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Taxonomy: A Discipline Central to Integrative Biology

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ABSTRACT

Taxonomists contribute to science in three ways: recognition of taxa, classification of taxa, and integration of information on taxa. Recognition of taxa is first performed at the species level. The fact that taxonomy at the species level is regarded as descriptive, rather than utilizing hypothesis testing, is perhaps why it is difficult for biologists other than taxonomists to understand taxonomy as a science, hence the low reputation of taxonomy. Most biologists consider, and refer to, as "science" only the disciplines of biology using hypothesis testing. Although a large part of a taxonomic paper is dedicated to description, however, taxonomy is itself a science based on hypothesis testing. If you wonder whether the specimen before you belongs to a described species or not, you first adopt a hypothesis that the specimen is an undescribed species, then begin to test this hypothesis using comparative morphology, distributional data, or any other tools available. You observe the specimen, describe it morphologically, compare it with those species close to it, decide that it is an undescribed species, name it, and finally publish a paper on the new species. Taxonomy has been misunderstood by people as *merely* descriptive, but in fact, it uses hypothesis testing *in addition to* description, and thus is as scientific as disciplines of biology other than taxonomy. In another respect, there is a basic difference between taxonomy at the species level and biology other than taxonomy. Taxonomy discovers a species, and then biology other than taxonomy does studies based on that species. In this sense, taxonomy at the species level is fundamental, whereas biology other than taxonomy is derived. Derived studies could not be performed if there were not outcomes from the fundamental biology, whereas fundamental studies can be done in the absence of derived studies. At the second level of taxonomy, currently the most popular method to classify taxa is according to phylogeny. There is a fundamental difference between phylogenetic and orthodox classification: the former classifies organisms by branching order or sharing the most recent common ancestor, based on derived characters, whereas the latter classifies organisms by all their features. Cell fate determination in the Ascidian embryo, as an analogy between phylogeny and embryology, helps to make a point. In ascidians, there is a polyphyletic origin of tissues, such as epidermis or nerve cord. Two cells with the most recent common ancestor can belong to entirely different tissues in an organism. Likewise, two terminal taxa with the most recent common ancestor can be entirely different in many features. If a species obtains a certain niche in the world of biodiversity, it doesn't matter what the process is. The scenario of ontogeny is opportunistic and casual, so is that of phylogeny. Common ancestry is a trivial event; only the result has meaning. These days, a vast amount of biological information is rapidly accumulating. Who might be interested in integration of these data? No one other than taxonomists would like to do, and can do, this kind of work. Taxonomists have already done some sorts of integrative work by publishing ency-

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clopedias, biodiversity series, classification series etc. Collaboration with informatics is crucial for taxonomy to construct databases, one of the ideal depositories for biological information. In this way, taxonomists can integrate the vast amount of biological information that is scattered across the various disciplines of biology, taken from the levels of genomes, cells, individuals, taxa and so on. So, we expect taxonomy in the future to be a discipline central to all of integrative biology.

Keywords: Taxonomy, Hypothesis testing, Descriptive, Classification, Integrative biology, Fundamental study, Derived studies

INTRODUCTION

For our 21st Century COE program to make forward progress, it is necessary first to correctly establish taxonomy as an important scientific subdiscipline of biology. The present situation, in which we have to demand a revival of natural history, results from the low status people accord to research in natural history, which in turn results from their low opinion of taxonomy. Without establishing the *Raison d'etre* of taxonomy, studies in phylogeny, biodiversity, and evolution can have no reality, and the goal of the COE program to create a new natural history will not be achieved. This is because research in natural history depends entirely upon the outcome of taxonomy.

Taxonomy contributes to biological science in three ways. First, taxonomy recognizes species, the most fundamental unit of taxa, and this contribution is called micro taxonomy or taxonomy at the species level, which used to be called α-taxonomy in the old sense of Ernst Mayr [1]. Second, taxonomists construct classifications, hierarchical systems of groups of organisms, in which categorical ranks are adopted and taxa above the species level are arranged hierarchically. The last role of taxonomy is to integrate various information obtained from other fields of biology, such as physiology, biochemistry, ethology, ecology, and so on into a kind of depository in an organized manner. In this paper, I illustrate the current nature of taxonomy by demonstrating some problems together with their solutions.

PROBLEMS OF TAXONOMY AT THE SPECIES LEVEL

1) Description versus Hypothesis Testing

It has been claimed that taxonomy is only descriptive, rather than involving hypothesis testing. This is the most important problem facing taxonomy and should be resolved as soon as possible. The fact that micro taxonomy is regarded as descriptive, rather than utilizing hypothesis testing, is perhaps why it is difficult for biologists other than taxonomists to understand taxonomy as a science, hence the low reputation of taxonomy. In general, biologists consider, and refer to, as "science" only those disciplines of biology using hypothesis testing. However, let's think about the procedure of micro taxonomy.

As an example to illustrate the procedure of taxonomy at the species level, I have chosen our study on the taxonomy of the genus *Sternomoera*, Crustacea, Amphipoda published in our papers [2, 3].

Before starting this study, we obtained from the literature the following information: In 1982, Barnard and Karaman [4] established *Sternomoera* as a new genus to which Japanese endemic species of *Paramoera* with sternal gills were assigned; *Sternomoera* is a ground-water genus endemic to Japan, and contained three species: *Sternomoera japonica* described by Tattersall in 1922 [5] from a stream on Honshu Island, *S. yezoensis* discovered by Uéno in 1933 [6] from a pond in Chitose, Hokkaido, and *S. hayamensis* described by Stephenson in 1944 [7] from a small river on Honshu Island.

