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한국산 길쭉먼지벌레족의 수리분류(II)

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Numerical Taxonomy of the Tribe Pterostichini Sloane from Korea(II)

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Abstract

A numerical taxonomy based on the phenetic characters of 59 Korean Pterostichini species is conducted to determine the effect on the assessment of the 7 different methods combined by 3 similarity or dissimilarity coefficients, using 87 morphological multistate characters.

Key words: Phenetics, Numerical taxonomy, Coleoptera, Pterostichini, Korea.

Introduction

The ground beetles belonging to the family Harpalidae are widely distributed all over the zoogeographical region of the world. Constituent species of the tribe Ptetrostichini are essentially predacious on many kinds of terrestrial arthropods including insects and mollusc with earthworms, slugs and land snails.

In Korea, the taxonomy of this group has been studied rarely, although primary classification system had been provided by Kwon and Lee (1986) and Shin *et al.*,(1994).

The purpose of this study is to reduce the existing identification problems and to revise this group taxonomically in accordance with the modern reasonable classification system. So, as one of the computation works to extensive verification of traditional systematics, a

phenetic classification, one of the largest used methods is attempted to show the placement status of Korean species by a numerical taxonomic method in accord with the traditional taxonomic view based on external structures and genitalia. Already the using the binary data matrix including 'NC' value was described by Park et Kwon (1996).

Materials and Methods

All the Korean species consisting of 59 operational taxonomic units (OTU's) were treated in this analysis (Table 1).

Table 1. List of OTU's (operational taxonomic unit) used.

OTU	Species
1	*Trigonognata coreana*
2	*Lesticus* (*Triplogenmius*) *magnus*
3	*Trigonotoma lewisii*
4	*Poecilus coerulescens encopoleus*
5	*Poecilus fortipes*
6	*Poecilus lamproderus*
7	*Poecilus nemotoi*
8	*Poecilus nitidicollis*
9	*Poecilus reflexicollis*
10	*Pterostichus* (*Badistrinus*) *aberrans*
11	*Pterostichus* (*Badistrinus*) *neglectus*
12	*Pterostichus* (*Bothriopterus*) *adstrictius*
13	*Pterostichus* (*Bothriopterus*) *subovatus*
14	*Pterostichus* (*Cryobius*) *coreicus*
15	*Pterostichus* (*Cryobius*) *kurosai*
16	*Pterostichus* (*Cryobius*) *horvatovichi*
17	*Pterostichus* (*Eosteropus*) *creper*
18	*Pterostichus* (*Eosteropus*) *prolongatus*
19	*Pterostichus* (*Euriperis*) *comorus*
20	*Pterostichus* (*Eurythoracana*) *haptoderoides*
21	*Pterostichus* (*Feroperis*) *pertinax*
22	*Pterostichus* (*Feroperis*) *probus*
23	*Pterostichus* (*Feroperis*) *rasilis*
24	*Pterostichus* (*Feroperis*) *seungmoi*
25	*Pterostichus* (*Lagarus*) *sulcitarsis*
26	*Pterostichus* (*Lyperopherus*) *rugosipennis*

