

Panel Discussion: Present and Future on Molecular Biology of *Useful Seaweeds*

Panel discussion was done to epitomize the 14th Natural History Symposium, which is entitled “Present and Future on Molecular Biology of Useful Seaweeds” consisting of 8 lectures at Natural History Museum and Institute, Chiba, Japan on November 29, 2002. This panel discussion was organized by Masahiro Notoya and Masahiko Miyata.

Notoya, M. (Tokyo University of Maritime Science & Technology, Chairman)

Now we would like to open the discussions. I would like to ask the speakers to talk about their impressions about the lectures today.

Miyata, M. (Natural History Museum and Institute, Chiba)

I think that genetic analysis is recognized as an indispensable method for the study of seaweeds. Molecular informations are powerful methods on taxonomic study, when we revalue the taxon constructed based on the morphology, especially, in the case that there are few characters and there are heavy morphological variations. In the lectures, I am very interested in that the molecular informations of Gelidiales and Laminariales are very clear and available to the taxonomy as same the morphological data.

Mizukami, Y. (National Fisheries University)

I am deeply impressed by that the molecular analyses are applied and contribute to the taxonomy of seaweeds. But, I also think that everybody have carried out the molecular phylogenetic analysis based on only a few gene: ribosomal gene, *rbcL* gene, and so on. If we are going to carry out the molecular analysis based on only a few gene, our study may not progress. We should call the specialists of molecular analysis many more to like this symposium. Then we may receive valuable suggestion from them on the useful gene. If minisatellite or microsatellite DNA have already been found, I think that the sequences of the DNA may be available for the phylogenetic analysis. But, there is little information of the gene. I had the feeling that there is a limit of the molecular phylogenetic study, because the used gene for the molecular

phylogenetic analysis is limited.

Nelson, W. (National Institute for Water and Atmospheric Research, New Zealand)

I think that molecular biological tool is helping in the wide range fields, and it is shown in the results of the study in many groups which have been discussed today. I would agree with Dr. Mizukami that we need to look at more tools and large parts of genome to provide us many sources of informations in possible. In the field of systematics, I think we are looking all the time new sources of the information for our works. And, similarly, in applied phycology, we should be looking for many tools which help us make progress. So, I think now molecular biology is indispensable element of the tool kits.

Kakinuma, M. (Mie University)

Today hearing the announcement of other speakers, I study very much since I have never study the molecular phylogeny. I think that we cannot elucidate the nature of the seaweeds when there are not all the informations of environment, morphology and molecular data.

Shimada, S. (Hokkaido University)

We study the molecular systematics in order to clarify the taxonomy based on the comparison of the nucleotide sequence. But, perhaps, we will able to find the interesting phenomenon from natural organisms through the molecular studies. Then, although we do not have techniques of gene introduction, gene isolation, and so on, we can collaborate with the researches who study the field. I strongly feel that taxonomist have the encouraging collaborators.

Yotsukura, N. (Hokkaido University)

I think that it may be possible that the molecular phylogenetic analysis is carried out based on other nucleotide sequence. These molecular data may contribute to the breeding of useful seaweeds. I strongly feel that we need a place like this symposium where various specialists who treat seaweeds participate and

discuss with a wide view.

Notoya, M

I think there are some problems in the molecular phylogeny of seaweeds. One is the problem of the distinction of species. While there is case the result of phylogeny based on the molecular data consists with the morphological data, it does not consist, and it produces taxonomic complex. And, there is the problem that how should we apply the molecular information to systematics of seaweeds?

Do you have any opinions about the application of molecular data to systematics?

Yoshizaki, M. (Toho University)

I think that taxonomy based on morphology and molecular biology are the thing that differs entirely. Seaweeds have simple thalli and have much individual variations and geographical variations. So, I learned that we should study the variations of morphology based on the materials from all over Japan, if I study the taxonomy of seaweeds. First of all, we should study the variations of morphology in order to determine the species name. When the species name is not able to be determined after the study, we should use the molecular data for the first time. However, I think that the biochemistry is not all-around tool to distinguish species. I think that we should study both morphology

and ecology to distinguish species of seaweeds. I think that the more the molecular data is increased, the more difficult problems appear. So, I do not think we should apply the molecular data to difficult taxa easily.