In addition to this published information, Dr Kuribayashi, the senior author of our papers had quite a few specimens from various localities in Hokkaido, and she was encountering difficulties with identification. Dr Kuribayashi collected vigorously around Japan and obtained *Sternomoera* samples from 174 localities across Hokkaido and Honshu Islands (Fig. 1).

Among the three species, *S. yezoensis* could be clearly distinguished because of two unique and invariable taxonomic characters, although the species was described based only on one immature female and one juvenile. All the individuals from the 80 inland populations on Hokkaido Island showed the two characters that define individuals of *S. yezoensis*: the round-cornered deep inferior antennal sinus on the head, and the presence of two notches

Fig. 1 Map showing the localities where *Sternomoera* samples were collected. Red Dots indicate the populations of *Sternomoera yezoensis* (Uéno, 1933). From Kuribayashi et al. (1996) [3]

on the posterior edge of epimeron 3. *Sternomoera yezoensis* was thus confirmed as a species distributed in inland waters across Hokkaido. In addition, we successfully collected mature male and female specimens of the species for the first time. These specimens gave us new information on sexual dimorphism; that is, the outer rami of pleopods 1–3 are modified to be stout and long in males. Moreover, some reproductive traits were discovered. For example, mature males and females occur at all seasons at two localities, but only from February to May at the other localities. Precopula could not be observed either in nature or under laboratory conditions. Copulation occurs just after female molting.

Sternomoera yezoensis [6] was thus distinguished and redescribed, but specimens from 96 localities on Hokkaido and Honshu remained unidentified. To discriminate specimens from these localities, a cluster analysis of 56 populations was performed, using Gower's similarity based on nine quantitative characters. A UPGMA phenogram divided populations into two distinct clusters, with low similarities between them (Fig. 2). One of the two was a cluster of inland populations, whereas the other contained populations situated along on the coast.

The next task was to define the entities of the two forms. At first, we compared the specimens from inland populations with two known species, *S. japon-*

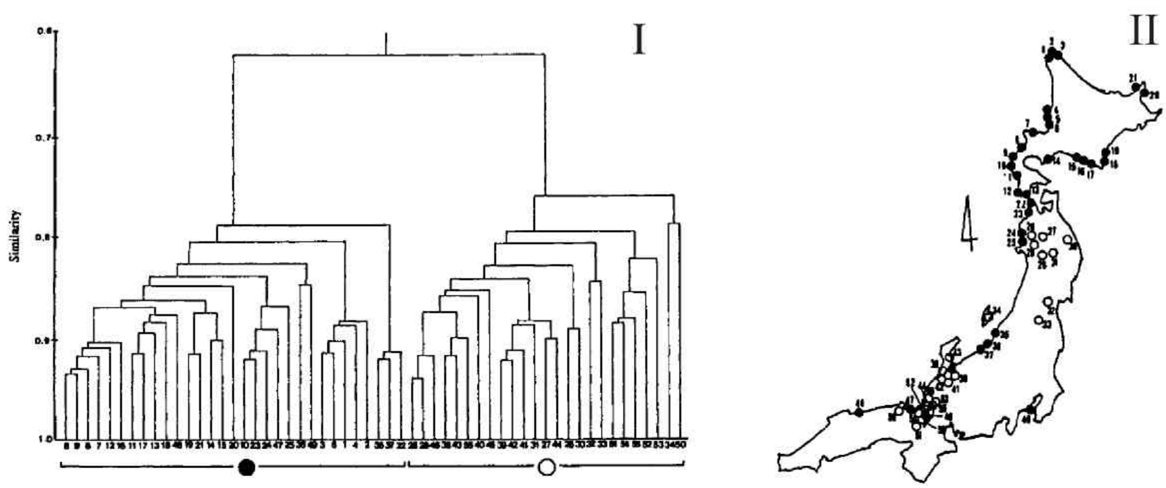

Fig. 2 I. UPGMA phenogram, using Gower's similarity, of 56 populations of *Sternomoera* spp. (except *S. yezoensis*. The coastal form (●) and the inland form (○). II. A map showing the distributions of populations in the two primary clusters. From Kuribayashi *et al.* (1996) [3]

ica and *S. hayamensis*. Judging from the original description of *S. japonica* and an examination of syntypes of *S. hayamensis*, we determined characters distinguishing those two species to be: 1) depth ratio of eye to head; 2) number of flagellar articles of the antenna 1; and 3) number of apical setae of the telson. These three characters were compared between specimens from Kitakomatsu, type locality of *S. japonica*, syntypes of *S. hayamensis*, and our specimens from the inland localities.

Scatter diagrams in two dimensions were drawn from ordination of the mean value of morphometric characters in populations of the inland form (Fig. 3). The depth ratio of eye to head is not so different between *S. japonica* and *S. hayamensis*, and these two species cannot be discriminated from populations of the inland form. However, the two species are different in the number of flagellar articles of antenna 1: *S. japonica* and *S. hayamensis* are plotted near the upper and lower extremity, respectively. Populations of the inland form bridge the two species. A similar relationship between the two species is found in the number of apical setae of the telson.

