

## Evaluation of Bat-Infesting Myobiidae (Acarina, Trombidiformes) as Indicators in Taxonomy and Phylogeny of Host Bats (Chiroptera)

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Received March 25, 1981

**ABSTRACT** Availability of Myobiidae as indicators in taxonomic and phylogenetic analyses of regional bat fauna was evaluated in light of data from a karyological study of bats. The speciation of mites of the genus *Neomyobia* parasitic on bats of the genus *Rhinolophus* seemed to have made progress concordant with the chromosomal differences among the named bats. Both the speciation of mites of the genus *Calcarmyobia* that infest *Miniopterus* and the divergence of bat karyotypes were thought to evolve much more slowly if all the *Miniopterus* bats proposed on general gross anatomy were valid species. The mites were, however, more divergent than the karyotypes in the bats, suggesting that mites are efficient indicators in the study of bat taxonomy and phylogeny. The mites of genus *Acanthophthirius* parasitizing Vespertilionidae were regarded as being more sensitive indicators than karyotypes in the taxonomy of bats. The mites of the genera *Acanthophthirius* and *Pteracarus* produced a suggested phylogeny of bats of the family Vespertilionidae comparable to that proposed on the karyological study of the bats.

Thus, the mites of the family Myobiidae are evaluated as indicators not less efficient than karyotypes in the taxonomy and phylogeny of bats. (*Zool. Mag.* 90: 351-361, 1981)

The bats or Chiroptera are small mammals specialized to the flying life. Because of their small size and convergence, taxonomy and phylogeny based merely on general gross anatomy come to difficult problems, and are sometimes misleading. Informations from various fields are necessary to improve so far constructed taxonomic and phylogenetic considerations of this particular group of mammals.

The karyological study of the bat has shed light on the phylogeny. The parasites, being considered as a part of the host, which are, as a rule, more conservative in morphology, may also be a better guide to the study of the ancestral history of the hosts than fur or feathers of hosts themselves (Jordan, 1942). The lice, Mallophaga and Anoplura, which have been thought to be the best indicators in the

taxonomy and phylogeny of their hosts, and have, in fact, contributed much to deduction of useful informations, are never found on Chiroptera. The acarine permanent parasites of the family Myobiidae commonly occurring on bats are expected to play a role in the taxonomy and phylogeny of the hosts as the lice do on birds and some mammals.

Both the karyological and parasitological studies carried out independently by the present authors are aiming not only at descriptive works but also at making taxonomic and phylogenetic deductions from the different fields of study. The informations as to the systematics and phylogeny of the bat fauna of Japan from both the sides have gradually compiled. The present paper deals with the results of analyses of the regional bat fauna using these data.

This is, in other words, a trial to evaluate the availability of recently obtained parasitological data in the host taxonomy and phylogeny in the light of knowledge from the further advanced karyological study.

The outline of the paper was read in the Acarology Section, the 16th International Congress of Entomology, Kyoto, Japan, 1980.

### Bat Fauna of Japan

The bat fauna of Japan comprises 33 species or subspecies as shown in Table 1. The bats of the genera *Pteropus* and *Hipposideros* are constituents of the fauna of the Oriental region, and the bat of the genus *Tadarida* is encountered by chance. These tropical or subtropical bats should be compared with respective allied species, data on which are scarce for the authors.

The other bats of the 3 families are endemic to wide ranges, including the domains of Japan, and the following discussions are exclusively concerned with the bats of these families.

#### Mites parasitic on the family Rhinolophidae

The mites of the genus *Neomyobia* are specific to the bats of the family Rhinolophidae. *Neomyobia plurihospitalis* is shared by *Rhinolophus cornutus* and *Rhinolophus* sp. distributed in southern-most islands of Japan. The mite and its relatives are found on several bats endemic to the Oriental region (Uchikawa and

Kobayashi, 1979; Uchikawa *et al.*, 1980). Further records on hosts are necessary to deduce taxonomic and phylogenetic informations on bats sharing the mite and their relatives.

*Neomyobia aberrans* infests the third bat of the genus *Rhinolophus*, which had long been regarded as the subspecies of the European horseshoe bat, *R. ferrumequinum*. *N. aberrans* and *N. rollinati* (Radford) parasitic on *R. ferrumequinum* are quite different from each other as shown in Fig. 1. Although the females of both the species are alike, the males are thought to be phylogenetically remote in that they have remarkably different genitalia. Since subspecies of a host species are, as a rule, parasitized with the same mite, this fact strongly suggests that the Japanese *Rhinolophus* can not be a subspecies of the European *R. ferrumequinum*.

