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Similarity of ectoparasitic gamasid mite (Acari: Parasitiformes: Mesostigmata) communities on small mammals in Yunnan, China*

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Abstract The ectoparasitic gamasid mite species on the body surface of a certain species of small mammal are regarded as a community of mites. The similarity of ectoparasitic gamasid mite communities on 17 species of small mammals was studied in Yunnan Province, China. Based on hierarchical clustering analysis, a similarity comparison of 17 mite communities was conducted with SPSS 11.5 software. Clustering analysis was based on the Pearson correlation coefficient for the nearest neighbor method. The results revealed these communities had high species abundance and diversity. The mite communities on the same genus of small mammals showed a high similarity and are classified into the same cluster. The clustering tendency of most mite communities was concordant with the taxonomic position of the corresponding small mammals on which the mites exist, but some of the mite communities are exceptions. The results suggest that ectoparasitic gamasid mite communities are related to host taxonomy and also possibly to host habitat [*Acta Zoologica Sinica* 53 (2): 208 – 214, 2007].

Key words Acari, Ectoparasitic gamasid mites, Community similarity, Hierarchical clustering analysis

中国云南小兽体表革螨的群落相似性*

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摘 要 运用系统聚类分析方法对中国云南省境内17种主要小型哺乳动物（小兽）体表革螨群落相似性进行研究，每一种小兽体表的所有外寄生革螨被定义为一个相应的革螨群落。运用SPSS 11.5软件完成17种革螨群落的相似性比较。研究结果表明：小兽体表革螨群落结构复杂，物种多样性高；隶属同一个属的小兽体表的革螨群落相似程度高，在系统聚类分析中聚为一类；大多数革螨群落相似性大小与相应小兽宿主在动物分类上的近缘性高低呈现高度一致，但也有一些革螨群落是例外的。这说明小兽体表革螨群落不仅受小兽宿主分类地位的影响，可能还受宿主生境的影响［动物学报 53（2）：208 – 214，2007］。

关键词 蜱螨亚纲 革螨 群落相似性 系统聚类分析

Research on the similarity of communities is an important aspect of community ecology, which helps illustrate the ecological relationship between communities and their environments. Although Guo (1999) and Guo et al. (1996, 2000) have studied the communities of ectoparasites, such as sucking lice, fleas and gamasid mites, and demonstrated the mutual relationship between ectoparasites and their hosts, there are still few systematic reports about ectoparasitic gamasid mite communities on small mammals.

Gamasid mites (Acari, Parasitiformes, Mesostigmata) (Deng et al., 1993) on the body surface of small mammal hosts (especially rodents and insectivores) are an important group of ectoparasites with complicated ecological behaviors. Some are suspected vectors of epidemic hemorrhagic fever and other zoonoses. Some ectoparasitic mites on small mammals may play an important role in harboring the pathogens of some zoonoses such as murine typhus, rabbit fever and plague (Chin and Li, 1991; Guo et al., 1996; Chin, 1999; Sasaki et al., 2002). Up to now, over 300 species of ectoparasitic gamasid mites have been found in China, with more new

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species continually appearing (Deng et al., 1993).

Some research on sucking louse communities and flea communities has been carried out in recent years (Guo et al., 1996; Guo, 1999; Guo et al., 2000). Research on gamasid mite communities, however, has been long neglected. The goal of the present research is to use hierarchical clustering techniques to classify the gamasid mite communities on small mammal hosts, and to interpret the resultant mite-host relationships, that is, to determine if gamasid mite communities on small mammals are related to host taxonomy and possibly to host habitat.

1 Materials and methods

1.1 Field investigations

All the gamasid mites and small mammals were collected from 25 counties, including indoor and outdoor cultivated habitats, in Yunnan Province of China from 1990 to 2004. The 25 counties were Baoshan, Yangbi, Jianchuan, Lijiang, Heqing, Xiangelila, Gongshan, Weishan, Nanjian, Simao, Puer, Dali, Binchuan, Xiangyun, Wenshan, Qiubei, Mengzi, Yuanjiang, Qiaojia, Suijiang, Yingjiang, Gengma, Maguan, Hekou and Menghai. According to a stratified sampling method (Guo et al., 2004), field investigations for collecting mites and small mammals were carried out both indoors (houses and stables, etc.) and outdoorhabitats (cultivated fields, dry lands and bush areas, etc.).

