Zoological Studies **35**(3): 178-187 (1996)

Zoological Studies

Morphometric Analysis between *Spinacus pagonis* Keifer and Its Affined Species (Acarina: Eriophyidae)

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(Accepted January 17, 1996)

Kun-Wei Huang, Tsan Huang and Chin-Fah Wang (1996) Morphometric analysis between *Spinacus pagonis* Keifer and its affined species (Acarina: Eriophyidae). *Zoological Studies* **35**(3): 178-187. Three species of eriophyid mites were found coexisting on leaves of mango trees in Tapu, Chiai, which is located in southwestern Taiwan. These mites were identified as *Cisaberoptus kenyae* Keifer, *Spinacus pagonis* Keifer (short setae type), and *Spinacus longinquus* sp. nov. (long setae type). Since the latter 2 species are similar to each other, morphometric analyses were used to discriminate between them. Distances between homologous structures (microtubercles) were measured and the ratio of these variables were calculated. Approaches used included cluster analyses, the principal component analysis, the minimum spanning tree, Burnaby's method for size adjustment, and non-metric multidimensional scaling. Males are distinguishable from females by size variables. The long setae type is separate from the short setae type by shape variables. However, the same variable could not be used to distinguish differences in sex and age of these 2 types. The major differences between the 2 *Spinacus* species are the length of dorsal setae (*S. pagonis* = 6-7, *S. longinquus* = 11-18), the distance between the 3rd coxal tubercles (*S. pagonis* = 18-27, *S. longinquus* = 19-23), and the distance between the 3rd ventral tubercles (*S. pagonis* = 12-15, *S. longinquus* = 11-15). This new species, *S. longinquus* was confirmed by the results of the above analyses.

Key words: Morphometric, Eriophyid mites, Homolog, New species, Taiwan.

Ten species of eriophyoid mites infesting mango trees have been recorded worldwide (Amrine and Stasny 1994). Among these, 3 have previously been reported from Taiwan. They are *Cisaberoptus kenyae*, *Tegonotus mangiferae* and *Tegonotus paramanfigerae* (Huang et al. 1989). We collected the eriophyoid mites on the leave trees at Tapu, Chiayi in 1994 and found 3 phenons coexisting. Preliminary identification indicated that 1 phenon belonged to *Cisaberoptus kenyae*, another belonged to *Spinacus pagonis* (a new record in Taiwan), and the other was close to *S. pagonis*. The latter differed from *S. pagonis* in the length of dorsal setae and the structure of the network. In this study, we temporarily defind this phenon as the "long setae type" of *S. pagonis* in contrast to the "short setae type" of *S. pagonis*, as described by Keifer (1979). *S. pagonis* was first recorded on Is. Samoa, and its occurrence in Taiwan is the 2nd record in the world.

The diagnostic characters of the length of dorsal setae and the structure of the network well support the idea that the long setae type should be a new species. However, it was necessary to use mass characters to objectively delimit the species boundary and to avoid misidentification. In this study, specimens were clustered into 2 types a priori according to the dorsal setae length. Different multivariate statistical methods were applied by measuring the data base of the homologous structures to prove that these 2 types are true separate species.

Few papers have dealt with the morphometric analysis of eriophyoid mites. The main reason is that the study of eriophyoid mites is still in the developing stages. Many new species of eriop-

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hyoid mites are being discovered every year. Additionally, scant knowledge of these species also hinders comparative studies. The eriophyoid mites are so tiny that it is difficult to distinguish the species by a few nominal characters. For example, there are about 800 species of the genus *Aceria* (Amrine and Stasny 1994). Most of them are distinguished by the structure of the network, and apt to cause confusion.

Morphometrics offers another way to distinguish the eriophyoid mites by analysis of assembled variables. In fact, it is useful to make morphometric measurements of the eriophyoid mites, because the microtubercles of eriophyoid mites are the homolog. Furthermore, the microtubercles are easy to inspect and quite stable in specific criteria.

The main aim of the present investigation is to try re-clustering the different data sets (size and shape) by a variety of techniques in order to see which combinations of the data set and the method give the best result that may provide a reliable means for species identification. This should also be of practical value in the taxonomy of eriophyoid mites.

All measurements in this study are given in micrometers (μm).

MATERIALS AND METHODS

Specimens

All 23 specimens used in this study were collected from the same mango tree at Tapu, Chiai, southwestern Taiwan. The specimens were oriented horizontally and mounted on slides for direct measurement. A priori grouping of specimens was based on the relative lengths of dorsal setae. There were 18 specimens belonging to the long setae type, including 12 females (F1-F12), 5 males (M1-M5) and one nymph (N) (Figs. 1a, 1b, 11a); the remaining 5 specimens belonged to the short setae type, including 3 female (F13-F15) and 2 male (M6-M7) (Figs. 1c, 11b).

Measuring method

To select the measuring point (landmark) it was necessary to base on the homolog, so that measurements would have the same standard. The most useful measurable homologous structure of the eriophyoid mites is probably the microtubercles, because they are common to all eriophyoid mites. Actually, some species lack the dorsal or the 1st or 2nd ventral setal tubercles which may be a result of reduction during the evolutionary process. In this study, 9 pairs of setal tubercles, as well as body, the width and the length of the dorsal setae were measured (Fig. 2). A total of 17 variables (M1 data set, Table 1) were selected for this study. The ratios between the variables were calculated except these for the high correlation variables (such as Gt-Gt/Sw and Gt-Gt/Lt-Lt). The total number of ratio values were 29 which were derived from 17 measured value (M2 data set, Table 2). The ventral setae length, as used by traditional taxonomists, was not accepted in this study, since such a character varies within the specimens themselves and may be affected by the preparation of slides. The length of dorsal setae was accepted because it is the main character used to distinguish these 2 type. The measuring process used in this studty follows that reported by Huang (1991).