The karyological studies of the bat have already revealed that the Japanese bat (Harada, 1973; Ando and Uchida, 1974) and *R. ferrumequinum* (Bovey, 1949; Capanna and Civitelli, 1964; Dulic, 1966; Capanna, 1968) differ from each other beyond the subspecies level. The karyotypes of both the bats are clearly different as shown in Fig. 1. And the Japanese bat has been elevated to a full species and is called *R. nippon*.

Thus, the comparable results are obtained in the karyological and parasitological studies, and the mite of the family Myobiidae is regarded as being a good indicator in the taxonomy of the *Rhinolophus* bats.

#### Mites parasitic on the family Miniopteridae

The family Miniopteridae represented by the genus *Miniopterus* has been elevated by Mein and Tupiner (1977) from the subfamily Miniopterinae in the family Vespertilionidae. Uchikawa (1978) followed them merely because only the bats are specific hosts for the mites of the genus *Calcaromyobia*, though they share many acarine parasites with the bats of the family Vespertilionidae. Accordingly, the

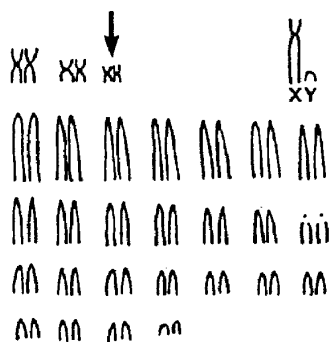
Table 1. Bat fauna of Japan

Family	No. of Gen.	No. of Sp. or Subsp.
Pteropidae	1	2
Hipposideridae	1	1
Rhinolophidae	1	3
Miniopteridae	1	2
Vespertilionidae	8	24
Molossidae	1	1
Total	13	33

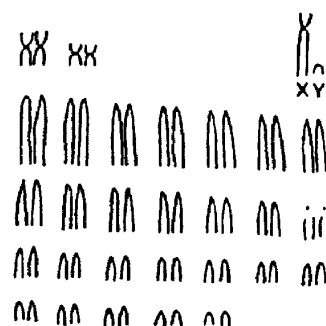
*Rh. ferrumequinum* subspp.  
(Japan)

*Rh. ferrumequinum*  
(Europe)

Karyotype



2n=58, FN=62, male



2n=58, FN=60, male

*Neomyobia aberrans*

*Neomyobia rollinati*

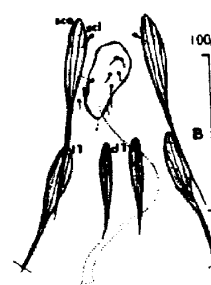
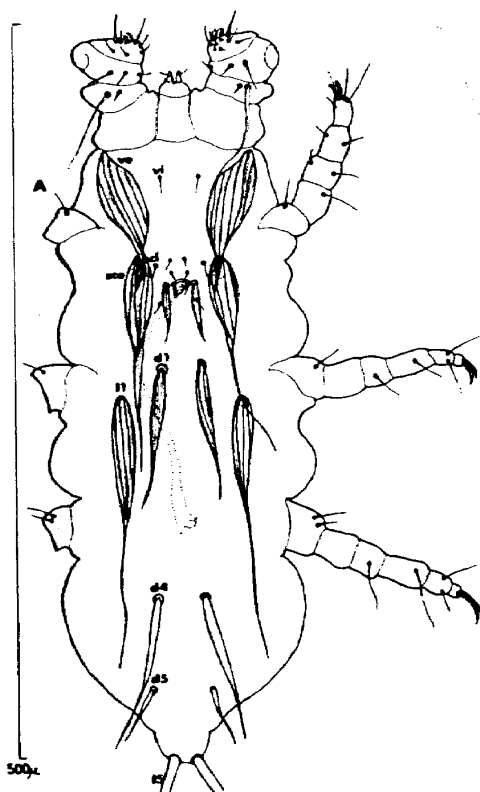


Fig. 1. *Rhinolophus* bats and their karyotypes and *Neomyobia* mites.

present authors do not necessarily agree with each other on the super-genetic classification of the bats.