1.2 Collection and identification

Small mammal hosts were randomly captured in 25 counties from 1990 to 2004, using live-capture traps (19.2 cm × 12.5 cm × 8.9 cm) baited with birdseed or peanuts. The small mammals were either artificially killed in the field or taken to a laboratory and anesthetized with 100% ether. Gamasid mites were collected from the small mammals with fine forceps and stored in labeled vials containing 70% ethanol until they were identified. Mites were cleared and mounted on slides (glass-meter manufactory, Haimen city, Jiangsu Province, China) (76.2 × 25.4 mm, 1 – 1.2 mm thick) in Hoyer's medium for identification using a microscope (Deng et al., 1993). Small mammal hosts were mainly identified in the field according to their body shape, size and color, and some measurements such as body length, ear length and length of the hind feet (Chin and Li, 1991; Guo et al., 2000). Some questionable hosts were preserved to verify identification. All small mammal specimens and gamasid mite specimens from this study are deposited in the Institute of Pathogens and Vectors, Dali University.

1.3 Definition of community of mites

The ectoparasitic mite species on a certain species of small mammal were treated as a community. More than 100 individuals for each of 17 small mammal species were sampled during the study, yielding 17 mite communities for study.

1.4 Statisticcal treatment of basic data

To define the communities, for each mite species, the constituent ratio (*Cr*) indicated the percentage of each species of gamasid mite in a certain community. The mite index (*Mi*) indicated the abundance per host individual, and the total mite index (*Mit*) indicated the total individuals of all the mite species on a certain host as the percentage of the total host individuals.

1.5 Measurement of community structure

The measurement of community structure includes four basic parameters: richness (*S*), diversity index (*Dii*), evenness (*E*), and dominance index (*Doi*). The diversity index and evenness are based on Shannon-Wiener's method. The richness, diversity index, evenness and dominance index of every mite community were calculated with the following formulae (Guo et al., 1996; Guo, 1999; Guo et al., 2000):

$$S = \sum S_i,\ Doi = \sum_{i=1}^{s} (N_i/N)^2,$$

$$E = Dii/\ln S,\ Dii = -\sum_{i=1}^{s} (N_i/N)\ln(N_i/N)$$

where S_i represents species i in a certain mite community, N_i and N represent the individuals of mite species i and the total mite individuals, respectively.

1.6 Calculation of similarity

A 17 × 59 primary matrix for the calculation of similarity was formed by 17 communities of mites (17 species of small mammal hosts) and 59 classification variables; 17 mite communities were regarded as 17 classification cases in the cluster analysis. The 59 classification variables included 28 constituent ratios (*Cr*), 28 mite indices (M_i), 1 total mite index (*Mit*) and 2 community parameters, richness (*S*) and diversity index (*Dii*). The primary matrix was then standardized according to the following formula (Gower, 1967; Xu, 1994; Guo et al., 2000; Sun and Xu, 2002):

$$X'_{ab} = (X_{ab} - \bar{X}_b)/\sqrt{\sum (X_{ab} - \bar{X}_b)/(n-1)}$$

$$(a = 1, 2, 3, \cdots\cdots n;\ b = 1, 2, 3, \cdots\cdots m)$$

where X_{ab} stands for the bth numerical figure of the ath classification case in the primary matrix before the standardization, while X'_{ab} represents the corresponding figures after the standardization. The n and m in the foumula represent the number of classification cases and classification variables. On the basis of standardizing the primary matrix, hierarchical clustering analysis based on the Pearson correlation coefficient for the nearest neighbor clustering method was used to compare the similarity between every two classification cases (small mammal hosts); the Pearson correlation coefficient (R_{ij}) was used as the similarity measure. The formula for the Pearson correlation coefficient (R_{ij}) is as follows (Lu, 2004; Pankhurst, 1991; Sneathand and Sokal, 1973; Yu et al., 2004):

$$R_{ij} = \sum(X_{ik} - \bar{X}_i)(X_{ik} - \bar{X}_i) \Big/ \sqrt{\left[\sum_{k=1}^{m}(X_{ik} - \bar{X}_i)\right]\left[\sum_{k=1}^{m}(X_{jk} - \bar{X}_j)^2\right]}$$, and here:

$$\bar{X}_i = (1/m)\sum_{k=1}^{m} X_{ik}, \bar{X}_j = (1/m)\sum_{k=1}^{m} X_{jk}$$