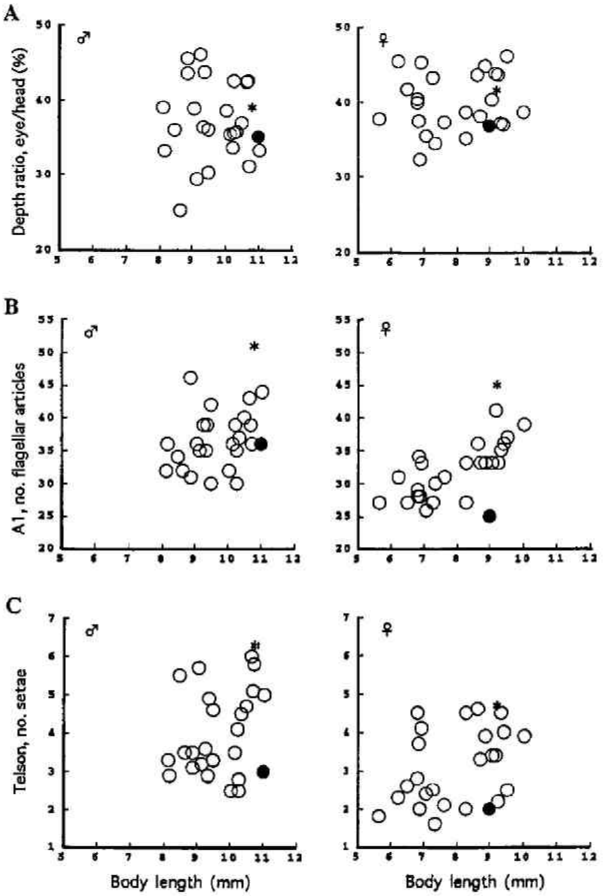

Fig. 3 Scatter diagrams in two dimensions from ordination of mean values of morphometric characters in populations of the inland form of Sternomoera. Population symbols: * = Kitakomatsu (type locality of *S. japonica*), ● = the syntype specimens of *S. hayamensis*, ○ = other populations: (A) a plot of populations by the depth ratio of the eye to head; (B) a plot of populations by the number of flagellar article of antenna 1; (C) a plot of populations by the number of setae on the apex of telson. From Kuribayashi et al. (1996) [3]

Thus, the inland form shows a wide range of morphological variation that bridges *S. japonica* and *S. hayamensis*. Neither clusters of the inland form nor the plots of three diagnostic characters form discrete groups. The original diagnostic characters of *S. japonica* and *S. hayamensis* were found to be continuously intergraded by intermediate populations, so that the two species cannot be distinguished from each other. Consequently, our second result was that the two species are conspecific, with *S. japonica* a senior synonym of *S. hayamensis*.

Next, we had to confirm the entity of the coastal form. As shown in Fig. 2, the coastal form is distinguished from the inland form statistically by some morphometric characters. Moreover, reproductive behavior is different between the coastal and inland forms (Table 1). Precopulation season is February to April for the coastal form, but October to January for the inland form. Thus, the two forms cannot interbreed.

Populations of *Sternomoera* spp. other than *S. yezoensis* are separable into two discrete groups, a coastal form and an inland form, which are distinguishable both morphologically and ecologically. The coastal form must be another species, because it is isolated reproductively from the inland form, that is, *S. japonica*. And the coastal form must be an undescribed species, because the taxonomic position of all the known three species had already been confirmed. We named the coastal population *Sternomoera rhyaca* sp. nov.

2) A General Account of Taxonomy at the Species Level

Taxonomy at the species level assumes that the taxonomist is aware of all known species in a taxon of interest and their positions in a multi-dimensional space, whose axes represent characters (Fig. 4). In this multi-dimensional space, each known species represents an assemblage of individuals. In practice, the specimen in question is located within the multi-dimensional character space as a new point. If the gap between the new point and its nearest known points is greater than the gap between the nearest and the other known points, and at the same time, it

Table 1 Results from morphometric analysis of the coastal and inland forms of *Sternomoera*: (10) breeding season when precopulae were observed in field; and (11) geographic and ecological distribution. Symbol: * = diagnostic characters of the two forms. From Kuribayashi et al. (1996) [3]

Characters	Coastal form				Inland form			
	♂		♀		♂		♀	
	range	mean	range	mean	range	mean	range	mean
(1) Boxy length(mm)	10·7–15·3	13·5	9·4–14·6	12·2	8·2–11·4	9·7	6·2–10·3	8·0
(2) Eye/head depth (%)	38·6–46·4	44·2	41·1–53·3	45·5	31·1–42·8	37·2	32·3–46·1	39·9
(3) Medial/lateral teeth, Maxilliped (%)	45·0–70·0	55·4	40·0–58·0	47·9	15·0–43·0	36·2	16·0–42·0	35·2
(4) No.setal bundles, article 1, Antenna 1*	3·0	3·0	3·0	3·0	2·0	2·0	2·0	2·0
(5) No.flagellar articles, Antenna 1	39–52	46·1	36–48	42·1	30–51	37·2	26–45	32·5
(6) Peduncular article 1 : 3, Antenna 1*	2·88–3·20	3·13	2·88–3·10	2·90	2·10–2·60	2·46	2·25–2·56	2·37
(7) Peduncular article 2 : 3, Antenna 1*	1·75–1·92	1·82	1·68–1·92	1·75	1·49–1·65	1·51	1·33–1·61	1·52
(8) No. spines Uropod 3	1–3	1·3	1–3	1·2	1–2	1·1	1	1·0
(9) No. setae, Telson	4–7	5·4	4–7	4·8	2–6	4·1	2–5	3·2
(10) Precopulatory season*	February-April				October-January			
(11) Distribution*	epigean waters along the coast of Hokkaido and Honshu				epigean waters in inland of Honshu			

is anticipated that the gap reflects reproductive isolation, then that new point is recognized as a new species. In other words, recognizing species involves clustering individuals as units, plus estimation of reproductive isolation, with the result that the position of a single species is determined in relation to adjacent species. In this way, a species is recognized in relation to others, and named if it is a new species. This is the process of taxonomy at the species level. A species is formally established by assigning a name.