The bats of the genus *Miniopterus* are

associated with the mite of the genus *Pteracarus*, which is thought to be very conservative in evolution. Although more than 40 species or subspecies have been described as the members

of the genus *Miniopterus*, only the two species of the mites, *Pteracarus faini* and *P. miniopteri*, have so far been known from them (Uchikawa, 1978a, b). Accordingly, it is now possible to sort out the bats into the two groups, the hosts of the former mite and those of the latter mite, which are regarded as being phylogenetically remote from each other. The two species of the bats distributed in Japan, the larger sized common bat and smaller sized one, share *P. faini*. This suggests that the two Japanese bats are phylogenetically close to each other regardless of their difference in size. Since the mite parasitic on the European *Miniopterus* is *P. miniopteri*, the Japanese bats are remote from the European bat. The larger sized Japanese bat had long been regarded as a subspecies of *Miniopterus schreibersi*, but its parasitic mite clearly suggests the impropriety of the above treatment.

The speciation of the mites of the genus *Calcarmyobia* is more advanced. Five species of the mites, including undescribed one, have so far been known, and a mite is usually shared by allied species. The two Japanese bats share *Calcarmyobia miniopteri*, while *Miniopterus schreibersi* harbours *C. parentzani* in Europe. This again shows that the two Japanese bats

are close to each other, and that any of them can not be a subspecies of European *M. schreibersi*.

The karyological study has revealed that the karyotypes of the examined bats are close to one another, and that the sex chromosomes and 2 pairs of large and a pair of small meta-submetacentric chromosomes are observed as in Fig. 2. And the karyotypic difference of the bats is usually confirmed by presence or absence of the smallest meta-submetacentric chromosomes, which are rather difficult to be clearly observed, and, if present, their nature. The karyotypes of the Japanese larger sized bat (Tsuchiya, 1971; Harada, 1973; Ando *et al.*, 1977) and European *Miniopterus schreibersi* (Capanna and Civitelli, 1965; Zima, 1978) have been studied. It seems that only the Japanese bat bears the fourth meta-submetacentric chromosomes (Fig. 2). The junior author is, however, of opinion that the karyotypes of the Japanese and European bats are hardly separable from each other.

Accordingly, only the above parasitological data suggest that the Japanese bat that had long been named as *Miniopterus schreibersi fuliginosus* should be regarded as being a full species different from *M. schreibersi*.

Recently, three of morphologically and ecologically different bat forms, being thought to be valid species with the similar karyotypes, were found in the same cave of Gomangton, Borneo, with the three respective valid species of *Calcarmyobia* and two species of *Pteracarus* on them (Harada and Kobayashi, 1980; Uchikawa *et al.*, 1980). This indicates that the mites are more easily discernible and more sensitive than the karyotypes of the hosts as the taxonomic and phylogenetic indicators.

Both the mites of the genus *Calcarmyobia* and karyotypes of the bats evolve more slowly than the general morphology of the bats, if all the bats of the genus *Miniopterus* proposed on general gross anatomy were valid species. The validity of the bats should, however, be reconfirmed basing on diversified studies. The

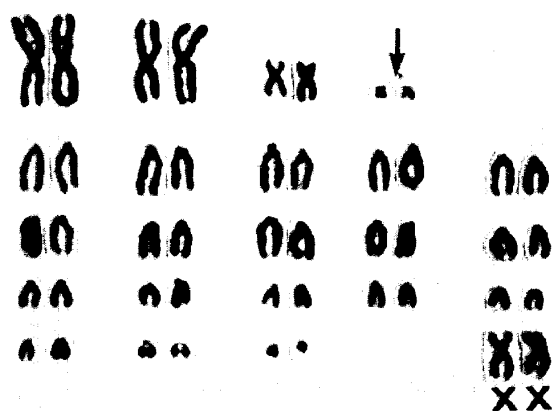


Fig. 2. Chromosomes of the Japanese *Miniopterus schreibersi* (female), with an arrow indicating key meta-submetacentric chromosomes for separating different karyotypes.

mites of the genera *Calcaromyobia* and *Pteracarus* are promising to present the most useful informations in the course of studies.

#### Mites parasitic on the family Vespertilionidae

The family Vespertilionidae are thriving in Japan, and are represented by 24 species belonging to the eight genera. And the taxonomy of this family is still in an unsatisfactory state.