27 *Pterostichus* (*Melanius*) *rotundangulus*
28 *Pterostichus* (*Metallophillus*) *interruptus*
29 *Pterostichus* (*Nialoe*) *audax*
30 *Pterostichus* (*Nialoe*) *ompoensis*
31 *Pterostichus* (*Nialoe*) *praedo*
32 *Pterostichus* (*Nialoe*) *raptor*
33 *Pterostichus* (*Nialoe*) *scurrus*
34 *Pterostichus* (*Nialoe*) *seunglaki*
35 *Pterostichus* (*Nialoe*) *jogaesanensis*
36 *Pterostichus* (*Nialoe*) *sincerus*
37 *Pterostichus* (*Nialoe*) *truncatus*
38 *Pterostichus* (*Phaenoraphis*) *acuspinus*
39 *Pterostichus* (*Phaenoraphis*) *peninsularis*
40 *Pterostichus* (*Platysma*) *fortis*
41 *Pterostichus* (*Platysma*) *sachtlebeni*
42 *Pterostichus* (*Rhagadus*) *microcephalus*
43 *Pterostichus* (*Rhagadus*) *solskyi*
44 *Pterostichus* (*Rhagadus*) *nimbatidius*
45 *Pterostichus* (*Steropus*) *coruscus*
46 *Pterostichus* (*Steropus*) *orientalis orientalis*
47 *Pterostichus* (*Steropus*) *orientalis tortuosus*
48 *Pterostichus* (*Koreonialoe*) *taebaegsanus*
49 *Pterostichus* (*Koreonialoe*) *apiculatiphallus*
50 *Pterostichus* (*Koreonialoe*) *bellator bellator*
51 *Pterostichus* (*Koreonialoe*) *belloter togyusanus*
52 *Pterostichus* (*Koreonialoe*) *bifidiphallus*
53 *Pterostichus* (*Koreonialoe*) *ishikawai*
54 *Pterostichus* (*Koreonialoe*) *palgongsanus*
55 *Pterostichus* (*Koreonialoe*) *teretis*
56 *Pterostichus* (*Koreonialoe*) *vicinus*
57 *Pterostichus* (*Koreonialoe*) *woongbii*
58 *Pterostichus* (*Microniloe*) *bifoveolatus*
59 *Pterostichus* (*Microniloe*) *chogyesanus*

A sum of 87 basic phenetic characters covering some 255 character states, either quantitative or qualitative, two-state or multi-state, ordered or unordered, were used here (Table 2).

Table 2. List of characters and coded character states: two-state and multi-state, orderd or unordered variables.

OTU	Species

(General)

1. Size of body : (1) long(>17mm), (2) intermadiate(14-17mm), (3) short(14m>).
2. Luster of Body : (1) polish, (2) mat, (3) not so.
3. Colour of luster : (1) green, (2) red, (3) copper, (4) not so.
4. Colour pattern of dorsal side : (1) black, (2) dark brown, (3) reddish brown, (4) brown.
5. Body appearance (length/ width) : (1) robust(<2.7mm), (2) medium(2.7-3.0mm), (3) elongate(>3mm).

(Head)

6. Size of head : (1) large(>2.5mm), (2) intermadiate(2.0-2.5mm), (3) small(<2.0mm).
7. Width of head : (1) wide(>3.5mm), (2) intermediate(3.0-3.5mm), (3) small (<3.0mm).
8. Punctuation of head : (1) strong, (2) weak, (3) absent.
9. Convexity of eye : (1) strong, (2) intermediate, (3) weak.
10. Size of mandible : (1) long, (2) intermediate, (3) short.
11. Width of mandible : (1) narrow, (2) intermediate, (3) wide.
12. Lateral apex of labrum : (1) strongly emarginate, (2) weakly emarginate, (3) not so.
13. Size of antenna : (1) long, (2) medium, (3) short.
14. Additional seta of antennal segment 2 : (1) 1, (2) 2, (3) 3, (4) absent.
15. Antennal segment 1-3 : (1) with flat angle, (2) cylindrical.
16. Form of clypeus : (1) trapizum, (2) rectangular, (3) not so.
17. Apical margin of clypeus : (1) straight, (2) slighly bent, (3) not so.
18. Shape of apical palpus : (1) round and elongate, (2) dilate.
19. Tip of maxillary palpus : (1) cuted, (2) blunt(round).
20. Apical segment of maxillary palpus : (1) longer than 2nd segment (2) same with 2nd segment (3) shorter than 2nd segment.
21. Length of frontal furrow : (1) reached at anterior supraorbital seta, (2) not reached at anterior supraorbital seta, (3) exceeding at anterior supraorbital seta.
22. Situation level of hind supraorbital seta : (1) before posterior margin of eye, (2) same level, (3) behind posterior margin of eye.
23. Convexity of gena : (1) large, (2) intermediate, (3) short.
24. Winkles of tempora at posterior margin of eye : (1) present, (2) abscent.
25. Convexity of tempora : (1) large, (2) medium, (3) small or absent.
26. Number of apical seta of ligula: (1) 2, (2) 4, (3) not so.
27. Mentum tooth : (1) bifid, (2) not so.