3) What is Description?

As the final result of our study, a revised diagnosis of the genus *Sternomoera*, a key to species, and detailed redescriptions and descriptions for each species are provided. During the study, the behavior of *Sternomoera* spp. was observed under laboratory conditions. Mate-guarding behavior is observed both for *S. rhyaca* and *S. japonica* in laboratory, but not

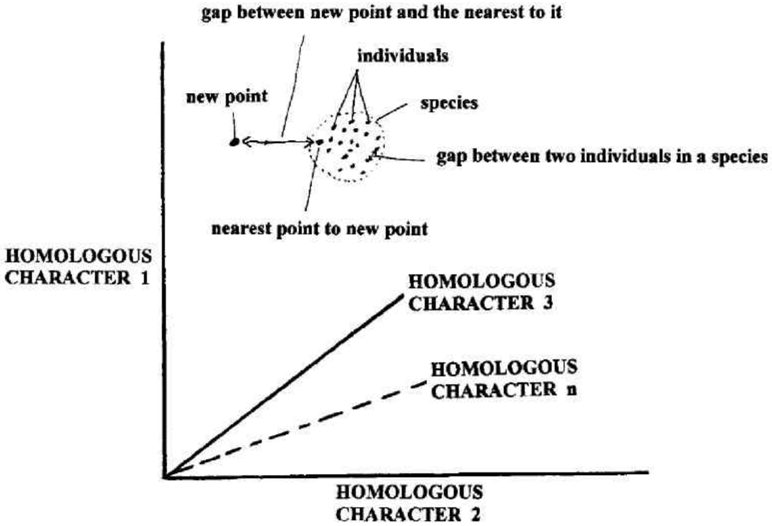

Fig. 4 General procedure of taxonomy at the species level. Taxonomist is aware of all the known species and their positions in a multi-dimensional character space, in which each known species represents an assemblage of individuals. In practice, the specimen in question is located within the multi-dimensional character space as a new point. If the gap between the new and its nearest known points is greater than the gap between the nearest and the other known points, and at the same time, it is anticipated that the gap will result in reproductive isolation, then that new point is recognized as a new species.

for *S. yezoensis*. That is, *Sternomoera rhyaca* and *S. japonica* are 'mate-guarders', whereas *S. yezoensis* is a 'non-mate-guarder'. *Sternomoera yezoensis* has stout outer rami of male pleopods as mentioned previously, whereas *S. rhyaca* and *S. japonica* have normal ones. Since there is a correlation between the sexual dimorphism and the reproductive behavior (Table 2), the taxonomic study of *Sternomoera* later developed into ecological studies of the relationship between sexual dimorphism and reproductive behavior, and their adaptive evolution.

As demonstrated thus far, the taxonomic study of *Sternomoera* did use hypothesis testing!! Judging from the specimens recently collected by one of the authors from Honshu Island and some information in the literature, we adopted a hypothesis that the specimens represented new species. The hypothesis was tested by comparative morphology, a distributional survey, and life history research. As a result, *S. yezoensis* was confirmed as the species distributed across inland waters on Hokkaido Island, *S. hayamensis* was confirmed as a junior synonym of *S. japonica*, and *S. rhyaca* was established a new species.

As shown by our taxonomic studies of *Sternomoera*, even the very first step of taxonomy at the species level has the feature that biologists other than taxonomists consider definitive of science, that is, hypothesis testing. Taxonomy has been misunderstood by people as *merely* descriptive, but in fact, it uses hypothesis testing *in addition to* description, and thus is as scientific as disciplines of biology other than taxonomy.

And so, we can ask what description is. In taxonomic practice, a taxon is recognized, namely, grasped, located, and then named, and hence derives its existence in our scientific world. Believe it or not, this procedure is done by "description," in which the taxon is explained with words, and the study finished by depositing the type specimens in some museum, institution, or university. After that, people recognize the species by knowing its name and reading its description, with help from the type specimens. Description is thus instrumental in recognizing species. Moreover, other studies will be done based on the description. In this sense, taxonomy at the species level is a study that mines those gemstones to be polished or refined by derived studies. The result of a taxonomic study is itself a hypothesis, which can be tested by more precise study of the species in future.

Anyway, description, name, and types are the Three Sacred Treasures of not the Imperial House, but of Our Holy Recognition.