The bats of the family are associated with the mites of the genera *Acanthophthirius* and *Pteracarus*. The former genus is divergent and almost host species specific, while the latter genus is conservative as already pointed out.

Of the twenty-four species of the known bats, *Murina tenebrosa* and *Myotis ozeensis*, which are known only from the type specimens, and *Myotis ikonnikovi* were found thus far free from any mite of the genus *Acanthophthirius*, though the specimens of these bats were examined. All the other twenty-one bats are the hosts of the twenty species or subspecies of the mites of the genus. Since *Myotis macrodactylus* is parasitized with the two specific mites, only the two pairs of the bats, *Vespertilio superans* and *V. orientalis* as well as *Eptesicus japonensis* and *E. nilssoni parvus*, harbour a common mite, respectively (Uchikawa, 1979, and in press). Thus, the mites of the genus *Acanthophthirius* must be good indicators in the taxonomy of the bats, and one can tell the name of a bat through examining particular mite or mites parasitic on it. If the mites are strictly host species specific, the two species of the bats each of the genera *Vespertilio* and *Eptesicus* that share respective common mite may be conspecific or different at merely the subspecies level, respectively (Uchikawa, in press).

Of the twenty species or subspecies of the mites, 5 taxa are thought to be conspecific with the mites distributed in Europe or India, and 15 taxa are so far indigenous to Japan. The hosts of the former group are *Plecotus auritus*,

*Barastella leucomelas*, *Nyctalus lasiopterus*, *Eptesicus nilssoni parvus*, *E. japonensis*, and *Myotis macrodactylus*. Thus, *P. auritus* from Japan and Europe, *B. leucomelas* and *B. barbastellus*, *N. lasiopterus* and *N. noctula*, *Eptesicus* from Japan and Europe, and *M. macrodactylus* and *M. longipes* from Kashmir, which share the same mite, respectively, are regarded as conspecific or different from each other at only the subspecies level, respectively (Uchikawa, in press). On the other hand, there are 3 bats among the hosts of the mites so far indigenous to Japan, which have been named the same with the European bats harbouring the different mites. These are *Myotis daubentoni*, *M. mystacinus* and *M. nattereri*. As the mites are synhospitalic on some hosts, it is possible to expect that, at least, a pair of the same mites might be found on each of the bats named as above in Japan and Europe. In this case, the above Japanese bats shall be regarded as being conspecific with the European bats, respectively. It is, however, also probable that the bats named the same harbour different mites in Japan and Europe, and, then, the three Japanese bats must be renamed as different full species in such the case (Uchikawa, in press).

Some morphological properties of the mites should be adopted to measure affinities among the mites which reflect the phylogenetic relationships among their hosts. Based on the remarkable differences in the legs and idiosomal outline of the male, 4 subgenera have been proposed for the genus *Acanthophthirius* (Fain, 1972a, b, 1976). The three subgenera occurring in Japan and their host genera are presented in Table 2. The subgrouping of the hosts by the subgenera of their parasitic mites considerably accords with the already presented data based on the gross anatomy of the hosts. However, the mites of the subgenus *Myotimyobia* are prevailing on a too wide range of the hosts than commonly expected. When the male genitalia and female opisthogastric sclerite are adopted as the criteria, different relation-

Table 2. Subgenera of *Acanthophthirius* distributed in Japan and their host genera

Mite Subgenus	Host Genus
1. <i>Acanthophthirius</i>	<i>Nyctalus</i> , <i>Plecotus</i> , <i>Vespertilio</i>
2. <i>Chiromyobia</i>	<i>Pipistrellus</i>
3. <i>Myotimyobia</i>	<i>Barbastella</i> , <i>Eptesicus</i> , <i>Myotis</i> , <i>Murina</i>

ships are deduced regardless of the subgenera of the mites. The male genital shields of the known Japanese species are as in Fig. 3. The shields Nos. 1 to 8 are essentially the same. The same is also for Nos. 18 and 19. The shields Nos. 9 to 17 are remarkably different from one another. Yet all the mites with these shields are parasitic exclusively on the bats of the genus *Myotis*, and, moreover, the two mites synhospitalic on *Myotis macrodactylus* bear remarkably different shields, Nos. 9 and 13. Accordingly, these divergent shields should be regarded as being of a single group (Uchikawa, in press).