In the above formulae, R_{ij} stands for the correlation coefficient between the ith and jth classification cases (mite communities); X_{ik} represents the kth classification variable of the ith classification case while X_{jk} the kth classification variable of the jth classification case in the standardized primary matrix; m represents the number of the classification variables. All the calculations for hierarchical cluster analysis were carried out with SPSS 11.5 software.

2 Results

2.1 Collection of small mammals and gamasid mites

A total of 10 803 small mammals were captured in Yunnan Province of China and identified as 9 families, 29 genera, and 53 species in five orders (Rodentia, Insectivora, Scandentia, Lagomorpha and Chiroptera). Of these, the 17 most abundant species including 10 098 individual were selected for study, consisting of mite communities on 17 species small mammals (Table 1). These included 13 species of rodents (Rodentia), 3 of shrews soricidae (Insectivora) and 1 tree shrew (Scandentia).

A total of 68 571 gamasid mites collected from the body surface of 51 species of small mammal hosts were identified as 10 families, 33 genera and 112 species, with 65 404 individuals of mites collected from 17 species of small mammals in 4 families, 12 genera and 29 species. The mites from the small mammals, together with their corresponding total mite indices (*Mit*), are also shown in Table 1. The total mite index is a component of the primary matrix in hierarchical cluster analysis.

2.2 Community structure and primary matrix

The primary matrix for calculating community similarity of the mites from 17 small mammal species consisted of 17 classification cases and 59 classification variables. It included 1 total mite index (*Mit*), 28 constituent ratios (*Cr*) of dominant mite species, 28 mite indices (*Mi*) of dominant mite species, and two community parameters, richness (*S*) and diversity index (*Dii*). The 17 classification cases and 59 classification variables formed a 17×59 primary matrix.

The results show that gamasid mites on the body surface of these small mammals was high in species richness, with a high diversity index. The diversity indices (Shannon-Wiener's diversity indices) for most communities of mites were greater than 1. The diversity indices for *Rattus flavipectus*, *Mus pahari* and *Rattus nitidus* were the highest, 53.89%, 44.67% and 27.80%, respectively. *Laelaps nuttalli* (Hirst, 1915) and *Laealps echidninus* (Berlese, 1887) were the most prominent species in the communities on *Rattus flavipectus*, *Rattus norvegicus* and *Rattus nitidus*. *Laelaps turkestanicus* (Lange, 1955) and *Laelaps traubi* (Domrow, 1962) were the more prominent species in the communities on *Niviventer confucianus* and *Niviventer fulvescens*. The constituent ratios and mite indices of the above mite species were the highest in comparison with the other mite species (Tables 2 – 4). The results revealed that most small mammals had two or more species of gamasid mites on their body surface and that the community structure of gamasid mites was quite diverse.

Table 1 The collected mite individuals and total mite indices from 17 main species of small mammal hosts

Community of mites		Mite individuals	Total mite indices (*Mit*)
Name of hosts	Individuals		
Rattus flavipectus	3 765	18 123	481.35
Apodemus chevrieri	1 451	2 478	170.78
Rattus norvegicus	1 123	5 417	482.37
Mus pahari	674	12 963	1 923.29
Eothenomys miletus	440	945	214.77
Rattus nitidus	359	10 131	2 822.01
Mus caroli	352	2 175	617.90
Rattus rattus sladeni	250	802	320.80
Suncus murinus	242	156	64.46
Crocidura attenuata	231	111	48.05
Tupaia belangeri	221	79	35.75
Apodemus draca	213	324	152.11
Niviventer confucianus	194	3 089	1 592.27
Niviventer fulvescens	182	5 998	3 295.60
Mus musculus	162	150	92.59
Anowrosorex squamipeis	134	2 389	1 782.84
Apodemus latronum	105	74	70.48
Total	10 098	65 404	647.69

2.3 Similarity of gamasid mite communities

On the basis of the primary matrix and its standardization, similarities between every pair of classification cases (small mammal hosts) were calculated. A correlation coefficient (R_{ij}) was used to measure community similarity. Finally a dendrogram formed through hierarchical cluster analysis was used to show affinitive relationship of the communities (Fig.1).