4) Fundamental versus Derived

Between taxonomy and biology other than taxonomy, however, exists an important basic difference in another respect. Taxonomy discovers a species, and then biology other than taxonomy does studies based on that species. The species is the outcome of taxonomy, and then becomes a unit for biology. In this sense, taxonomy is fundamental, whereas biology other than taxonomy is derived. Derived studies could not be performed if there were not outcomes from the fundamental biology, whereas fundamental studies can be done in the absence of derived studies. As shown in Fig. 5, taxonomy, a fundamental study, is located on the border between the worlds of science and non-science, though derived studies are located within the world of science. Taxonomy plays a vital role in recognizing natural units in nature and bringing them into the scientific world. In other words, taxonomy brings taxa from the world of non-science to our world of science. This demanding work has to be done using very limited information starting at almost zero. Taxonomists discover natural groups of organisms, which are called 'species,' by taxonomy at the species level. It is only after this process that human beings can recognize a group of organisms. Those organisms that are not described cannot be handled in sci-

Table 2 Sexually dimorphic characters and mating types of the males of *Paramoera* and *Sternomoera*. References to mating types: *Sternomoera koysama* (Kuribayashi, personal observation); *P. erimoensis* (Kyono, personal communication); *P. mohri* (Conlan, 1991). From Kuribayashi et al. (1996) [3]

	Sternomoera yezoensis	*S. japonica*	*S. rhyaca*	*Paramoera koysama*	*P. erimoensis*	*P. mohri*
Gnathopod enlargement	no	enlarged and massive	enlarged massive	enlarged	enlarged	no
Pleopod modification	medium	no	no	slight	strong	?
Mating type	non-mate-guarder	mate-guarder	mate-guarder	mate-guarder	non-mate-guarder	non-mate-guarder

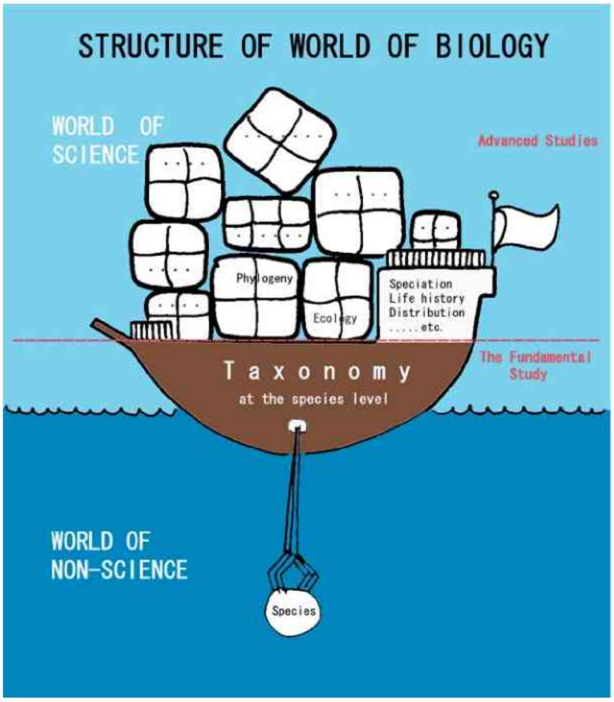

Fig. 5 Structure of world of biology

ence, because they are not recognized by human beings. In another word, taxonomy is a study that puts unknown organisms upon a cutting board. Science cannot cook anything that is not on the cutting board. Undescribed organisms cannot be a subject of other fields of biology. Biology starts with taxonomy.

By contrast, other fields of biology do derived studies which are always situated above the fundamental level, that of taxonomy. On the basis of taxonomy, these derived studies clarify the relationships of things and discover something more understandable and of more direct concern to the life of human beings. Taxonomy, the fundamental study, may be seen as simple and primitive, while derived studies are viewed as complex, important and attractive for people.

That's why the derived studies always take priority, and get money easily from our world. These differences of structural rank, of character of study, and of economical situation make researchers in derived fields seem superior. I repeat once again that derived studies are structurally placed above taxonomy. However, any discipline that is placed lower in the world of science can't be inferior to those disciplines at higher levels. This low and high structure of the world of science stems from the nature of science. Derived studies include not only biology other than taxonomy as well as some offshoots of taxonomy, such as studies of life history, distribution, reproductive traits, the internal structure of species, speciation, and so on. These used to be called as γ-taxonomy in the old sense of Ernst Mayr.

TOWARDS A NATURAL CLASSIFICATION

1) Orthodox Classification

Taxonomy above the species level is called classification, or macro taxonomy, or β-taxonomy in the old sense of Ernst Mayr. In classification above the species level, taxa are nested in hierarchically arranged ranks. For this procedure, only the clustering of taxa is accomplished, without any biological concept, in contrast to the recognizing of species, in which the biological species concept is adopted. Taxonomists are aware of all the known taxa and their positions in a multi-dimensional space (Fig. 4), in which the coordinates represent characters. In this multi-dimensional space, each known taxon represents an assemblage of taxa of the next lower rank.

In practice, a species in question is located within the multi-dimensional character space as a new point. If the gap between the new and its nearest known points is greater than the gap between the nearest and the other known points within a genus, then that new point is recognized as a new genus. In other words, classifying a genus involves clustering species as units, with the result that the position of a single genus is determined in relation to adjacent genera. In this way, a genus is recognized in relation to others, and named if it is a new genus. In the same way, a family is recognized in relation to others, and so on. This is the process of taxonomy above the species level. A taxon is determined by assigning a name.

If you find an undescribed species close to a described one, it is easy to define the species by recognizing small differences against the background of many common characters, but is not easy to infer the presence of reproductive isolation, because of the small difference in characters between the species. In this case, anyhow, the undescribed species takes a distinct position in the multi-dimensional character space. If you cannot find any species close to the undescribed one concerned, it is difficult to define the species by recognizing many differences against the background of few common characters, but is undoubtedly clear that the undescribed species is reproductively isolated from all known species. The undescribed species cannot take a distinct position in the multi-dimensional character space already existing.