The opisthogastric sclerites of the female mites are as in Fig. 4. The sclerites of the partner females for the males with the genital shields numbered 1 to 8 resemble one another. These shields are forcibly subdivided into the two groups, Nos. 1 to 5 with round process and Nos. 6 to 8 with triangular process. The sclerites of the mites parasitic on the bats of the genus *Myotis*, Nos. 9 to 17, are too divergent to divide them into some subgroups, though Nos. 10 and 11 as well as 14 and 16 resemble each other, respectively. Thus, adopting the male genital shield and female opisthogastric sclerite as criteria, the mites are divided into the three groups, one of which is further divided into the two subgroups. This suggests a phylogenetic relationship among the eight genera in the family Vespertilionidae as follows: The genera *Nyctalus*, *Pipistrellus* and *Vespertilio* are close to one another, and constitute a group together with the other

three genera, *Plecotus*, *Barbastella* and *Eptesicus*, which are closer to one another than to the former three genera; and *Myotis* and *Murina* each forms a group separately (Uchikawa, in press). Table 3 is the schematic expression of the above.

The mites of the genus *Pteracarus* are conservative. A mite is usually shared by several host bats of the same genus or even of some allied genera. The mites themselves are very small sized and round, and almost the same in the outline. As Dusbábek (1973) paid much attention, the structure of the male genitalia seems to be the best clue to deduce relationships among the mites. Table 4 is a scheme of phylogenetic grouping of the bats of the family Vespertilionidae suggested by similarity or divergence of the genitalia of parasitic mites. Mites infesting the bat genera *Vespertilio* and *Barbastella* are not known yet, and mites occurring on the bats of the genus *Myotis* have not so far been thoroughly clarified. These mites should be located hereafter, and, then, becoming mites may bring much informations on the phylogenetic relationships of the host bats. Although any mite is not found on the bats of the genus *Eptesicus* in Japan, Fain and Lukoschus (1979) have recorded *Pteracarus chalinolobus* from bats of the genera *Chalinolobus*, *Nycticeius* and *Eptesicus* in Australia. Because of a slowness of the mite in evolution, it is reasonable to presume that the bats of the genus *Eptesicus* are associated with mites identical with or very close to *P. chalinolobus*, which bears the genitalia similar

Table 3. Subgrouping of bat genera with types of genital shields of parasitic *Acanthophthirius*

Mite Genital Shield	Host Genus
Type I	<i>Pipistrellus</i> , <i>Nyctalus</i> , <i>Vespertilio</i> , <i>Plecotus</i> , <i>Barbastella</i> , <i>Eptesicus</i>
Type II	<i>Myotis</i>
Type III	<i>Murina</i>