(Thorax)

28. Size of pronotum : (1) long(>3.5mm), (2) intermdiate(2.5-3.5mm), (3) short(<2.5mm).
29. Width of pronotum : (1) wide(>5.0mm) (2) intermediate(4.0-5.0mm), (3) small (<4.0mm).
30. Luster of pronotum : (1) strong, (2) weak, (3) abscent
31. Appearance of pronotum PA(width of apical angles) /PB(width of hind angles) : (1) >1, (2) 0, (3) <1.
32. Shape of pronotum : (1) cordate, (2) rectangular, (3) oval, (4) not so.
33. Punctuation of pronotum (besides near to basal fovea) : (1) strong, (2) weak, (3) absent.
34. Widest position of pronotum from apical angle : (1) before about 1/3, (2) about 1/2, (3) behind about 1/3.
35. Transverse winkles of pronotum : (1) distinct, (2) weak, (3) absent.
36. Shape of apical angle in pronotum : (1) Sharply prominant, (2) feebly prominant, (3) not so.
37. Sinuation before basal angle of pronotum : (1) strong, (2) weak, (3) not so.
38. Number of basal linear fovea in pronotum : (1) 1, (2) 2, (3) 3, (4) absent.
39. Basal linear fovea to median line in pronotum: (1) parallel, (2) not so, (3) absent.
40. Hind angle of pronotum : (1) acute, (2) rectangular, (3) obtuse(round).
41. Point of hind angle in pronotum : (1) sharp, (2) weak, (3) absent.
42. Border of proserternal process : (1) distinct, (2) weak, (3) absent.
43. Punctuation of proepisternum : (1) strong, (2) weak, (3) absent.

(Elytron)

44. Length of elytron : (1) long(>8.5mm), (2) intermediate(7.0-8.5mm), (3)short(<7mm).
45. Width of both elytron : (1) wide(>5.5mm) (2) intermediate(4.5-5.5mm), (3) small (<4.5mm).
46. Shape of elytra : (1) oval, (2) oblong, (3) not so.
47. Luster of elytron : (1) strong, (2) weak, (3) absent.
48. Color of elytron : (1) black, (2) dark brown, (3) reddish brown, (4) brown, (5) not so.
49. Denticle of shoulder : (1) distinct, (2) weak, (3) absent.
50. Basal pore of elytron : (1) present, (2) absent.
51. Shape of elytral stria : (1) regular, (2) irregular.
52. Sculpture of elytral stria : (1) deep, (2) weakly deep, (3) superficial.
53. Beginning point of 1st stria : (1) basal pore, (2) not so.
54. Punctuation of stria : (1) distinct, (2) weak, (3) absent.
55. Basal linear pore : (1) with, (2) not distinct, (3) without.
56. Length of basal linear pore : (1) long, (2) intermediate, (3) short.

57. Pore of interval 3 : (1) 2, (2) 3, (3) ≥4, (4) absent.
58. Level of anterior pore from base : (1) before 1/2, (2) behind 1/2, (3) absent.
59. Position of anterior pore : (1) adjoining stria 2, (2) adjoining stria 3, (3) not so.
60. Additional pores of interval 4-7 : (1) present, (2) absent.
61. Form of interval pores : (1) normal, (2) abnormal(deeper and wider), (3) absent.
62. Punctuation of mesepisternum : (1) strong, (2) weak, (3) absent.
63. Punctuation of metepisternum : (1) strong, (2) weak, (3) absent.

(Leg)

64. Ventral setae of 5th tarsus : (1) present, (2) absent.
65. Dorsal scarina of tarsus : (1) present, (2) absent.

(Abdomen)

66. Protuberance of last abdominal sternite : (1) present, (2) absent.
67. Position of last abdominal protuberance : (1) apex of sternite, (2) on middle plate, (3) absent.
68. Shape of protuberance : (1) symmetric, (2) asymmetric, (3) absent.
69. Concavity of last abdominal sternite : (1) strong, (2) weak, (3) not so.
70. Lateral punctuation of abdominal sternite 3-5 : (1) strong, (2) weak, (3) absent.
71. Lateral depression of abdominal sternite 1 : (1) deep, (2) weak, (3) absent.