Analytical methods

The analytical data were sorted into 2 sets:

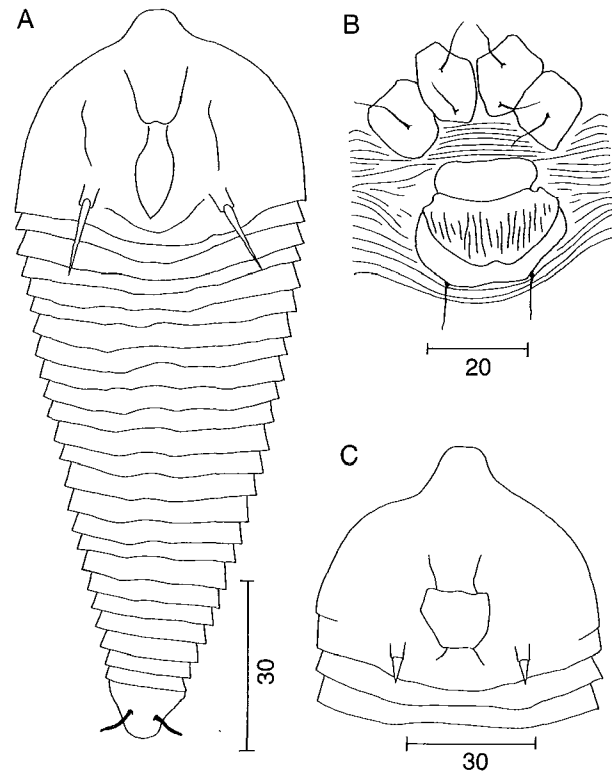

Fig. 1. *Spinacus longinquus* sp. nov.: A, Dorsum; B, Female genitalia and coxae. *Spinacus pagonis* Keifer: C, Shield. (units = μm)

the measured data set (M1 set), and the ratio data set (M2 set). These 2 data sets were standardized before multivariate analysis. The analytical methods included SHAN clustering, minimum spanning tree, principal component analysis, nonmetric multidimensional scaling (in the NTSYS program package), and Burnaby's method for size adjustment according to N. MacLeod (Rohlf and Bookstein 1990).

RESULTS AND DISCUSSION

Clustering analysis

The M1 data set was used with the average taxonomic distance coefficient (DIST) and UPGMA method to produce a phenogram (Fig. 3). The phenogram shows that the OTUs (Operational Taxonomic Units) fall into 3 groups, named M1a, M1b, and M1c. M1a consists of OTUs that are all females; M1b consists of a single nymph (N); and M1c consists of OTUs that are all males. The directly measured data (M1) best represent the meaning of size. The results indicate that the female, male, and nymph can clearly be distinguish by size. The 2 types of *S. pagonis* show a difference in size by sex and age from the clustering analysis.

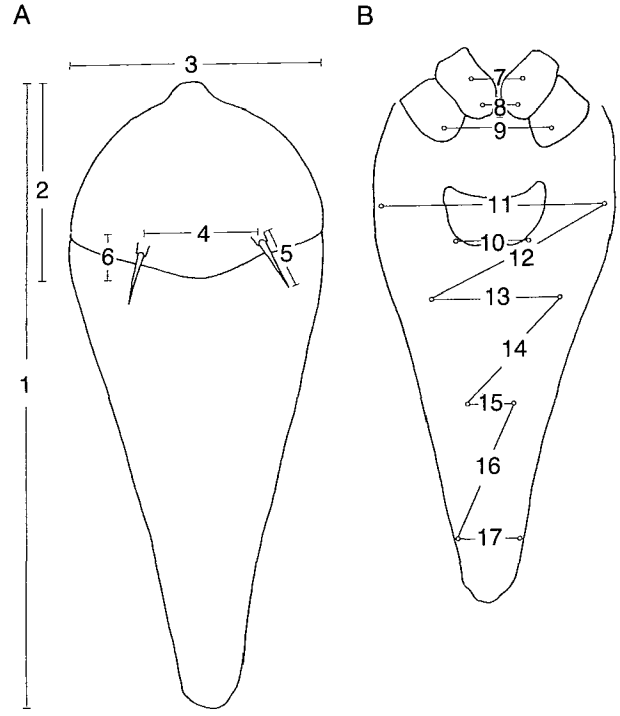

Fig. 2. Outline drawings of *Spinacus longinquus* showing the variables used for comparing the morphometric data: A, dorsal view; B, ventral view. The numbers representing the variables are listed in Table 1.

Table 1. Seventeen variables of the M1 data set and their abbreviations

1.	Body length (Bl)
2.	Shield length (Sl)
3.	Shield width (Sw)
4.	Distance between the dorsal tubercles (Dt-Dt)
5.	Dorsal setae length (Ds.l)
6.	Distance from dorsal tubercle to rear margin of shield (Dt-Sr)
7.	Distance between the 1st coxal tubercles (Ct1-Ct1)
8.	Distance between the 2nd coxal tubercles (Ct2-Ct2)
9.	Distance between the 3rd coxal tubercles (Ct3-Ct3)
10.	Distance between the genital tubercles (Gt-Gt)
11.	Distance between the lateral tubercles (Lt-Lt)
12.	Distance from lateral tubercle to the 1st ventral tubercle (Lt-Vt1)
13.	Distance between the 1st ventral tubercles (Vt1-Vt1)
14.	Distance from the 1st to 2nd ventral tubercle (Vt1-Vt2)
15.	Distance between the 2nd ventral tubercles (Vt2-Vt2)
16.	Distance from the 2nd to 3rd ventral tubercle (Vt2-Vt3)
17.	Distance between the 3rd ventral tubercles (Vt3-Vt3)