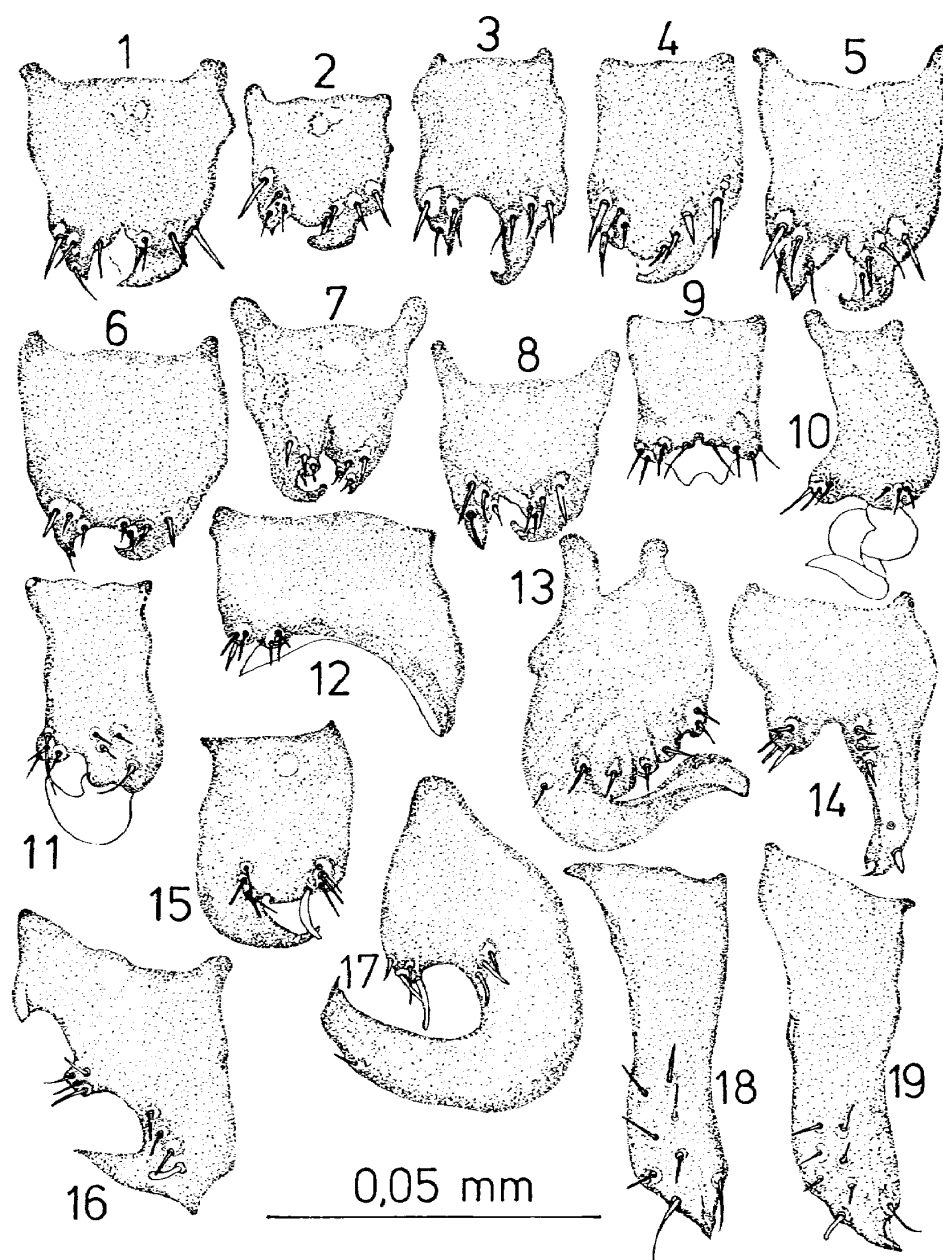


Fig. 3. Male genital shields of *Acanthopthirius* spp. Hosts: 1—*Nyctalus lasiopterus*; 2—*N. furvus*; 3—*Pipisterellus abramus*; 4—*P. endoi*; 5—*Vespertilio orientalis* and *V. superans*; 6—*Plecotus auritus*; 7—*Barbastella leucomelas*; 8—*Eptesicus nilssoni parvus* and *E. japonensis*; 9—*Myotis macrodactylus*; 10—*M. daubentoni*; 11—*M. pruinus*; 12—*M. hosonoi*; 13—*M. macrodactylus*; 14—*M. nattereri*; 15—*M. mystacinus*; 16—*M. frater*; 17—*M. formosus*; 18—*Murina curata*; 19—*M. leucogaster*. The names of the bats are those currently used in Japan. (From Uchikawa, in press).

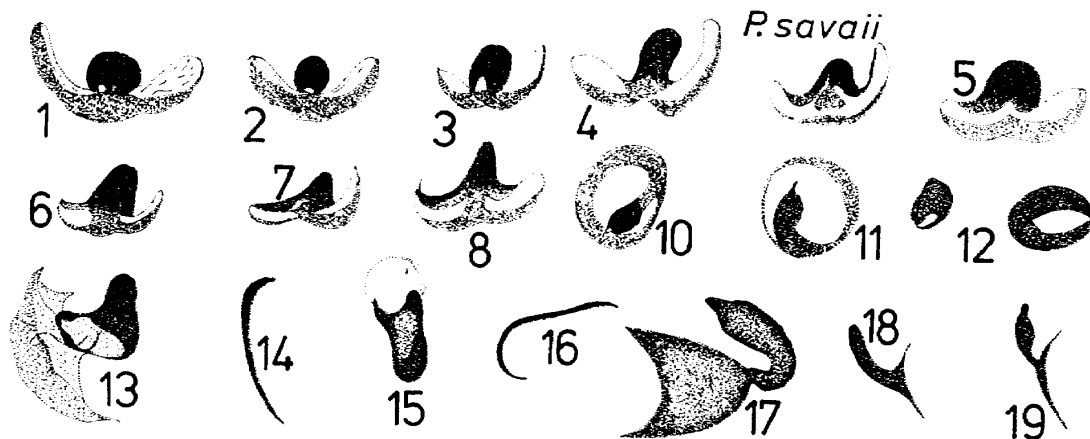


Fig. 4. Female opisthogastric sclerites of *Acanthophthirius* spp. Hosts: As in male genital shield and *P. savaii* shows directly the name of the host. The partner female for the male with the genital shield No. 9 lacks opisthogastric sclerite.