The dendrogram shows that the clustering tendency of most mite communities was concordant with the taxonomic position of the corresponding small mammals where the mites existed. For example, the mitecommunities on *Rattus norvergicus*, *Rattus flavipectus*,

Table 2 Contituent ratios of 29 dominant mite species on host species

29 dominant mite species	*Rattus flavipectus*	*Apodemus chevrieri*	*Rattus norvegicus*	*Mus pahari*	*Eothenomys miletus*	*Rattus nitidus*	*Mus caroli*	*Rattus rattus sladeni*	*Suncus murinus*	*Crocidura attenuata*	*Tupaia belangeri*	*Apodemus draca*	*Niviventer confucianus*	*Niviventer fulvescens*	*Mus musculus*	*Anourosorex squamipeis*	*Apodemus latronum*
Laelaps nuttalli	16.31	0.23	3.29	0.00	0.01	7.92	0.27	0.37	0.07	0.04	0.00	0.19	0.02	0.02	0.02	0.05	0.03
Laelaps echidninus	7.83	0.44	2.26	0.03	0.02	6.75	0.01	0.28	0.01	0.02	0.00	0.07	2.09	2.09	0.01	0.08	0.00
Laelaps guizhouensis	0.00	0.07	0.01	15.27	0.00	0.02	0.01	0.00	0.00	0.00	0.00	0.08	0.00	0.00	0.00	0.00	0.00
Laelaps turkestanicus	0.11	0.13	0.01	0.04	0.00	0.00	0.05	0.25	0.00	0.01	0.01	0.05	3.98	3.98	0.00	0.00	0.00
Laelaps traubi	0.13	0.06	0.00	0.00	0.00	0.01	0.00	0.01	0.00	0.00	0.04	0.00	3.00	3.00	0.00	0.00	0.00
Ornithonyssus bacoti	1.97	0.01	2.28	0.00	0.00	0.19	0.00	0.02	0.02	0.02	0.01	0.00	0.00	0.00	0.16	0.00	0.00
Dipolaelaps anourosorecis	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.01	0.00	0.01	0.00	0.00	0.00	3.42	0.00
Laelaps algericus	0.00	0.00	0.01	0.03	0.00	0.00	2.87	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.04	0.00	0.00
Laelaps paucisetosa	0.00	0.01	0.00	2.77	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Laelaps chini	0.00	0.07	0.01	0.06	0.93	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.0	00.01
Hirstionyssus sunci	0.20	0.54	0.19	0.09	0.02	0.21	0.01	0.14	0.02	0.02	0.02	0.01	0.00	0.00	0.00	0.07	0.02
Laelaps xingyiensis	0.00	0.00	0.00	1.34	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Eulaelaps shanghaiensis	0.00	1.15	0.00	0.00	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02
Eulaelaps dremomydis	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00
Proctolaelaps pygmaeus	0.25	0.06	0.13	0.03	0.01	0.31	0.03	0.02	0.02	0.03	0.00	0.00	0.01	0.01	0.00	0.00	0.00
Haemogamasus oliviformis	0.00	0.16	0.02	0.02	0.18	0.00	0.00	0.01	0.00	0.00	0.00	0.01	0.01	0.01	0.00	0.01	0.04
Laelaps liui	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Laelaps jettmari	0.00	0.46	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.00
Hypoaspis pavlovskii	0.02	0.09	0.01	0.02	0.08	0.03	0.01	0.03	0.02	0.00	0.00	0.01	0.00	0.00	0.00	0.01	0.00
Tricholuelaps myonysognathus	0.33	0.00	0.02	0.00	0.00	0.01	0.01	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Haemolaelaps glasgowi	0.02	0.09	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
Liponyssoides muris	0.33	0.00	0.00	0.00	0.00	0.01	0.00	0.01	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00
Laelaps fukienensis	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.01	0.00	0.00	0.00
Eulaelaps substabularis	0.00	0.13	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.05	0.02	0.02	0.00	0.00	0.00
Hypoaspis miles	0.07	0.02	0.00	0.03	0.01	0.00	0.04	0.01	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Hypoaspis lubrica	0.12	0.01	0.01	0.01	0.00	0.00	0.00	0.01	0.02	0.00	0.00	0.00	0.01	0.01	0.00	0.00	0.00
Haemogamasus dorsalis	0.00	0.00	0.00	0.04	0.13	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Haemogamasus gongshanensis	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Androlaelaps singularis	0.01	0.02	0.02	0.03	0.00	0.01	0.01	0.03	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