Table 2. Twenty-nine variables[a] of the M2 data set

1.	Sl/Bl	16.	Vt3-Vt3/Sw
2.	Dt-Dt/Sw	17.	Lt-Vt1/Bl
3.	Ct1-Ct1/Ct2-Ct2	18.	Lt-Vt1/Sl
4.	Ct2-Ct2/Ct3-Ct3	19.	Vt1-Vt2/Bl
5.	Lt-Lt/Vt1-Vt1	20.	Vt1-Vt2/Sl
6.	Vt1-Vt1/Vt2-Vt2	21.	Vt2-Vt3/Bl
7.	Vt2-Vt2/Vt3-Vt3	22.	Vt2-Vt3/Sl
8.	Lt-Vt1/Vt1-Vt2	23.	Lt-Vt1/Sw
9.	Vt1-Vt2/Vt2-Vt3	24.	Vt1-Vt2/Sw
10.	Ct1-Ct1/Sw	25.	Vt2-Vt3/Sw
11.	Ct2-Ct2/Sw	26.	Gt-Gt/Vt1-Vt1
12.	Ct3-Ct3/Sw	27.	Dt-Sa[b]/Dt-Sr
13.	Lt-Lt/Sw	28.	Ds.l
14.	Vt1-Vt1/Sw	29.	Sl/Sw
15.	Vt2-Vt2/Sw		

[a]The abbreviations are in Table 1.
[b]Anterior margin of shield.

The M2 data set used the product-moment correlation coefficient (CORR) and UPGMA method to produce a phenogram (Fig. 4). The phenogram fall into 3 groups, named M2a, M2b, and M2c. M2a consists of OTUs that are all males (but excluding M7); M2b consists of all females of the short setae type, a male of the same type and a nymph (N) of the long setae type; and M2c consists

of OTUs that are all females of the long setae type. It is interesting to compare Fig. 3 with Fig. 4. The M2 data set is a ratio transformation from the M1 data set. The phenogram of Fig. 4 separates the females of the short setae type from those of the long type, but that of Fig. 3 does not. This may indicate that the ratios simultaneously stand for both the shape factor and the size factor. So the M2 data set can separate the females of the long setae type from those of the short type, but can not separate sex or age well, because sex and age are size factors.

Principal component analysis

The 17 character loadings and eigenvalues of the M1 data set are given in Table 3. The combination of the first 3 components explains 77.2 % of the sample variance. The amount of phenetic variation which is explained by the 1st component (PC1) is 60.8 % and appears to be heavily influenced by overall size as indicated by the invariably positive and high loadings of the 1st component, except characters 5, 7, and 17 with low loadings. Humphries et al. (1981) pointed out when the character loadings of PC1 were not equal "thus PC1 is not strictly 'size', but contains information about allometric respects of shape as well." In this study, the low loadings of PC1 are the length of dorsal setae (character 5), the distance between the 1st coxal tubercles (character 7), and the distance between the 3rd ventral tubercles (character 17). The last 2 characters are similar to the anterior part and posterior part of the body form, respectively. For example, when the 2 loadings are low, then the body form of this eriophyoid mite is worm-like; when the loading of character 7 is high and that of character 17 is low, then the body form is spindle shaped. The dorsal setae length represents the differentiation of dorsal setae, so it can be used to discriminate between the long and the short types. The largest loading value in PC1 is Lt-Vt1, 0.949, which presents the body length. The smallest loading is Vt3-Vt3, 0.409. The ratio between the largest and the smallest loading values is 2.32. When the low loadings in PC1 are deleted (characters 5, 7, and 17), the smallest loading is Dt-Dt, 0.683. The ratio

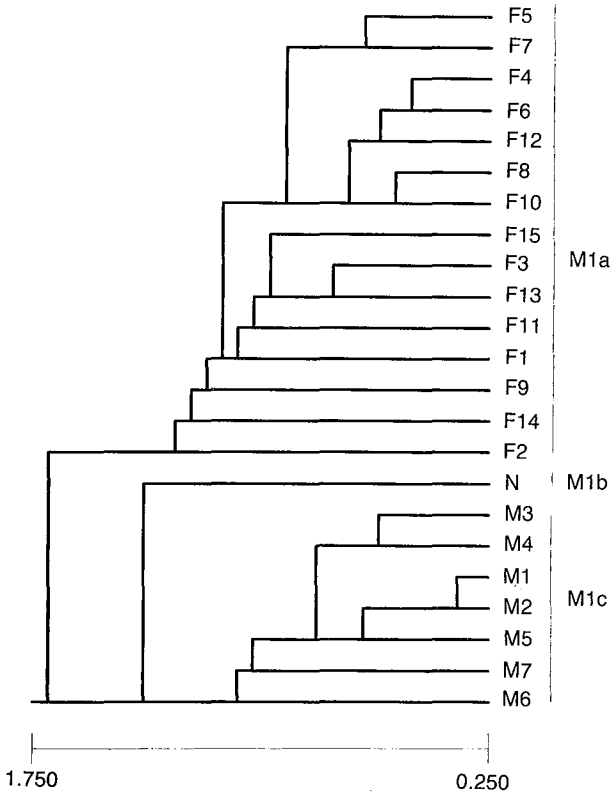

Fig. 3. An UPGMA phenogram for the M1 data set based on the average taxonomic distance coefficient.

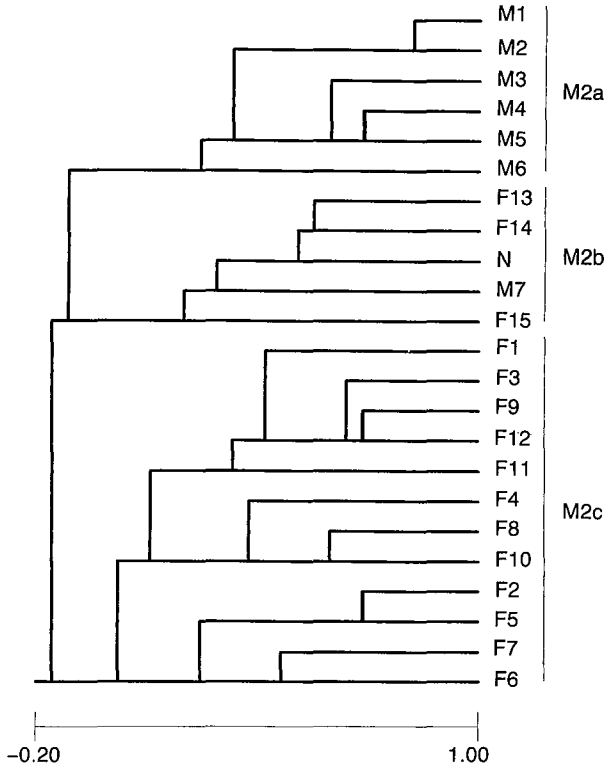

Fig. 4. An UPGMA phenogram for the M2 data set based on the average taxonomic distance coefficient.