(Genitalia)

72. Shape of aedeagus : (1) slender, (2) medium, (3) robust.
73. Curvature of aedeagus : (1) strongly curved, (2) weakly curved (3) not so.
74. Additional lobe of aedeagus : (1) distinct, (2) weak, (3) absent.
75. Placement of additional lobe : (1) dorsal, (2) ventral, (3) lateral, (4) latro-ventral, (5) latro-dorsal, (6) without.
76. Direction of additional lobe : (1) anterior, (2) posterior, (3) absent.
77. Length of apical lamella : (1) long, (2) intermediate, (3) short.
78. Shape of lamella tip : (1) round, (2) angle, (3) not so.
79. Form of apical lamella : (1) straight, (2) weakly sinuate, (3) fully twisted.
80. Length of apical lamella (Length /width in of apical lamella) : (1) long(>2), (2) medium(1-2), (3) short(<1).
81. Protuberance of apical lamella in dorsal view : (1) present, (2) absent.
82. Width of aedeagal anterior part (width of anterior part /width of posterior part) : (1) elongate (<1), (2) intermediate(1-2), (3) dilate (>2).
83. Ostium of aedeagus : (1) strongly twisted, (2) weakly twisted, (3) not so.
84. Shape of female apical segment of stylus : (1) strongly bent, (2) weakly bent, (3) not so.

85. Spine of apical segmental stylus at ventral outer margin : (1) present, (2) absent.
86. Spine of apical segmental stylus at ventral inner margin : (1) present, (2) absent.
87. Pore of apical segment stylus at latro-dorsal view : (1) present, (2) absent.

In the coding scheme, some unknown characters were scored as '-' to accommodate the missing value when computing.

Cluster analyses based on similarity or dissimilarity computation for each OTU were carried out through suits of Fortran, SPSS/PC+. The designated Fortran program reads an input primary data matrix and record this matrix to the output binary data matrix, and another output binary data matrix which include 'no comparison' coded to prevent comparison of unavailable particular characters (cf. Dunn and Everitt, 1982). For the agglomerating hierarchical clustering procedures, either 1 binary matching similarity or 2 dissimilarity coefficients were made through the Fortran run on the computers, which carried out an analysis using each binary data matrix by computing the information content of each character as well as the joint and mutual information content of all character pairs.

For the comparative proper classification, 7 different cluster methods combined with 3 coefficient measures were conducted (Table 3).

Table 3. The coefficient measures and clustering methods used (coefficient measures between x and y, cf. Norusis 1985).

Coefficient measure	Clustering method
Simple matching similarity $SM(x, y) = \frac{a+d}{a+b+c++d}$	Average linkage between groups (unweighted pair group method average) Average linkage within group Single linkage (nearest neighbor) Complete linkage (furthest neighbor)
Variance dissimilarity $VARIANCE(x, y) = \frac{b+c}{4(a+b+c+d)}$	Average linkage between groups (unweighted pair group method average) Average linkage within group Single linkage (nearest neighbor) Complete linkage (furthest neighbor)
Binary squared Euclidean distance $BSEUCLID(x, y) = b+c$	Centroid (unweighted pair group method centriod) Median (weighted pair group method centriod) Ward's method

Results

1. Excluding 'NC' value

This analysis was carried out to show the relationships among the species of the tribe Pterostichini for more easily understand the between allied species.

To compare the effect of using similarity or dissimilarity coefficients as well as different clustering methods, 7 different clustering methods jointed with 3 measures were carried out here. And also, out of the comparing procedures, centroid, median and Ward's methods can only work with the binary squared Euclidean distance, among the clustering methods (Noru is, 1985, SPSS, 1988).

① Average linkage within groups

The phenograms given by the simple matching and variance coefficients measures were well agglomerated with their groups.