Table 3 Mite indices of 29 dominant mite species on host species

29 dominant mite species	*Rattus flavipectus*	*Apodemus chevrieri*	*Rattus norvegicus*	*Mus pahari*	*Eothenomys miletus*	*Rattus nitidus*	*Mus caroli*	*Rattus rattus sladeni*	*Suncus murinus*	*Crocidura attenuata*	*Tupaia belangeri*	*Apodemus draca*	*Niviventer confucianus*	*Niviventer fulvescens*	*Mus musculus*	*Anowrosorex squamipeis*	*Apodemus latronum*
Laelaps nuttalli	283.32	10.48	191.81	0.00	0.91	1 442.90	50.85	96.40	19.01	12.55	0.91	56.81	15.98	8.79	6.17	23.88	16.19
Laelaps echidninus	136.10	19.92	131.70	3.26	3.41	1 229.81	1.70	74.00	3.72	6.93	1.36	20.66	333.51	749.45	4.94	38.06	0.00
Laelaps guizhouensis	0.03	3.38	0.45	1 482.20	0.68	3.62	2.56	0.00	0.41	0.87	0.00	23.47	2.58	0.00	0.62	0.00	0.00
Laelaps turkestanicus	1.83	6.00	0.80	3.86	0.00	0.84	8.81	66.40	0.83	2.16	2.26	14.55	749.48	1 431.87	0.00	0.75	0.00
Laelaps traubi	2.28	2.76	0.00	0.00	0.45	2.23	0.00	3.20	0.00	0.00	10.86	0.94	424.74	1 078.57	0.00	0.00	0.00
Ornithonyssus bacoti	34.16	0.28	132.68	0.00	0.00	34.54	0.28	5.60	5.37	4.33	3.62	0.00	0.00	0.00	63.58	0.00	0.00
Dipolaelaps anourosorecis	0.00	0.62	0.00	0.30	0.00	0.00	0.00	0.40	3.72	1.73	0.00	2.35	0.52	0.00	0.00	1 670.15	0.00
Laelaps algericus	0.05	0.00	0.80	3.12	0.00	0.00	533.24	0.00	0.00	0.00	0.00	0.00	0.00	0.00	14.20	0.00	0.00
Laelaps paucisetosa	0.00	0.41	0.00	268.40	0.00	0.56	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.55	0.62	0.00	0.00
Laelaps chini	0.08	3.24	0.45	5.34	138.64	2.23	0.57	0.40	0.41	1.30	0.45	0.00	1.03	0.00	0.00	0.00	4.76
Hirstionyssus sunci	3.48	24.53	11.04	9.05	2.95	38.72	1.14	37.60	4.13	5.19	4.98	1.88	3.09	1.65	0.00	32.09	10.48
Laelaps xingyiensis	0.03	0.00	0.00	130.12	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Eulaelaps shanghaiensis	0.00	51.83	0.18	0.00	4.32	0.00	0.00	0.80	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	9.52
Eulaelaps dremomydis	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.26	0.00	0.52	0.00	0.00	0.00	0.00
Proctolaelaps pygmaeus	4.30	2.76	7.30	2.67	2.05	55.99	5.11	5.20	5.79	9.09	0.00	1.41	1.55	3.85	1.23	1.49	0.00
Haemogamasus oliviformis	0.00	7.10	1.16	1.78	27.05	0.56	0.00	3.20	0.41	0.00	0.00	3.29	1.03	3.30	0.00	4.48	25.71
Laelaps liui	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4.12	0.00	0.00	0.00	0.00
Laelaps jettmari	0.00	20.95	0.09	0.00	0.68	0.00	1.42	0.00	0.00	1.30	0.00	7.04	0.00	0.00	0.00	0.00	0.95
Hypoaspis pavlovskii	0.37	3.93	0.62	1.93	12.27	5.57	1.14	8.40	4.55	0.87	1.36	3.76	1.55	1.65	0.00	5.97	2.85
Tricholuelaps myonysognathus	5.79	0.21	0.89	0.00	0.00	1.11	1.42	0.40	5.79	0.00	0.00	0.00	1.03	0.00	0.00	0.00	0.00
Haemolaelaps glasgowi	0.29	3.86	0.27	0.00	0.45	0.28	0.00	0.80	0.00	0.00	0.00	0.94	0.00	1.65	0.62	2.99	0.00
Liponyssoides muris	5.71	0.00	0.27	0.00	0.00	1.11	0.00	2.00	0.00	0.00	6.79	0.00	0.00	0.00	0.62	0.00	0.00
Laelaps fukienensis	0.00	0.00	0.00	0.30	0.68	0.00	0.00	0.00	0.00	0.00	0.00	0.00	43.30	3.85	0.00	0.00	0.00
Eulaelaps substabularis	0.00	5.86	0.00	0.45	0.23	0.28	0.00	1.60	0.00	0.00	0.00	14.55	0.00	6.59	0.00	0.00	0.00
Hypoaspis miles	1.22	0.90	0.09	3.26	0.91	0.00	7.95	3.20	2.48	0.43	0.00	0.00	1.55	0.55	0.00	0.75	0.00
Hypoaspis lubrica	2.05	0.83	0.71	0.59	0.00	0.00	0.57	2.40	4.55	0.43	0.45	0.00	2.58	2.75	0.00	0.00	0.00
Haemogamasus dorsalis	0.03	0.00	0.00	3.86	18.86	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.55	0.00	0.00	0.00
Haemogamasus gongshanensis	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Androlaelaps singularis	0.24	0.96	1.07	2.82	0.23	1.67	1.14	96.40	3.31	0.87	0.45	0.47	4.12	0.00	0.00	2.24	0.00