Table 3. Factor matrix from a 17-variable principal component analysis of the M1 data set showing the character loadings on the first 3 components

Measurement	PCI	PCII	PCIII
1	0.778	0.206	0.144
2	0.848	0.342	-0.194
3	0.869	-0.013	-0.247
4	0.683	-0.109	0.444
5	0.494	-0.771	-0.266
6	0.795	-0.017	-0.251
7	0.521	-0.505	0.073
8	0.685	0.280	0.436
9	0.817	0.148	-0.055
10	0.715	-0.458	-0.065
11	0.938	0.202	0.041
12	0.949	0.137	0.063
13	0.871	0.054	0.133
14	0.915	0.244	-0.048
15	0.841	-0.058	-0.142
16	0.859	-0.053	-0.280
17	0.409	-0.459	0.588

between 0.949 and 0.683 is then 1.39 and the standard deviation and mean of the 14 characters are 0.086 and 0.83, respectively. The difference between the largest and the smallest loadings is very small, and therefore allometrics are not so apparent in this study.

The 3 dimensional plot of the first 3 components and its minimum spanning tree of the M1 data set (Fig. 5) reflect 3 groups: the male, the female, and the nymph. The distinction between females of the long and the short setae types is considerably enhanced by the addition of the minimum spanning tree. Thouth the nymph (N) is associated with the male group, its sex can not be discriminated by this result.

The plot of component I against II of the M1 data set reveals 3 clusters: females, males, and the nymph, respectively, corresponding to sex and age. The clusters are vertical to the PCI axis, and clearly show that size can be used to discriminate both sex and age. The result clearly reflects the importance of overall size. The largest females (mean body length = 123.5) cluster predominately in the right half of the plot, males (mean body length = 105.9) more towards the middle to the left of the plot, and the nymph (body length = 77.2), the smallest, on the extreme left.

If the 1st principal component is a measure of size in this study, more information about the relevant structure among the OTUs might be obtained by plotting the 2nd principal component against the 3rd, rather than a plot of components I and II. The plot of PCII against PCIII of the M1 data set reveals that 2 clusters are oblique to the axes. The long setae type and the short setae type are separated by PCII and PCIII simultaneously. The discrimination between these 2 types is based on characters that reflect differences in Ds.l, Ct1-Ct1, and Vt3-Vt3. These character match with shapes relating differences in body form and dorsal setae form. Plots of PCI against PCII and PCII against PCIII show that the size factor of PCI suppresses the shape factor of PCII in distinguishing the long setae type from the short type. In the plot of PCI against PCII, PCII does not separate the long setae type from the short type owing to the effect of PCI. But when PCII accompanies PCIII, these 2 types can be separated.

The character loadings and eigenvalues of the M2 data set are given in Table 4. The cumulative percentage of sample variance represented by the first 3 components is 58.8 %, with 29.3 % for the 1st component alone. The factor matrix indicates that the 1st component is heavily influenced by the characters 3, 7, 9, 13, 14, 15,17, 18, 19, 20, 23, and 24. The components of II to VII, respec-

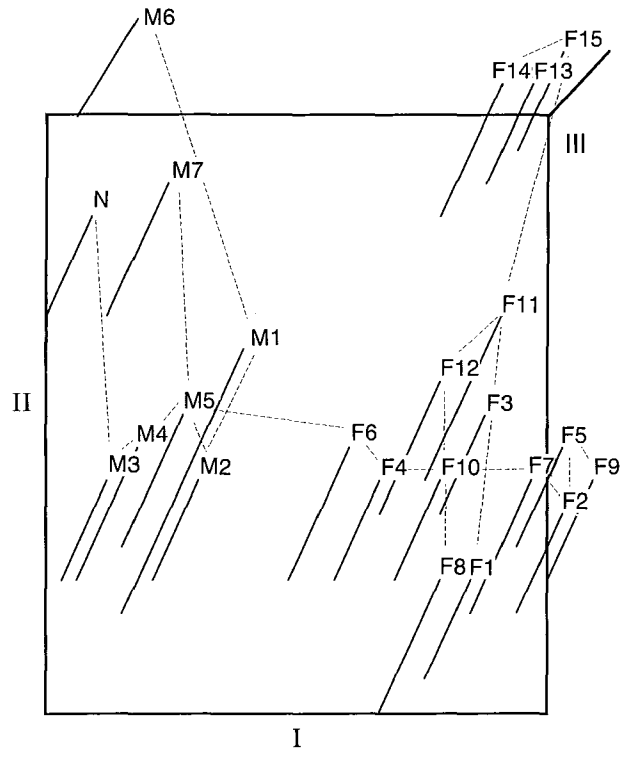

Fig. 5. Three-dimensional plot of PCI, PCII, and PCIII from a principal component analysis of the M1 data set. A minimum spanning tree is superimposed (dotted lines). X axis represents PCI. Y axis represents PCII. Z axis represents PCIII.