The undescribed species deviates from the multi-dimensional character space. In this case, a new higher taxon, for example a phylum, is established. In this way, more than 30 animal phyla have been recognized, including four discovered within the last 50 years: these newcomers are the Placozoa, Loricifera, Gnathostomulida, and Cycliophora. A taxon that cannot be grouped with another taxon due to a large difference in characters is given the highest rank, that of Phylum. Taxonomists have a poor grasp of the relationships between Phyla, and the same applies to the relationships between Classes, Orders, and Families. The criteria by which a certain group of organisms attains a rank of Class, for example, rather than that of Order, are unclear. Moreover, there is inconsistency between taxonomists: I might give a rank of Order to an animal group, whereas you might give a rank of Suborder to the same group.

Is there any possibility to make an objective and natural classification? Since Darwin, we have understood that present biodiversity results from the evolution of organisms in the past. Phylogeny was born as a new scientific discipline that looks for the history of present organisms and the historical relations among them. Phylogeny gives the framework of evolution to taxonomy. That is, taxonomy came to depend on phylogeny to make classification based on evolution. Taxonomy and phylogeny fused into a phylogenetic classification, or what is called phylogenetic systematics.

Since evolution is a unique, one-time event, a classification based on phylogeny must be unique, objective, and natural. All taxonomists dreamed that the classification based on phylogeny would solve the problems of classification. Taxonomists continuously explored the possibility of a phylogenetic classification by using various disciplines of biology as tools, namely, morphology, physiology, biochemistry, embryology, genetics etc., testing a lot of different characters, such as chromosomes, larval types, sperm morphology, etc. In other words, taxonomists looked for a common language that tells us the history of organisms.

The results were miserable. Taxonomists failed to find a phylogenetic classification, and their trust in a phylogenetic classification has been completely ridiculated.

2) Cladistics

When taxonomists were looking for a phylogenetic Messiah, Willi Hennig came along and developed cladistics [9]. Cladistics discards primitive characters as the basis for recognizing taxa and adopts branching order determined by derived characters as the primary focus. One of the main goals of cladists was to classify organisms according to branching order, that is, to achieve a phylogenetic classification. A phylogenetic classification adopts only monophyletic groups as taxa and rejects paraphyletic groups. Orthodox classification, on the other hand, recognizes groups using all characters and adopts some paraphyletic groups that can be recognized by a gap in the clustering of characters. Nowadays, cladistic methodology applied to DNA sequence data is flourishing, and there is an increasing trend to incorporate the results in classifications. In contrast, orthodox classification is going downhill.

Mark Ridley, a prophet of cladistics, claimed that cladistics is objective [10]. I agree with him. He also wrote that "Evolutionary classification was the orthodox school from the 'modern synthesis' of the 1930s (or even from Darwin's time in the 1860s) until about 20 years ago." I will never agree with him on this point. I would say "Evolutionary classification is the orthodox school from the 'modern synthesis' of the 1930s until forever." But in reality, I am one of the relatively few proponents.

However, in several aspects there are serious problems with adoption of a universal phylogenetic classification, e.g., nomenclatural systems such as the Phylocode. As paraphyletic genera now exist across animal groups in the current classification, e.g., the shrimp genus *Pandalus* paraphyletic to *Pandalopsis* [11], so can species also be paraphyletic. An example is paraphyly of grizzley bears against monophyletic polar bears [12–13]. Paraphyly is likely to be a common byproduct of speciation events in which a new species arises as an offshoot population from a group of phylogenetically structured populations of the mother species. Furthermore, a phylogenetic classification is incoherent in the face of reticulate evolution, such as when species hybridize to produce new species; an example is found in wheat tetraploids [14].

On the other hand, orthodox classification has a defect too. Orthdox classification insists that basal lineages sharing a suite of primitive characters be defined as a taxon separate from a terminal clade united by many synapomorphic characters. However, "many" is a term of degree, and subjective; it is unclear how many apomorphies are necessary for a derived terminal group to be separated from a paraphyletic basal group. If there were a natural way to determine the threshold of apomorphic characters necessary, the orthodox classification would win the game.

Taxonomy is the wisdom that came to the brain of human beings when they first observed biodiversity in nature. There existed organisms as classes of characters, and so humans began to classify organisms according to their features. Orthodox taxonomy similarly classifies organisms by all their features. Cladistics is primarily concerned with branching order, and is thus fundamentally a discipline of phylogeny rather than a discipline of taxonomy. Though taxonomists have long dreamed of a phylogenetic classification, which cladistics promised to produce in an objective manner; what is emerging is different from the original dream. And so, cladists claim to abandon the orthodox classification, whereas orthodox taxonomists claim that a cladistic approach to classification cannot explain nature in a useful way. What shall I hope for as an orthodox taxonomist — some other possibility, a phylogenetic classification based on something other than cladistics, or an entirely different system of natural classfication?

3) Is Phylogenetic Classification Plausible?

Whatever classification we adopt, what is ultimately important is taxonomy at the species level. An analogy between phylogeny and embryology may help to make this point. In a group of sea urchins (Fig. 6.), an egg of one species takes one developmental pathway to become an adult, whereas an egg of another species develops into an adult through another route, and a third species takes yet a different route from either [15]. Adult form cannot be predicted by embryology.