Table 4　Community structure parameters of gamasid mite on the main hosts

Parameters of community	*S*	*Dii*	*E*	*Doi*
Rattus flavipectus	19	53.89	18.3	331.61
Apodemus chevrieri	21	2.46	0.81	2.18
Rattus norvegicus	19	0.7	0.24	21.2
Mus pahari	18	44.67	15.45	242.77
Eothenomys miletus	17	4.77	1.68	0.93
Rattus nitidus	17	27.8	9.81	108.47
Mus caroli	15	1.98	0.73	8.32
Rattus rattus sladeni	19	7.84	2.66	0.3
Suncus murinus	15	0.89	0.33	0.01
Crocidura attenuata	14	0.67	0.25	0
Tupaia belangeri	12	0.5	0.2	0
Apodemus draca	14	1.31	0.5	0.05
Niviventer confucianus	18	1.28	0.44	7.53
Niviventer fulvescens	15	9.89	3.65	29.23
Mus musculus	9	0.58	0.27	0.03
Anowrosorex squamipeis	11	3.49	1.46	11.72
Apodemus latronum	7	4.53	2.33	0.00

Rattus rattus sladeni and *Rattus nitidus* were clustered together in the same group in the dendrogram. The mite communities on *Apodemus chevrieri* and *Apodemus draca* (belonging to the same genus, *Apodemus*) merged into the same group and then with *Anowrosorex squamipeis* (belonging to order Insectivora). The mite community on *Apodemus latronum* (belonging to *Apodemus*), however, was an exception. The mite communities on *Niviventer confucianus* and *Niviventer fulvescens* were in the same group. The mite community on *Tupaia belangeri* (belonging to order Scandetia) was far removed from other mite communities in the dendrogram.

Some mite communities, however, were not consistent with the taxonomic affinities of their corresponding hosts in the dendrogram. For example, the mite community on *Apodemus latronum* was quite different from those on *Apodemus chevrieri* and *Apodemus draca*, and they did not cluster in the same group. The mite communities on the three species of Mus did not cluster in the same group.