Table 4. Factor matrix from a 29-variable principal component analysis of M2 data set showing the character loadings on the first 3 components

Measurement	PCI	PCII	PCIII
1	0.214	0.060	0.334
2	−0.289	0.537	−0.185
3	0.621	−0.238	−0.196
4	−0.256	0.539	0.266
5	0.385	0.527	0.217
6	0.191	−0.401	0.181
7	−0.642	−0.062	−0.101
8	0.135	0.052	−0.346
9	−0.734	−0.026	0.574
10	0.230	0.528	−0.320
11	−0.403	0.804	−0.108
12	−0.342	0.571	−0.403
13	−0.823	0.356	0.032
14	−0.815	−0.237	−0.153
15	−0.734	0.250	−0.332
16	−0.082	0.368	−0.432
17	−0.813	−0.387	−0.011
18	−0.809	−0.343	−0.182
19	−0.797	−0.411	0.217
20	−0.818	−0.344	0.037
21	0.118	−0.461	−0.639
22	−0.044	−0.442	−0.703
23	−0.851	0.288	−0.184
24	−0.827	0.238	0.064
25	0.016	0.370	−0.745
26	0.535	0.200	−0.393
27	0.445	−0.006	0.020
28	−0.111	−0.604	−0.585
29	0.053	0.858	0.026

tively, have some of the greatest loading by the characters 2, 4, 5, 6, 8, 10, 11, 12, 16, 21, 22, 25, 26, 27, and 28. This means that the size factor of the 1st component of the M2 data set is less significant than that of the M1 data set.

The 3 dimensional plot of the first 3 component analysis and its minimum spanning tree of the M2 data set (Fig. 6) show the OTUs massed into 3 groups: females of the long setae type; females and 1 male (M7) of the short setae type with the nymph (N) of the long setae type; and all other males. From the minimum spanning tree, females of the short setae type are distributed sparsely on the terminal of the branches, but those of the long setae type are connected to each other to form a group. The ratio separates the long setae type from the short setae type but does not separate males from females. If the ratio (M2 data set) represents the shape factor, then these 2 types differ in shape but not in size. The result is close to those shown in Fig. 4 and the plot of PCII against PCIII of the M1 data set. This result explains that the shape factor is the main factor to distinguish between the long and the short setae types and the size factor is to distinguish sex and age.

The plot of PCI against PCII of the M2 data set reveals 2 groups. The clusters are oblique to the PCI and PCII axes. PCI does not strictly mean "size factor" owing to the ratio effect, so males being distributed in the right part of PCI (with larger values) does not mean males are larger than females. In the plot of PCII against PCIII, the clusters are oblique to the 2 axes. The separation of the 2 types is based on the characters 2, 4, 5, 10, 11, 12, 21, 22, 25, 28, and 29. The M2 data set for the principal component analysis shows the ratio which stands for the size factor decreasing and the shape factor obviously increasing.

Burnaby's method for size adjustment

In order to distinguish the long from the short setae type by the shape factor, Burnaby's method for size adjustment was used to get rid of the size factor in the M1 data set. In all 2 dimensional plots of component I against II, I against III, and II against III (Fig. 7), the long setae type and the

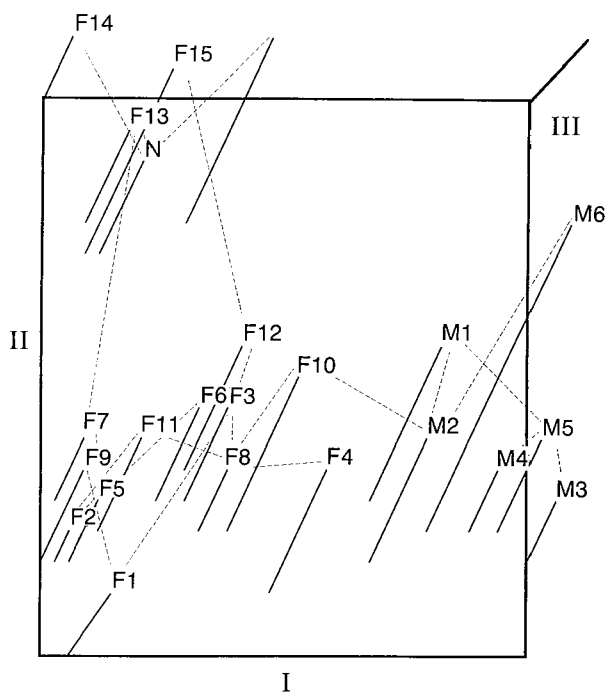

Fig. 6. Three-dimensional plot of PCI, PCII, and PCIII from a principal component analysis of the M2 data set. A minimum spanning tree is superimposed (dotted lines). X axis represents PCI. Y axis represents PCII. Z axis represents PCIII.