In the analysis using simple matching coefficient (Fig. 1), species of the *Trigonognata*(1), *Trigonotoma*(3), *Lesticus*(2), *Koreonialoe*(48-57) and some *Nialoe*(30,37,36) species were segregated from remainder groups as the primary 2 main clusters. Again in the 2nd one, they were mainly divided into 2 subgroups: species of the *Steropus* (46,47,45) and the remainder subgroup splitted from *Pterostichus*. However, some species (30, 36, 37) of the Nialoe were placed to the unexpected position with *Koreonialoe*. The rest groups combined well in accordance with all the their subgenera and genera, among them *Poecilus* species were well linked from their known group.

As a rule, the position of most species presented a phenetic classification in accordance with the traditional taxonomic view, although several species were not included to the expected places.

The phenograms given by the variance dissimilarity (Fig. 5) were generally accorded with simple matching measure.

② Average linkage between groups

In the analysis using simple matching coefficient (Fig. 2), *Koreonialoe* and remainder groups were segregated as the primary 2 main clusters.

As a secondary cluster group, *Trigonognatha coreana* (1), *Lesticus magnus* (2) and *Trigonotoma lewisii* (3) were isolated from the rest groups, and also, species of the *Steropus*, *Eosteropus* and *Nialoe* were segregated from the remainder groups.

The position of most species presented a phenetic classification in accordance with the traditional taxonomic view, whereas, *P. ompoensis* (30) was not linked properly to the expected position.

The dendrogram given by the variance dissimilarity (Fig. 6) was mostly coincieded with the above measure.

③ Single linkage

The phenograms based on the simple matching and variance coefficients (Figs. 3, 7), given by this method were well agglomerated within their known

subgeneric and generic groups. In the first one,

they were firstly divided into both *P. ompoensis* (30) and the rest groups. The rest groups were subsequently grouped into 2 parts: the one is the species of the *Micronialoe*(58,59) and rest groups wihich ares continuely saperasted to *Trigonognatha*, *Lesticus* and *Trigonotoma*, the other is the rest groups. Again, the remainders splitted into 3 subgroups as their expected places.

So, most species were linked together with their known subgeneric and generic groups in the phenogram using this method, although some species were not included to the expected places.

④ Complete linkage

The analysis using this method (Figs. 4, 8) was made up to 2 main clustering groups: the one is merged with *P. interruptus* (28), 4 species of the *Feroperis*(21-24), 2 species of the *Platysma*(40,41), 3 species of the out from *Pterostichus*(1-3), *P. ompoensis* (30) and 10 species of the *Koreonialoe*(48-57), the other is divided into 3 subgroups.

As a rule, most intersubgeneric and intergeneric relationships corresponded to conventional taxonomic views, but some species were not linked to the expected places.

Both the phenograms produced by the simple matching and variance coefficients showed a very similar clustering pattern, except for only minor degree of linked points in some allied species.

⑤ Centroid method

The analysis using this method (Fig. 9) can work with the binary squared Euclidian distance. The *Pterostichus ompoensis* (30) was segregated from others, as in the cases of single linkage methods.

Most species were grouped with their known groups. As a whole, the yields from this analysis was similar to those shown by the above methods. And all the phenograms seemed to be closely accorded to the traditional view. In the subspecific view, *P. orientalis orientalis* (46) and *P. orientalis tortuosus* (47) were linked as a nearest position, and also, *P. bellator bellator* (50) and *P. bellator togyusanus* (51) were placed into their known group.

⑥ Median method

The present method was also used with the binary squared Euclidian distance. In this method (Fig. 10), *Pterostichus ompoensis* (30) was isolated from the others and linked to unexpected place. And also, species of the *Koreonialoe* (48-57) were segregated from other groups.

In each genus, the intersubgeneric and interspecific relationships were nearly coincided with the expected groups as in the view of traditional taxonomy.

⑦ Ward's method

The analysis using this method (Fig. 11) can be worked only with binary

suared Euclidian distance,

as in case of the previous both centrioid and median methods. Particularly, Pterostichus ompoensis (30) was linked together with their known subgeneric group.