Urchins can take any of a number of ways to arrive at the same destination. As shown in Fig. 7, cell fate determination in the ascidian embryo is another example of the analogy [16, 17]. There is a polyphyletic origin of tissues, such as epidermis or nerve cord.

The process of ontogeny is opportunistic and casual, just as is that of phylogeny. It isn't a coincidence; instead, there must be some logical relationship between the two processes. Two cells with the most recent common ancestor can comprise entirely different tissues in an organism. The two cells are not treated as a kind of group, because they play different roles either in developmental process or the adult body. There is no absolute linkage between the cell lineage and the tissue into which the cell differentiates. Common ancestry is a trivial event. The same result can be achieved by a variety of processes, and only the result has meaning.

Likewise, two terminal taxa with the most recent common ancestor can be entirely different in features. They can play different roles either in the process of evolution in the past or in the present world of biodiversity, and so, orthodox classification does not put two terminal taxa into one group just because they share the most recent common ancestor. If a taxon obtains a certain niche in the world of biodiversity, the process involved doesn't matter. In the sense that only the result has meaning, common ancestry is a trivial event even in phylogenetic classification.

There is no fatalism between the phylogenetic position of a taxon and the new taxon into which it evolves. Just as in the situation in which the site to which a cell moves determines the cell's fate, where a taxon evolves determines that taxon's fate, that is, the particular adaptive features it will show in the environment in which it evolves. There is no fatalism between the lineage and the diversity at the end of the lineage. Is there any fatalism between the past and present?

Various kinds of classifications can exist: phylogenetic, physiological, biochemical; classification by chromosomes, larval forms, etc. You can choose

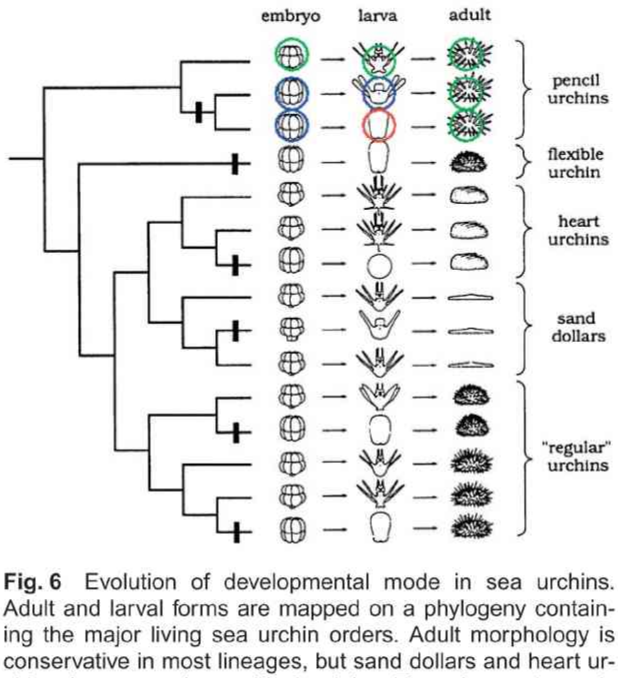

Fig. 6 Evolution of developmental mode in sea urchins. Adult and larval forms are mapped on a phylogeny containing the major living sea urchin orders. Adult morphology is conservative in most lineages, but sand dollars and heart urchins have greatly modified adults. The pluteus larva is maintained by most lineages, and is the primitive mode of development. Direct development has arisen independently in over 20 lineages of sea urchin. Modified from Raff (1996) [15]