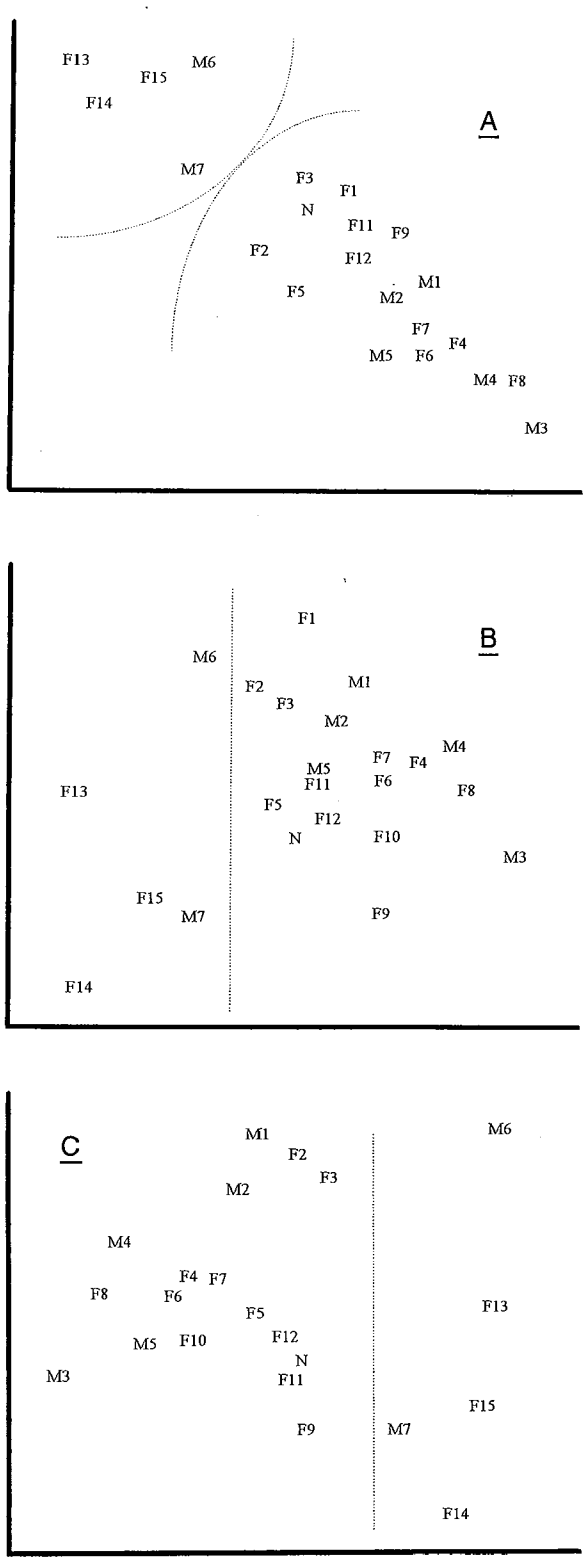

Fig. 7. Two-dimensional plot from Burnaby's method: A, X axis represents shape vector I, Y axis represents shape vector II; B, X axis represents shape vector I, Y axis represents shape vector III; C, X axis represents shape vector II, Y axis represents shape vector III. (Dotted lines denote the direction of clustering gap.)

short setae type are well separated by character 5, the dorsal setae length. The adjusted shape vector is used with the average taxonomic distance coefficient and UPGMA method to produce the phenogram. The OTUs are clustered into 2 groups: the long setae type (L) and the short setae type (S). The plot of adjusted shape vector II against PCI (Fig. 8) clearly shows that the size factor separates sex and age, and the shape factor separates the long setae type from the short type. From Burnaby's method, the M1 data set, after removing the size factor, indeed distinguishes the long setae type from the short type, but does not distinguish sex and age.

Multidimensional scaling

The stress value, 0.13, obtained after analyzing the M1 data set by the non-metric multidimensional scaling, indicates a result which falls between fair and good. From the plot of the first 2 axes and its minimum spanning tree (Fig. 9), the X axis at −0.5 separates the sexes. The nymph (N) is affined to the males, and this result is similar to

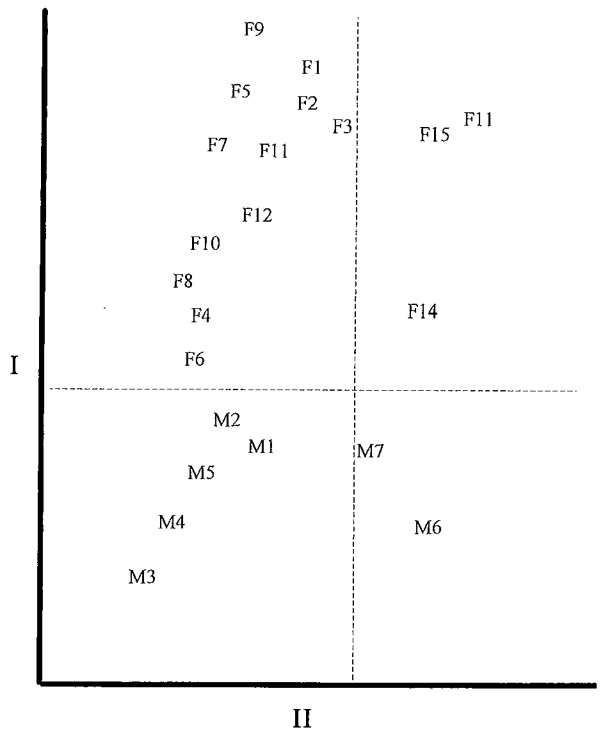

Fig. 8. Two-dimensional plot of shape vector II against component I of the M1 data set. X axis represents shape vector II. Y axis represents PCI. (Dotted lines denote the direction of clustering gap.)

that of Fig. 3. Analysis of the M1 data set by non-metric multidimensional scaling is unable to separate these 2 types, and the result is similar to the clustering analysis and the principal component analysis. The M1 data set (size factor) can only be used to distinguish sex and age.

The stress value, 0.15, obtained after analyzing the M2 data set by non-metric multidimensional scaling indicates a result which is poor, meaning the result is unreliable. The plot of the first 2 axes and its minimum spanning tree are given in Fig. 10. The X axis at 0.5 separates the sexes but does not separate the long setae type from the short type. The result of the M2 data set after non-metric multidimensional scaling is different from that of the clustering and the principal component analyses which may be due to the former's unreliability.

The M1 data set, with the greatest amount of size factor in the clustering analysis and non-metric multidimensional scaling, separates sex and age. The principal component analysis and Burnaby's method use the shape factors (PCII and PCIII) to separate the long setae type from the short type. The M2 data set simultaneously incorporates the shape factor and the size factor and, in the clustering analysis and the principal component analysis, it separates not only the long and the short setae types but also the sexes. The M2 data set after non-metric multidimensional scaling only separates the sexes. Besides, the stress is low, so the M2 data set does not fit this method.