As in the Ward's method, most species were placed into their known groups.

Discussion

This methods attemped to know the relationships among the species by the cluster analysis based on the quantitative or gualitative characters. And also, it may be more easy to understand the relationships among the species of this tribe by the dendrograms output from the present analysis.

Totally 7 clustering methods jointed with 3 measures, including 'NC' (no comparison) values, and similarity or dissimilarity coefficients were used here.

In the analysis, the phenograms of most methods showed to the resemblant patterns. And the position of most constituent species presented a relevant phenetic classification in accordance with the traditional taxonomic view. The species of the genera other than genus *Pterostichus*, *Trigonognata*, *Lesticus*, *Trigonotoma* and *Poecilus*, were placed to their expected position by characteristics of the each genera. Whereas, *Pterostichus ompoensis* of the subgenus *Nialoe* was usually placed to the unexpected position, it may be due to the setae of ventral tarsus. In the *Nialoe*, absence of ventral setae in tarsus is one of the their main characters.

In addition to, we examined the analysis based on the only genitalic characters using the same measures and methods, but we didn't mentioned here, because the results revealed unsatis-factory clustering trends under the classical taxonomic point of views than those yielded by using the all characters. It may be due to the existence of the numerous missing values in the data matrix.

Already, Park & Kwon(1996) decribed the using the data matrix including 'NC' value, but it was quite minor with excluding 'NC' value, indiscriminately.

摘　　要

韓國産 길쭉먼지벌레族을 대상으로 "NC" 값을 인정하지 않은 상태에서 定性的 形態形質을 根據로 表現論的 數理分類方式을 利用한 群分析을 실시하였다. 그 結果, 비록 일부 種에서는 傳統分類 結果와 다소 一致하지 않은 경우도 있었으나 대부분 經驗的 分類와 類似한 傾向을 나타내었다. 그리고 대부분 種들이 期待한 屬 또는 亞屬내에 分布하였다.

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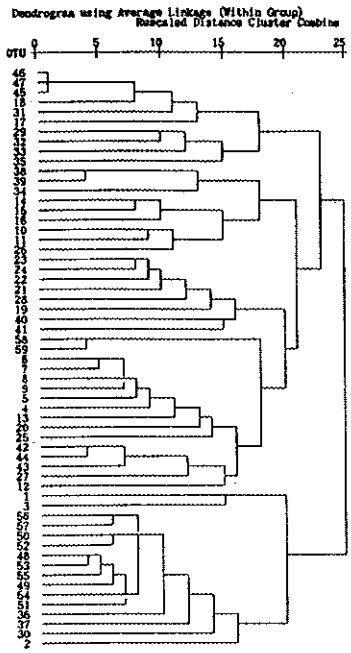
EXPLANATION OF FIGURES

The Simple matching similarity measure (1: average linkage within group, 2: average linkage between group, 3: single linkage, 4: complete linkage).

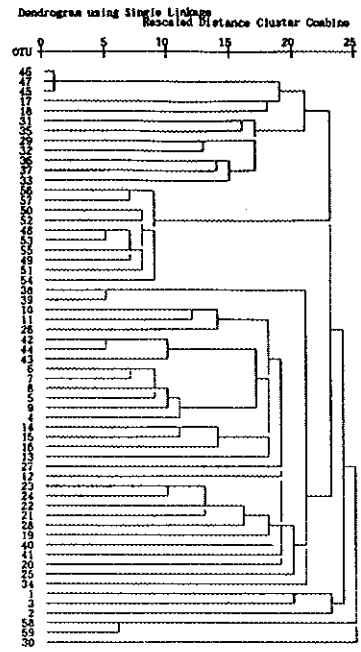
The Variance dissimilarity measure (5: average linkage within group, 6: average linkage between group, 7: single linkage, 8: complete linkage).

The binary squared Euclidean distance measure (9: centriod method, 10: median method).