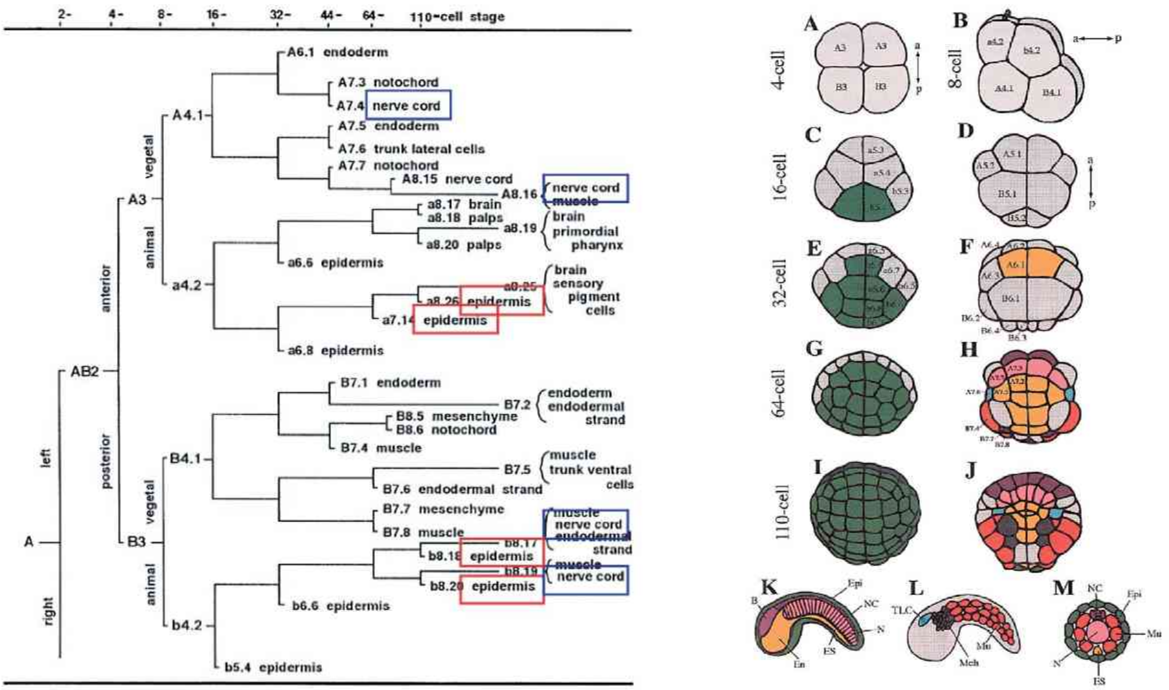

Fig. 7 I. Cell lineage and segregation of developmental fates in Halocynthia roretzi embryo. Because the lineage is bilaterally symmetrical, only the left half of the embryo is shown. Divisions of cells that are tissue restricted are abbreviated. From Nishida (1987) II. Cleavage pattern, nomenclature of blastomeres, lineage and gradual restriction of developmental fates of ascidian embryonic cells. Blastoneres are colored when the developmental fate is restricted to give rise to cells of a single type of tissue. Epidermis is marked by green and nerve cord by light purple. Modified from Sato (1999) [17]

one of them according to what you want to know, whether you want to know phylogeny, or taxonomy, or whatever else. If you adopt any kind of classification, however, the status of the taxonomy at the species level must remain stable. If there were no taxa, neither phylogenetic history nor characters would exist in the world of science. In a world without taxonomy at the species level, there would be no biological problems to be solved.

4) Possibility of Integrative Biology

These days, a vast amount of biological information is rapidly accumulating. Who might be interested in the integration of these data? No one other than taxonomists would like to do, and could do, this kind of work. Taxonomists have already done some sorts of integrative works by publishing encyclopedias, biodiversity series, classification series etc. Recently, It has been said that databases are going to develop and can be one of the ideal depositories for biological information. Of course, collaboration with informatics is crucial for taxonomy to integrate the vast amount of biological information that is scattered across the various disciplines of biology, taken from the level of genomes, cells, individuals, taxa and so on. In the future, therefore, we expect taxonomy to be a discipline central to all of integrative biology.

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REFERENCES

1. Mayr, E., 1968. *Principles of Systematic Zoology*, McGraw-Hill, New York.
2. Kuribayashi, K., Ishimaru, S. and Mawatari, S.F., 1994. Redescription of *Sternomoera yezoensis* (Ueno, 1933) (Amphipoda: Uusiridae) with reference to sexual dimorphism on pleopod 2. *Crustacean Res.*, 23, 79–88.
3. Kuribayashi, K., Mawatari, S.F. and Ishimaru, S., 1996. Taxonomic study on the genus *Sternomoera* (Crustacea: Amphipoda), with redefinition of *S. japonica* (Tattersall, 1922) and description of a new species from Japan. *J. Nat. Hist.*, 30, 1215–1237.
4. Barnard, J.L. and Karaman, G.S., 1982. Classifactory revisions in gammaridean Amphipoda (Crustacea). *P. Biol. Soc.Wash.*, 95, 167–187.
5. Tattersall, W.M., 1922. Zoological results of a tour in the Far

East, Part 8. Amphipoda with notes on an additional species of Isopoda. *Memoirs of the Asiatic Society of Bengal*, 6, 435–459, pls. 18–21.

6. Uéno, M., 1933. Three noticeable freshwater Crustacea of Hokkaidô. *Annot. Zool. Japon.*, 14, 115–122.
7. Stephenson, K., 1944. Some Japanese amphipods. *Videnskabelige Meddelelse fra Dansk Naturhistorika Forening*, 108, 25–88.
8. Wilson, E.O., 1992. *The Diversity of Life*, Harvard University Press, Cambridge.
9. Hennig, W., 1965. Phylogenetic Systematics. *Ann. Rev. Ent.*, 10, 97–116.
10. Ridley, M., 2004. *Evolution*, Third Edition, Blackwell.
11. Komai, T., 1999. A revision of the genus Pandalus (Crustacea: Decapoda: Caridea: Pandalidae). *J. Nat. Hist.*, 33(9), 1265–1372.
12. Cronin, M., Amstrup, S.C., Carner, G.W. and Vyse, E.R., 1991. Interspecific and intraspecific mitochondrial DNA variation in North American bears (*Ursus*). *Can. J. Zool.*, 69, 2985–2992.
13. Sandra, L.T. and Gerald F.S., 1996. A phylogeny of the bears (*Ursus*) inferred from complete sequences of three mitochondrial genes. *Mol. Phylogenet.* Evol., 5(3), 567–575.
14. Kihara, H., 1954. Considerations on the evolution and distribution of *Aegilops* species based on the analyser-method. *Cytologia*, 19, 336–357.
15. Raff, R.A., 1996. *The Shape of Life: Genes, Development, and the Evolution of Animal Form*, The University of Chicago Press, Chicago and London.
16. Nishida, H., 1987. Cell lineage analysis in ascidian embryo by intracellular injection of a tracer enzyme. III. Up to the tissue restricted stage. *Dev. Biol.*, 130, 737–766.
17. Sato, N., 1999. Cell fate determination in the ascidian embryo. In: A.A. Moody (ed.), *Cell Lineage and Fate Determination*. Academic Press, 59–74.