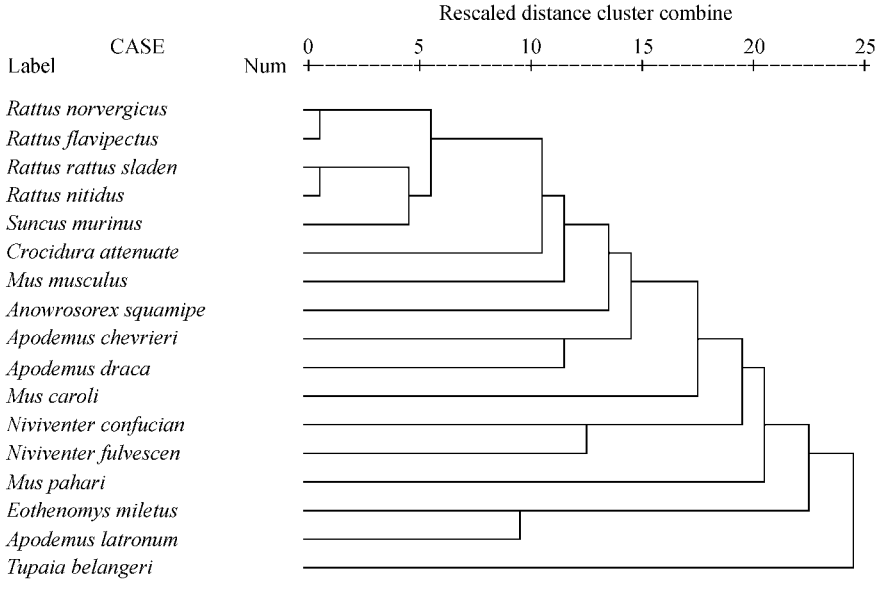

Fig.1　Cluster dendrogram of the mite communities on 17 main species of small mammal hosts in hierarchical cluster analysis

3　Discussion

The results in this paper reveal that the species of gamasid mites (112) are much greater in number than the species of their hosts (53). Most small mammals have two or more species of gamasid mites on their body surface. The diversity indices for most small mammals are greater than 1, and the community structure of gamasid mites is characterized by abundance and high species diversity.

Our research shows that the mite communities on *Rattus norvergicus*, *Rattus flavipectus*, *Rattus rattus sladeni* and *Rattus nitidus* have a higher similarity than any of the others, and they cluster in the same group in the dendrogram, Probably because of similar evolutional relationship.

Some mite communities, however, are not consistent with the taxonomic affinities of their corresponding hosts. For example, the mite community on *Apodemus latronum* is quite different from those on *Apodemus chevrieri* and *Apodemus draca*, and do not cluster in the same group in the dendrogram. The mite communities on *Mus caroli*, *Mus pahari* and *Mus musculus* also do not cluster in one group. Their habitats varie from each other although these three species of mice (belonging to the same genus) are phylogenetically close. *Mus caroli* usually lives in outdoor

habitats (cultivated fields, dry lands and bush areas, etc.), *Mus pahari* usually lives in woodland habitats (brushy forests and green broadleaved forests, etc.), whereas *Mus musculus* is typical of extensively inhabitable mice. On the other hand, their parasite load vary from each other, the habitats where the hosts live also possibly influence their parasite load. For example, *Mus pahari* has a higher parasite load (13 species of mites), *Laelaps guizhowensis* is the dominant species (15.27%), followed by *L. pancisetosa* (2.77%) and *L. xigytensis* (1.34%). *Mus caroli* and *Mus musculi* have none of these. *Mus caroli* has a lower parasite load (11 species of mites) than *Mus pahari*, The main mite (over 1.0%) of *Mus caroli* is *L. algericus* (2.87%), while *M. musculus* has very depauperate mite fauna, with only 4 mite species, none of them dominant. *O. bacoti* is the main mite species on *Mus musculus*, but it is not even found on either of the other two *Mus*. The reason that *M. musculus* is so distant from both other *Mus* species is because it is depauperate. The difference in mite host habitats and their parasite load might explain the above results. For some closely related hosts, their habitat and parasite load differences may lead to differences in the gamasid mites.