The Ward's method of binary squared Euclidean distance measure (11)


Dendrogram using Average Linkage (Within Group)
Rescaled Distance Cluster Combine
OTU
0
5
10
15
20
25

1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Rescaled Distance Cluster Combine
OTU
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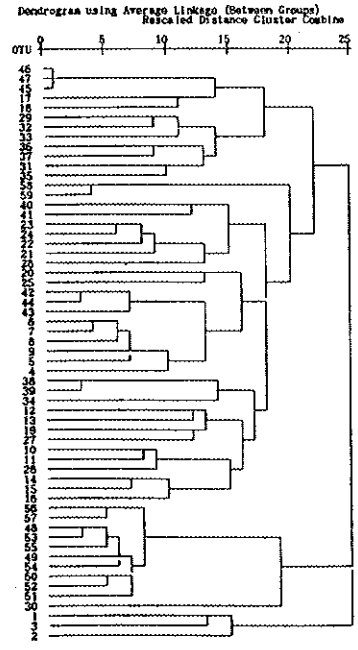
10
15
20
25

3


Dendrogram using Average Linkage (Between Groups)
Rescaled Distance Cluster Combine
OTU
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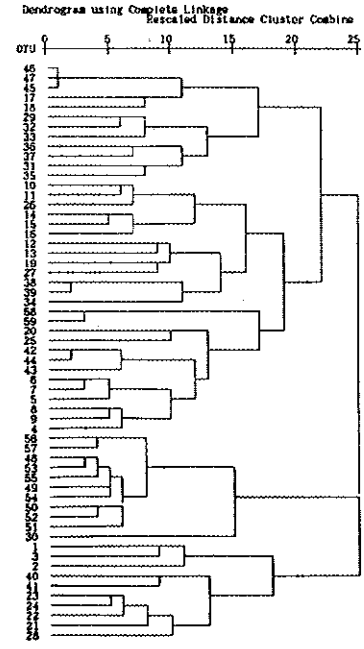
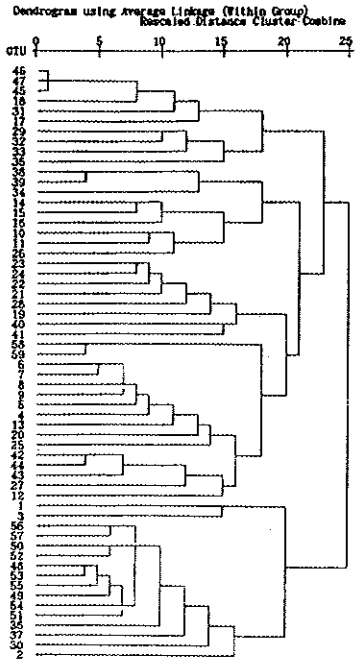
5
10
15
20
25

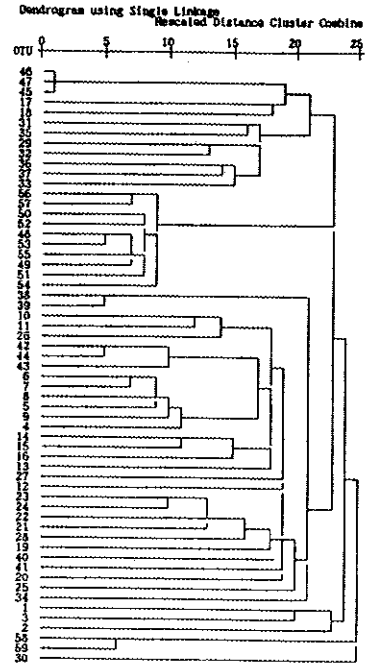
2


Dendrogram using Complete Linkage
Rescaled Distance Cluster Combine
OTU
0
5
10
15
20
25

