	0.360	1.022
* <i>A. planci</i> vs <i>E. luzonicus</i>	0.417	0.875

The data except *A. planci* and *E. luzonicus* were quoted from Matsuoka *et al.*(1994). The genus names are that *A*: *Asterias*, *Ap*: *Aphelasterias*, *C*: *Coscinasterias*, *D*: *Distolasterias* and *P*: *Plazaster*.

Kimura (personal communication) who proposed the neutral theory (Kimura, 1983) suggested that the echinoderm species from deep-sea would have larger population size than those from shallow water, and thus the larger population size make it possible to hold the higher genetic variation within populations. In order to confirm the difference of genetic variation between shallow water and deep-sea echinoderms, further extensive population genetic studies in various marine invertebrates from different environments would be required.

Gojobori (1982) examined the relationship between the enzyme groups and heterozygosity by using data on 20 different enzymes from 14 *Drosophioa* species, 14 *Anolis* species and 31 other species. As a result, he found that enzymes with various functional constraints tend to have low heterozygosity. The present study showed that esterase (EST) or peroxidase (PO) of non-specific enzymes are more variable than dehydrogenases of higher substrate-specificity. These findings support the neutral theory of Kimura: the more strictly functional constraints would decrease the neutral regions of the molecules and the probability of amino acid replacement being selective neutral becomes smaller for enzymes with strictly functional constraints.

To estimate the degree of genetic differentiation between the two starfish species studied here, I calculated the genetic identity (*I*) and genetic distance (*D*) from allele frequencies data by the method of Nei (1972). As a result, the genetic identity was $I=0.417$ and the genetic distance was $D=0.875$. Previously, we reported the phylogenetic relationships among five asteroid species of the family Asteriidae by allozyme analysis(Matsuoka *et al.*, 1994). Table 3 summarizes the *I* and *D* values obtained between the five asteroids and the present data. As evident from this table, the *I* and *D* values between *A. planci* and *E. luzonicus* were comparable to those obtained between asteroids of different genera. As described in Matsuoka and Sugiyama (2005), Thorpe (1982) examined the relationship between the taxonomic rank and genetic identity in various organisms and prepared the figure showing the positive correlation between them. According to the figure, the range of genetic identity(*I*) in each taxonomic rank is as follows: conspecific local populations are $I=0.9-1.0$, closely related species of the same genus $I=0.7-0.89$, distinct species of the same genus $I=0.5-0.7$, and different genera of the same family $I=0.2-0.49$. When compared the present data with his figure, the *I* value ($I=0.417$) between *A. planci* and *E. luzonicus* was comparable to those observed between different genera in many other animals. The traditional taxonomic system that the

present two asteroids should be classified into two different genera is consistent with the present allozyme study.

In comparison between allozyme analysis and mtDNA analysis, Nei (1987) suggested that the resolving power of mtDNA is not necessarily higher than that of allozymes. This is particular so when the restriction enzyme technique is used. According to the estimation of Nei (1987), electrophoresis is expected to survey about 100 nucleotides per locus. If we examined 30 loci by electrophoresis, it is equivalent to studying 3,000 base pairs at mtDNA level. Therefore, the resolving power of allozyme analysis is not lower than mtDNA analysis which has been using extensively until now. Murphy *et al.* (1996) claimed that in phylogenetic and population genetic studies many molecular characters should be used and that the enzyme loci at allozyme analysis are the important molecular characters. The number of molecular characters adopted in protein electrophoresis is more enough than that of mtDNA study. Although protein electrophoresis is one of the traditional methods, it is one of powerful techniques for estimating genetic variation within population and genetic differentiation between related taxa.

In conclusion, I would like to propose that the shallow water echinoderms tend to show lower genetic variability than those from deep-sea and that the degree of genetic variability within populations is closely related to the population size.