Table 4. Subgrouping of Japanese *Pteracarus* by male genital shield and hosts

Group	Mite species	Host
	—submedianus.....	<i>Plecotus</i>
<i>Pipistrellus</i> gr.	—(chalinolobus).....	<i>Eptesicus</i>
	—pipistrellus .....	<i>Pipistrellus</i> , <i>Nyctalus</i>
	—subsp. daubentoni ..	<div style="display: inline-block; vertical-align: middle;"> <i>Myotis frater</i>  <i>M. nattereri</i>  <i>M. pruinosis</i> </div>
	—minutus —subsp. A. ....	<i>M. hosonoi</i>
<i>Minutus</i> gr.	—subsp. japonicus.....	<i>M. macrodactylus</i>
	—macfarlarei .....	<i>Murina</i>
<i>Miniopteri</i> gr.	—faini .....	<i>Miniopterus</i>

to those of the mites infesting *Pipistrellus* and *Nyctalus*. Thus, the genus *Eptesicus* is added in Table 4. The position of this genus is different from that in Table 3 suggested by the mites of *Acanthophthirius*. In such the case, the authors incline to rely on the information from the mites of the genus *Pteracarus*. Integrating the deductions drawn by the mites of both the genera, *Acanthophthirius* and *Pteracarus*, a suggested phylogeny of the bats of the family Vespertilionidae is shown in Fig. 5. This figure will be improved with becoming

records on mites of the genus *Pteracarus*.

On the other hand, the karyological studies of the bats of the family have already contributed many attractive data to the phylogeny of the bats (*e.g.*, Capanna and Civitelli, 1970). The generic difference in the karyotype is usually discernible, and a suggested phylogeny of the family Vespertilionidae has been presented as in Fig. 6. This suggested phylogenetic scheme well accords with that proposed on the parasitological data as in Fig. 5. The ramification of each evolutionary branch is almost



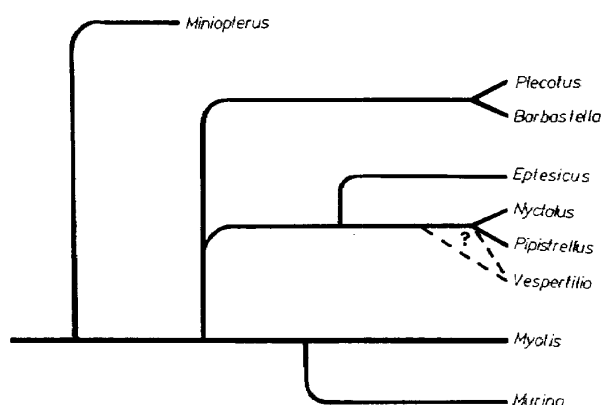


Fig. 5. Phylogeny of Vespertilionidae suggested by the mites of the genera *Acanthophthirius* and *Pteracarus*.

the same in both the figures, though the two genera, *Eptesicus* and *Vespertilio*, are not yet located exactly in either of them. The above deductions from the karyological and parasitological data contrast with the so far constructed phylogeny on the general morphology of the bats (Fig. 7).

As to the species level, the karyotypes of *Pipistrellus* are divergent from species to species, and are thought to be parallel with the general gross anatomy in evolution. It is not *Nyctalus fuscus*, which had been regarded

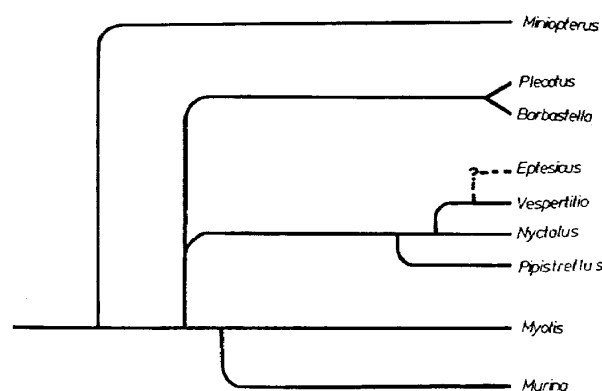


Fig. 6. Phylogeny of Vespertilionidae suggested by the bat karyotypes.