The results of this research reveal that the gamasid mite communities on their hosts is similar if the taxonomic position and habitats of the hosts are similar. This suggests that the types of gamasid mite communities on small mammals are influenced not only by their hosts but also by the habitats where the hosts live. The host factor may be more important than the habitat factor.

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References

Chin TH, Li KC, 1991. The Anoplura and Siphonaptera of Guizhou Guiyang, China. Guizhou: Guizhou Science and Technology Publishing House, 155 – 388 (In Chinese).

Chin DX, 1999. Taxonomy and Fauna of Sucking Lice (Anoplura) in China. Beijing: Science Press, 1 – 132 (In Chinese).

Deng GF, Wang DQ, Gu YM, 1993. Economic Insect Fauna of China. Vol. 40. Acari: Dermanyssoideae. Beijing: Science Press (In Chinese).

Gower JC, 1967. Multivariate analysis and multidimensional geometry. Statistician 17: 13 – 28.

Guo XG, Qian TJ, Guo LJ, Dong WG, 2004. Similarty comparison and classification of sucking louse communities on some small mammals in Yunnan, China. Entomologia Sinica 11 (3): 199 – 209.

Guo XG, Gong ZD, Qian TJ, Feng XG, Duan XD, Li W, Zhang XK, 2000. The comparison between flea communities on ten species of small mammals in the foci of human plague in Yunnan, China. Entomologia Sinica 7 (2): 169 – 177.

Guo XG, 1999. Cluster of ectoparasitic gamasid mites and their small mammal hosts in different habitat regions in western Yunnan. Systematic and Applied Acarology 4: 39 – 48.

Guo XG, Ye BH, Gu YM, Chen YM, 1996. Studies on the similarity and classification of gamasid mite communities on small mammals in the west of Yunnan Province. Chinese Journal of Parasitology & Parasitic Diseases 14 (1): 42 – 45 (In Chinese).

Lu WD, 2004. SPSS (Statistical Package for the Social Science) for Windows Statistical Analysis. 2nd edn. Beijing: Publishing House of Electronics Industry.

Pankhurst RJ, 1991. Practical taxonomic computing. Cambridge: Cambridge University Press, 110 – 161.

Sasaki T, Kobayashi M, Agui N, 2002. Detection of *Bartonella quintana* from body lice (Anoplura: Pediculidae) infesting homeless people in Tokyo by molecular technique. Journal Medical Entomology 39: 427 – 429.

Sneath P, Sokal R, Translated by Zhao Tie-Qiao, 1973. Numerical Taxonomy: The Principles and Practice of Numerical Classification. Beijing: Science Press (In Chinese).

Sun ZQ, Xu YY, 2002. Medical Statistics. Beijing: Science Press (In Chinese).

Xu KX, 1994. Numerical Taxonomy. Beijing: Science Press (In Chinese).

Yu H, Xiao SG, Li HT, 2004. Practice of numerical taxonomic on insect taxonomy in China. Journal of Henan Forestry Science and Technology 24: 32 – 34 (In Chinese).

邓国藩, 王敦清, 顾以铭, 1993. 中国经济昆虫志. 第四十册, 蜱螨亚纲, 皮刺螨总科. 北京: 科学出版社.

金大雄, 李贵真, 1991. 贵州吸虱类、蚤类志. 贵阳: 贵州科技出版社, 155 – 388.

金大雄, 1999. 中国吸虱的分类和检索. 北京: 科学出版社, 1 – 132.

郭宪国, 叶炳辉, 顾以铭, 陈渊民, 1996. 云南西部小兽革螨群落相似性及分类研究. 中国寄生虫学与寄生虫病杂志 14 (1): 42 – 45.

卢纹岱, 2004. 统计分析软件 SPSS for Windows 统计分析 (第二版). 北京: 电子工业出版社.

P. 史尼斯, R. 索卡尔 (赵铁桥译), 1973. 数值分类学——数值分类的原理和应用. 北京: 科学出版社.

孙振球, 徐勇勇, 2002. 医学统计学. 北京: 人民卫生出版社.

徐克学, 1994. 数值分类学. 北京: 科学出版社.

喻 泓, 肖曙光, 李海涛, 2004. 数值分类在我国昆虫分类工作中的应用. 河南林业科技 24 (4): 32 – 34.