Abstract

Enzyme polymorphism was studied in the populations of two tropical starfish species, *Acanthaster planci* of the family Acanthasteridae and *Echinaster luzonicus* of the Echinasteridae from Ryukyu Islands (Okinawa) in Japan by allozyme analysis of 11 different enzymes. In 35 genetic loci scored, the proportion of polymorphic loci (P) was 12.5 % and 22.9 %, the average heterozygosity per locus (H) was 6.1 % and 9.3 %, for *A. planci* and *E. luzonicus*, respectively. These values were comparable to those observed in many other asteroids and echinoids living in shallow water as well as the two starfish studied here, and lower than those of echinoderms from deep-sea. The author suggested that the extent of genetic variation is closely related to the population size: Echinoderms from deep-sea have large population size, and thus they can maintain high genetic variability within population. Furthermore, the substrate specific enzymes (dehydrogenases) of strict functional constraints showed the lower genetic variability than the non-specific enzymes such as esterase (EST) or peroxidase (PO) of weak functional constraints. The result is consistent with the neutral theory of Kimura. The genetic identity (I) and genetic distance (D) between the two starfish species were $I=0.417$ and $D=0.875$. These values were comparable to those obtained between different genera in other asteroids and many animal groups. The maintenance mechanism of genetic variation in echinoderm populations was discussed in some detail from the viewpoints of population genetics and the neutral theory with putting the allozyme data of echinoderms obtained until now together.

References

- AVISE, J.C. and SELENDER R.K. (1972) Evolutionary genetics of cave-dwelling fishes of the genus *Astyanax*. *Evolution*, 26: 1-19.
- AYALA, F.J. and VALENTINE, J.W. (1974) Genetic variability in the cosmopolitan deep-water ophiuran *Ophiomusium lymani*. *Mar. Biol.*, 27: 51-57.
- AYALA, F.J., VALENTINE, J.W., HEDGECOCK, D. and BARR, L.G. (1975) Deep-sea asteroid: High genetic variability in a stable environment. *Evolution*, 29: 203-212.
- GOJOBORI, T. (1982) Means and variances of heterozygosity and protein function. In *Molecular Evolution, Protein Polymorphism and the Neutral Theory* (Edited by Kimura, M.), pp. 137-148. Japan Scientific Societies Press, Berlin, Springer-Verlag.
- KIMURA, M. (1983) *The Neutral Theory of Molecular Evolution*. Cambridge University Press, Cambridge.
- MATSUOKA, N. (1981) Phylogenetic relationships among five species of starfish of the genus, *Asterina*: An electrophoretic