From the above results, the M1 data set after principal component analysis uses the size factor (PCI) to separate sex and age and uses the shape factors (PCII, PCIII) to separate the long setae type from the short one. The M1 data set combined with the principal component analysis is the best way to conduct a morphometric analysis of mango eriophyoid mites. In general, the size factor discriminates sex and age, and the shape factor separates setae types. If size is a variable which originates in the environment, and is influenced by sex and age, then shape is the main factor for

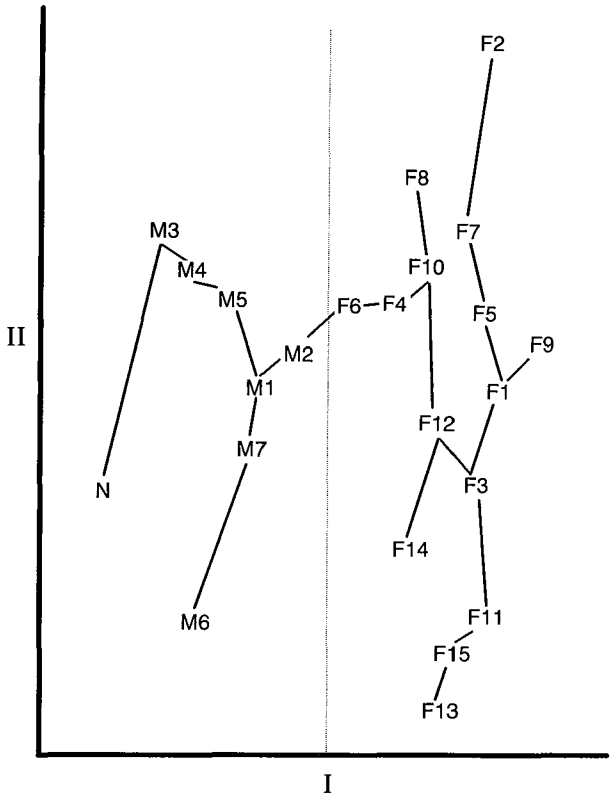

Fig. 9. Two-dimensional plot of the first 2 factors of the M1 data set by non-metric multidimensional scaling. A minimum spanning tree is superimposed. X axis represents factor I. Y axis represents factor II. (r = 0.0078) (A dotted line denotes the clustering gap.)

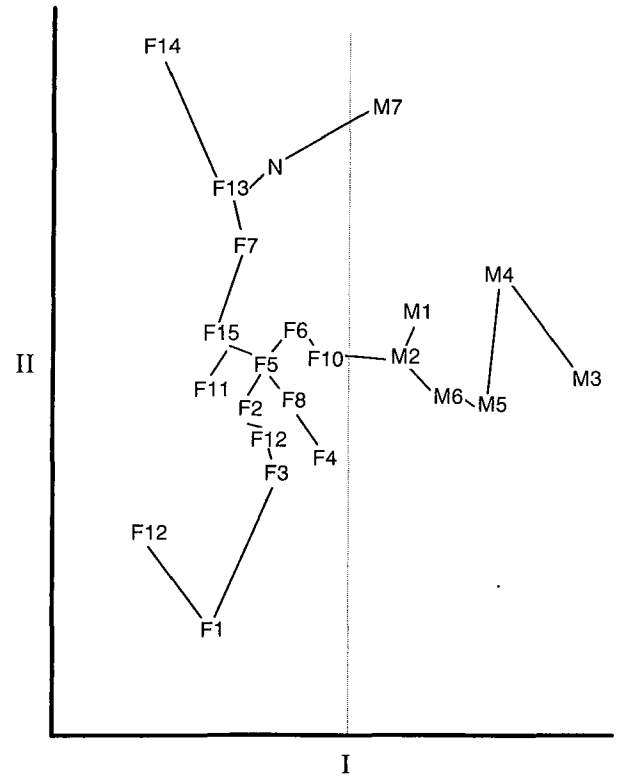

Fig. 10. Two-dimensional plot of the first 2 factors of the M2 data set by non-metric multidimensional scaling. A minimum spanning tree is superimposed. X axis represents factor I. Y axis represents factor II. (r = 0.02) (A dotted line denotes the clustering gap.)

classification. Thus, these 2 types are 2 species, namely the short setae type, *S. pagonis* Keifer, and the long setae type, *S. longinquus* sp. nov.

TAXONOMY

Spinacus longinquus sp. nov.
(Figs. 1a, b, 11a)

Female: Body spindle form, with wax, 112-132 long. Shield with anterior lobe, 35-42 long, 40-50 wide. Shield design with median line absent; admedian lines U-shaped, about one-third from the anterior margin, with concavity at center, arching laterally and joined centrally to form an inverse conical apex ahead of rear margin; submedian lines incomplete, subparallel, present in front of dorsal tubercles. Dorsal tubercle 19-25 apart, distance to rear shield margin 5-9; dorsal setae projecting to rear or lateral or upper, 11-18 long; Ct1-Ct1 6-11 apart, Ct2-Ct2 5-8 apart, Ct3-Ct3 19-23 apart; claw ending as a knob, foretibial seta missing, femoral seta sets at lateral side; featherclaw simple, 6-rayed.

Abdomen: about 23-26 tergites and 66-72 sternites, tergites with a central furrow; lateral seta 21-26 long, Lt-Lt 40-50 apart, Lt-Vt1 36-48; 1st ventral seta 13-17 long, Vt1-Vt1 25-30, Vt1-Vt2 24-34, 2nd ventral seta 38-47 long, Vt2-Vt2 9-15, Vt2-Vt3 26-34, 3rd ventral seta 20-25 long, Vt3-Vt3 11-15; accessory setae missing.

Coverflap: 26-29 wide, 19-20 long, with about 20-25 longitudinal lines; Gt-Gt 10-13, genital seta 7-9 long.

Male: 98-110 long; shield 31-37 long, 35-41 wide; coverflap 14-16 wide, 7-8 long, Gt-Gt 9-11, genital seta 6-10 long.

Etymology: The species epithet is an adjective meaning "long", in reference to the length of dorsal setae.

Type data: Holotype, ♀, from *Mangifera indica* L. Tapu, Chiai, Taiwan. 1994-I-14. K. W. Huang et C. F. Wang. Paratypes, 11♀♀, 5♂♂, 1 nymph same data as holotype.

Relation to host: A vagrant on the lower leaf surface. No apparent damage was observed.

Note: This new species is similar to *S. pagonis* Keifer, 1979 except for the length of dorsal setae and the structure of the network. According to the morphometric analysis, these 2 species mainly differ in the length of dorsal setae, the distance between the 1st ventral setae, and the distance between the 3rd ventral setae. These 2 species were found coexisting on the leaves of mango trees at Tapu, Chiai.