(Imaizumi and Yoshiyuki, 1968) as being close to European *N. noctula*, but *N. lasiopterus* is really close to *N. noctula* in the karyotype (Harada, 1973; Ando *et al.*, 1977). The same is demonstrated with the mites of the genus *Acanthophthirius* (Uchikawa, in press) as pointed out above. *Plecotus auritus* and *Barbastella leucomela* are almost identical with each other and with respective relatives distributed in Europe in the karyotype (Uchida and Ando, 1972; Harada, 1973; Bovey, 1949; Williams *et al.*, 1970). The karyotypes of the two species of the common bats of the genus

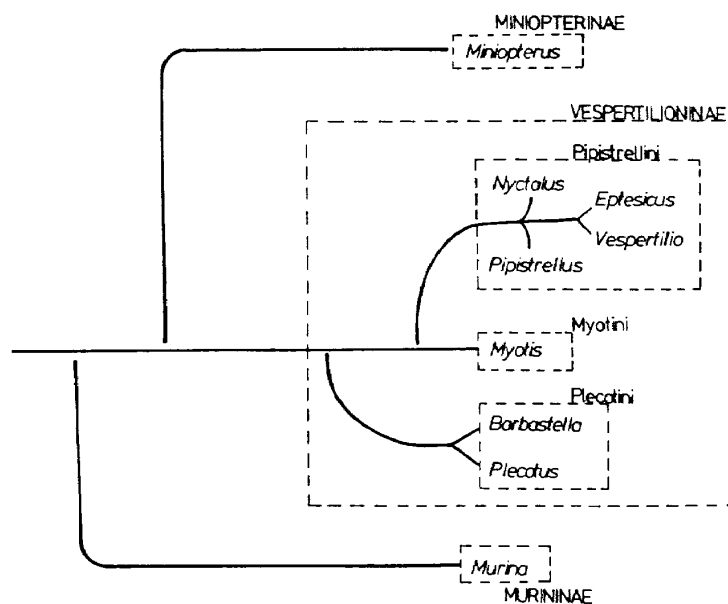


Fig. 7. Phylogeny of Vespertilionidae based on the general morphology.

*Murina* representing the fauna of Japan are considerably different from each other. Many species of the genus *Myotis* bear 22 pairs of chromosomes with 50FN and almost the same karyotype formula (*e.g.*, Baker and Patton, 1967). Evolution in the karyotype of these bats is thought to be much slower as compared with the general anatomical properties or not to be parallel to that of the external morphology of the bats. Karyotypic difference is sometimes found in the structure of a single pair of the key chromosomes. Nevertheless, it is barely possible to find out specific karyotype for the majority of the bats known from Japan, and *M. hosonoi*, *M. macrodactylus*, *M. frater* and *M. pruinus* have been proved to have the particular karyotypes remarkably different from others (Harada and Yoshida, 1978).

As described above separately, the mites of the genera *Acanthophthirius* and *Pteracarus* and karyotypes of the bats are useful in the taxonomy and phylogeny of the family Vespertilionidae. The mites of the genus *Acanthophthirius* are so divergent, that is, strictly host species specific, that they are excellent indicators comparable to or better than the karyotypes in the taxonomy of the family Vespertilionidae. Especially in such the bats as *Myotis* spp. with the least differential morphological properties to discriminating them and with karyotypes alike to one another, the validity of the bats is easily proved through inspecting their mites. The suggested phylogenetic schemes proposed on both the parasitological and karyological studies, Figs. 5 and 6, are comparable to each other as pointed out above. Thus, the mites of the family Myobiidae are regarded as being good indicators not less useful than the karyotypes in the taxonomy and phylogeny of the bats. There are, however, some discordances between the parasitological and karyological data. And many parasitological findings are contradictory to thus far constructed taxonomy of the bats. These problems are left to all biologists, who are concerned in the taxonomical and phylo-

genetic studies of the bats, for further discussions.

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