Notoya, M.

I think so to some extent. I think that it is the general opinion to the molecular phylogeny. However, I think that if a morphological character is supported by the molecular data, the character is very clear in the classification.

I am interested in the taxonomic complex, for example, *Enteromorpha* and *Ulva*, *Bangia* and *Porphyra*, and Laminariaceae. How should we study the taxonomic complex?

Shimada, S.

I think that it is very important that the other useful gene is used for the molecular phylogenetic study in order to clear the taxonomic complex. However, there is the problem whether the classification of species based on the sequence of spacer region is correct. We should clear the morphological and ecological character to establish the taxonomy of seaweeds. For example, we should study the protein structure and its role to the morphogenesis. We may not be able to clear the taxonomy, if we do not study it, even if we analyze the sequence of other useful gene.



Fig. 1. A scene of panel discussion, *Present and Future on Molecular Biology of Useful Seaweeds* at auditorium, Natural History Museum and Institute, Chiba, Japan on November 29, 2002. Above (left to right): Masahiro Notoya and Masahiko Miyata (co-organizer), Yuzuru Mizukami, Wendy A. Nelson, Makoto Kakinuma, Satoshi Shimada, Norishige Yotsukura.

Nelson, W.

I think that we are looking for the tool that both clarify relationships and define the phylogeny, but also have a practical use. We are looking for the character that are well defined and clearly different from those of near species.

But, actually, in the taxonomy of many organisms we have to rely on chemistry, we have to rely on non-structural features, may be the characteristics of the organisms has growing in culture, may be aspects about the physiology. And, when we actually look at wide area of characteristics we employ, morphology is only one part of entire story.

When we see the work that was introduced today, about the impact of salinity on morphology of species we have to be careful about how much lay special emphasis of particular characters. We have to be careful whether the character appeared with what kind of condition.

So therefore, again I would take the broadest possible view that we will take informations from the every resource we can work it.

And we studied worked the agar molecules on members of Gracilariales, particular genus *Curdiea*, and Gelidiales, working with different species *Gelidium* in New Zealand, and we have obtained rarely information. It is difficult to study the chemistry of agar molecules, but we also have be able to obtain the phylogeny.

So, I have the feeling that when we look back 5 years and 10 years, the situation of molecular sequences data has changed during this period. If we will be sitting the room in another 5 years, we will be looking at tools which are very much rapid and differentiate more easily. So, I am looking forward to the future what kind of development of the study and to applying wide range of techniques of molecular at more rapid pace.

Miyata, M.

I think that there is a difficulty still regarding the method of molecular analysis, and there is the flow that develops it toward the future. But, I think that it is important that the result and process are used for the basic and applied sciences.

Since I am working in the natural history museum, I emphasize that the molecular data may provide the important informations to the problem of the extinction of organisms. I am looking forward to the development of the important discussion about the conservation biolo-

gy based on the molecular informations.

Notoya, M.

Finally, please comment about the future direction of application of molecular biology of seaweeds.

Mizukami, Y.

I have the feeling that it is very important that various specialists, for example, taxonomy, molecular analysis, and so on, gather and discuss periodically. We should be going to hold such a meeting to obtain the important information from other specialized fields. I am looking forward to the good results from the meeting in future.

Notoya, M.

Thank you for your attention to this panel discussion.



Photographs of the Participants

The 14th Natural History Symposium, “*Present and Future on Molecular Biology of Useful Seaweeds*” (Chiba, Japan on November 29, 2002)

The front row (from left side): **K. Mochizuki** (Natural History Museum and Institute, Chiba), **M. Chihara** (Chair, Natural History Museum and Institute, Chiba), **W. A. Nelson** (National Institute for Water and Atmospheric Research, New Zealand), **M. Notoya** (Program Committee Chair, Tokyo University of Marine Science & Technology), **Y. Mizukami** (National Fisheries University)

The back row: **M. Kakinuma** (Mie University), **N. Yotsukura** (Hokkaido University), **S. Shimada** (Hokkaido University), **M. Miyata** (Secretary General, Natural History Museum and Institute, Chiba)