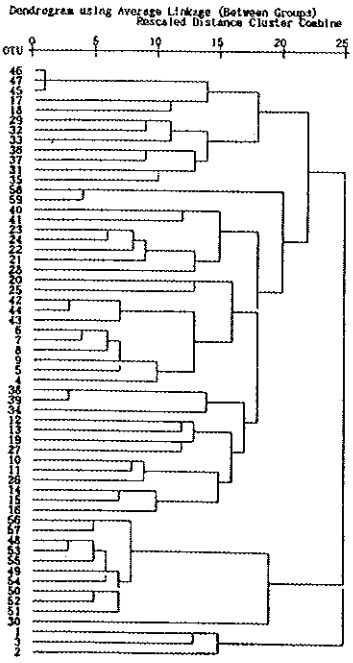
4


Dendrogram using Average Linkage (Within Group)
Rescaled Distance Cluster Combine
OTU
0
5
10
15
20
25

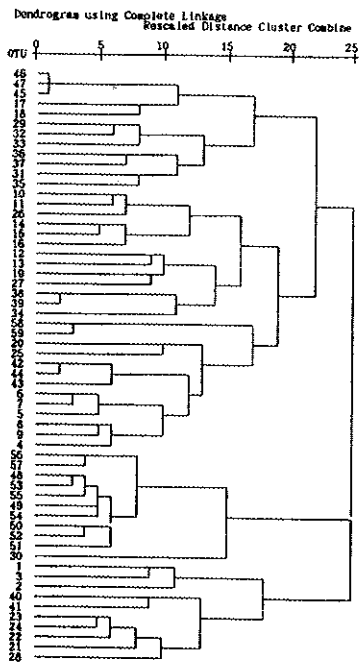
5


Dendrogram using Single Linkage
Rescaled Distance Cluster Combine
OTU
0
5
10
15
20
25

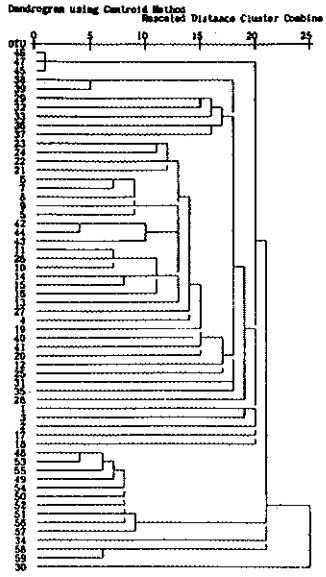
7


Dendrogram using Average Linkage (Between Groups)
Rescaled Distance Cluster Combine
OTU
0
5
10
15
20
25

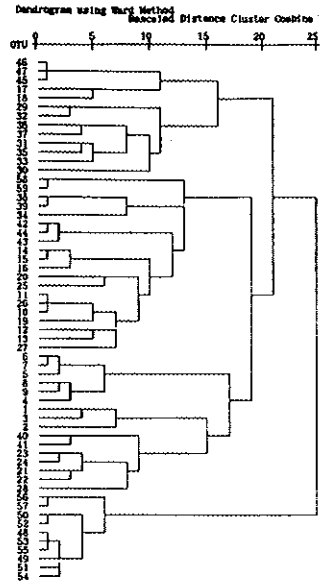
6


Dendrogram using Complete Linkage
Rescaled Distance Cluster Combine
OTU
0
5
10
15
20
25

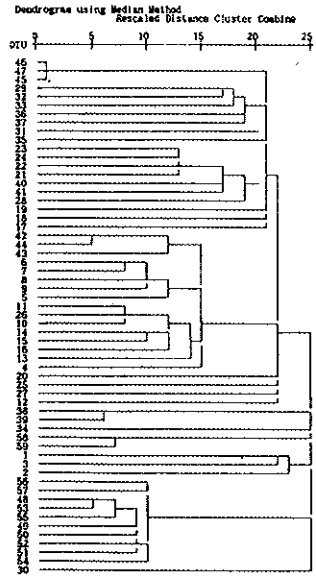
8


Dendrogram using Centroid Method
Rescaled Distance Cluster Combine
OTU
0
5
10
15
20
25

9


Dendrogram using Ward Method
Rescaled Distance Cluster Combine
OTU
0
5
10
15
20
25

11


Dendrogram using Median Method
Rescaled Distance Cluster Combine
OTU
0
5
10
15
20
25

10