Spinacus pagonis Keifer, 1979
(Figs. 2c, 11b)

Spinacus pagonis Keifer, 1979: 11-12.

Female: Body 128-135 long, shield 38-44 long, 37-46 wide. Dorsal tubercles 22-23 apart, distance to rear shield margin 6-7; dorsal setae 6-7 long. Ct1-Ct1 8-9 apart, Ct2-Ct2 7-10 apart, Ct3-Ct3 18-27 apart.

Abdomen: Lt-Lt 42-49 apart, Lt-Vt1 40-44; Vt1-Vt1 24-28 apart, Vt1-Vt2 30-36; Vt2-Vt2 11 apart, Vt2-Vt3 25-27; Vt3-Vt3 12-15 apart.

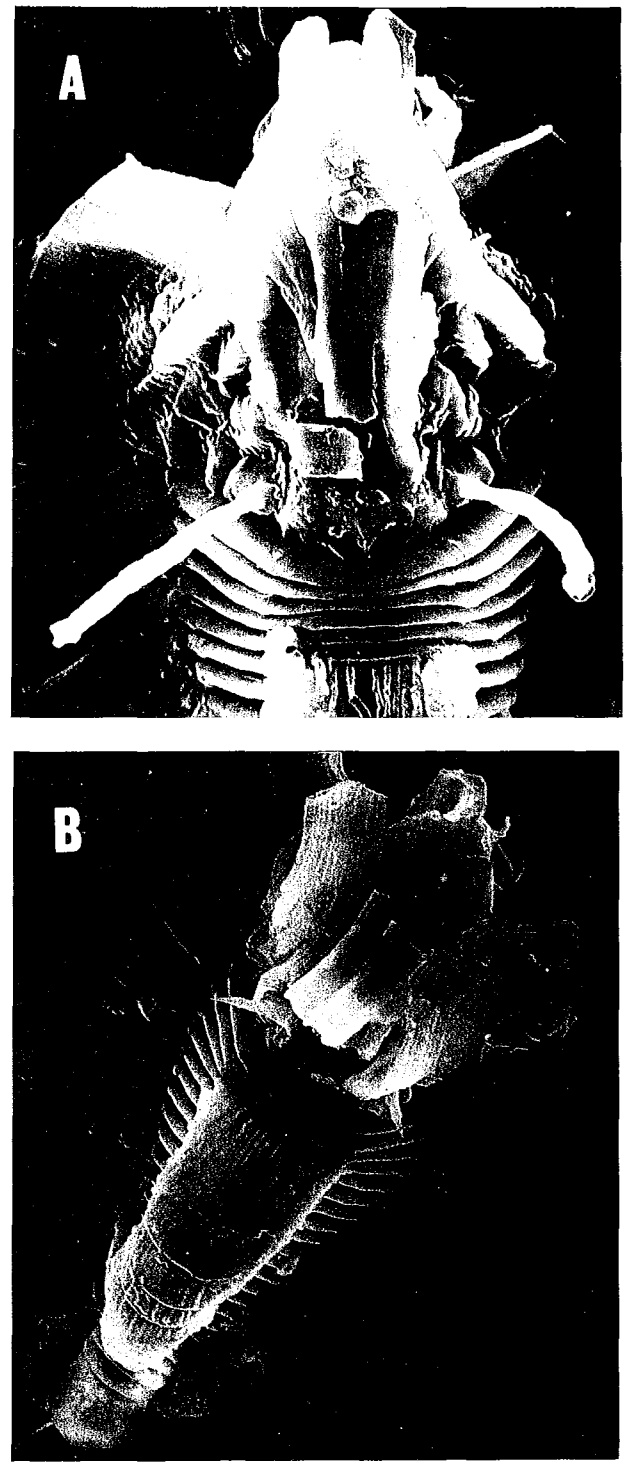

Fig. 11. SEM micrographs: A, *Spinacus longinquus* sp. nov. shield; B, *Spinacus pagonis* Keifer dorsum.

Coverflap: 26-29 wide, 18-21 long, Gt-Gt 9-11.
Male: Body 104-105 long, shield 35 long, 36-41 wide; Gt-Gt 6-9.

Specimens examined: 3♀♀, 2♂♂, from *Mangifera indica* L. Tapu, Chiai, Taiwan. 1994-1-14. K. W. Huang et C. F. Wang.

Acknowledgements: We thank Dr. JT Yang (Chung-Hsing University), Miss HJ Chang and Mr. YP Huang (National Museum of Natural Science) for their assistance with the preparation of this manuscript, and Dr. MM Yang (Natl. Mus. Nat. Sci.) for her valuable comments.

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以形態測量分析 *Spinacus pagonis* Keifer 及其近緣新種 (Acarina: Eriophyidae)

黃坤煒[1] 黃 讚[2] 王進發[2]

於嘉義大埔同一棵芒果樹的葉片上，發現有三種節蜱，分別爲 *Cisaberoptus kenyae, Spinacus pagonis* 及一種類似於 *S. pagonis* 的種類，後者因其背毛較長而暫定爲 *S. pagonis* 的長毛型，以相對於原敍述種類的短毛型。本文藉由測量同源點間的距離及計算測量值間的比值，分別以類聚分析、主成分分析、Burnaby 校正大小方法，最短樹及非計量多度空間尺度，來分析這二型節蜱是否爲不同種。結果顯示，雌、雄性可由大小的變數來區別，而形狀變數可以區別長、短型，但無法有效區別性別及年齡上的差異。這二種的主要區別在於背毛的長度(*S. pagonis* = 6−7, *S. longinquus* = 11−18)，第三足基節瘤的間距(*S. pagonis* = 18−27, *S. longinquus* = 19−23)，第三腹毛瘤的間距(*S. pagonis* = 12−15, *S. longinquus* = 11−15)。依據形態分析結果，應可將長毛型定爲新種 *Spinacus longinquus* sp. nov.。

關鍵詞：形態測量, 節蜱, 同源性, 新種, 臺灣。

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