- study. *Comp. Biochem. Physiol.*, 70 B(4) 739-743.
- MATSUOKA, N. (1987) Biochemical study on the taxonomic situation of the sea-urchin, *Pseudocentrotus depressus*. *Zool. Sci.*, 4: 339-347.
- MATSUOKA, N. (1989) Biochemical systematics of four sea-urchin species of the family Diademidae from Japanese waters. *Biochem. Syst. Ecol.*, 17: 423-429.
- MATSUOKA, N., FUKUDA, K., YOSHIDA, K., SUGAWARA, M. and INAMORI, M. (1994) Biochemical systematics of five asteroids of the family Asteroiidae based on allozyme variation. *Zool. Sci.*, 11: 343-349.
- MATSUOKA, N. and HATANAKA, T. (1991) Molecular evidence for the existence of four sibling species within the sea-urchin, *Echinometra mathaei*, from Japanese waters. *Zool. Sci.*, 8: 121-133.
- MATSUOKA, N. and INAMORI, M. (1999) Phylogenetic relationships among four echinoids of the family Cidaridae (Cidaroida) based on allozymes. *Zool. Sci.*, 16: 529-534.
- MATSUOKA, N., INAMORI, M. and SUGAWARA, M. (1993) High genetic variability in the starfish, *Distolasterias nippon*. *Comp. Biochem. Physiol.*, 104B(1) 75-79.
- MATSUOKA, N., KOHYAMA, K., ARAKAWA, E. and AMEMIYA, S. (2004) Molecular evidence for the existence of two sibling species within the echinothurioid echinoid *Asthenosoma iijimai* from Japanese waters. *Zool. Sci.*, 21:1057-1061.
- MATSUOKA, N. and SUGIYAMA, T. (2005) Molecular taxonomy of two different types of body color in the fish *Sebastes inermis* from Japanese waters. *Bull. Fac. Agric. & Life Sci, Hiroshima Univ.*, No.7: 1-8 (in Japanese)
- MATSUOKA, N. and SUZUKI, H. (1989) Electrophoretic study on the phylogenetic relationships among six species of the sea urchins of the family Echinometridae found in Japanese waters. *Zool. Sci.*, 6: 589-598.
- MIYATA, T. (1994) *Invitation to Molecular Evolution*. Blue Backs, Kodansha, Tokyo (in Japanese)
- MURPHY, R.W., SITES, J.W., BUTH, P.G. and HAUFLER, C.H. (1996) Protein: Isozyme Electrophoresis. In *Molecular Systematics* (Edited by Hills, D.M., Moritz, C. and Mable, D.K.) pp.51-120, Sinauer Associates, MA, USA.
- NEI, M. (1972) Genetic distance between populations. *Am. Nat.*, 106: 283-292.
- NEI, M. (1983) Genetic polymorphism and the role of mutation in evolution, In *Evolution of Genes and Protein* (Edited by Nei, M. and Koehn, R.) pp.165-190. Sinauer Associates, Sunderland, Mass.
- NEI, M. (1987) *Molecular Evolutionary Genetics*. Columbia Univ Press, New York.
- NEI, M. and GRAUR, D. (1984) Extent of protein polymorphism and the neutral mutation theory. *Evol. Biol.*, 17: 73-118.
- O'BRIEN, S.J. and 9 other authors (1985) Genetic basis for species vulnerability in the cheetah. *Science*, 227: 1428-1434.
- SCHOPF, T.J.M. and MURPHY, S. (1973) Protein polymorphism of the hybridizing sea-star *Asterias forbesi* and *Asterias vulgaris* and implications for their evolution. *Biol. Bull.*, 145: 589-597.
- SELENDER, R.K., SMITH, M.H., YANG, S.Y., JOHNSON, W.E. and GENTRY, J.B. (1971) Biochemical polymorphism and systematics in the genus *Peromyscus*. I. Variation in the old-field mouse (*Peromyscus polionotus*) In *Studies in Genetics VI*, pp.49-90. University of Texas, University of Texas Publication 7103, Austin, Texas.
- SHIGEI, M. (1974) Echinoids. In *Systematic Zoology*, Vol.8 (Edited by Uchida, T) pp.208-332, Nakayama, Tokyo (in Japanese).
- THORPE, J.P. (1982) The molecular clock hypothesis: Biochemical evolution, genetic differentiation, and systematics. *Ann. Rev. Ecol. Syst.*, 13: 139-169.
- VALENTINE, J.W. and AYALA, F.J. (1978) Adaptive strategies in the sea. In *Marine Organisms: Genetics, Ecology, and Evolution* (Edited by Battaglia, B. and Beardmore, J.A.) pp.323-345, Plenum Press, New York.

棘皮動物ヒトデ類のオニヒトデとルソンヒトデ集団における遺伝的変異

松 岡 教 理

弘前大学農学生命科学部分子進化学研究室

海産無脊椎動物の集団内に存在する遺伝的変異の保有機構に関しては、報告例が少なく未だ不明な点が多い。著者は、インド・西太平洋の熱帯・亜熱帯海域のサンゴ礁に生息している棘皮動物ヒトデ類・オニヒトデ科のオニヒトデ (*Acanthaster planci*) と、ルソンヒトデ科のルソンヒトデ (*Echinaster luzonicus*) の沖縄集団の遺伝的変異を、アロザイム分析により調査した。その結果、11 酵素で検出された 35 酵素遺伝子座において、多型的遺伝子座の割合 (P) は、オニヒトデで 12.5 %、ルソンヒトデで 22.9 %であった。また平均ヘテロ接合体率 (H) は、オニヒトデで 6.1 %、ルソンヒトデで 9.3 %であった。これらの数値は、深海産の棘皮動物で報告されている値よりかなり低いものであり、浅海産の棘皮動物での数値と同等の値であった。これまでの一連の棘皮動物

(ウニ類・ヒトデ類) の集団遺伝学的研究から、深海産の棘皮動物は高い遺伝的変異を示すが、浅海産の棘皮動物は低い変異性を示す。これは集団サイズの大小と密接に関係していると推察された。また機能的制約の強弱と酵素多型の程度の関係調べた結果、機能的制約の強い基質特異性の高い酵素 (脱水素酵素群など) は、非特異的酵素であるエステラーゼ (EST) やパーオキシダーゼ (PO) などより遺伝的変異が低い傾向にあった。この結果は中立説と一致する。また 2 種の遺伝的分化の程度を示す遺伝的距離 (D) は $D=0.875$ であり、他の棘皮動物での数値と比較した場合、別属間で観察される値と同等な D 値であった。

弘大農生報 No. 8 : 9 - 16, 2005