A NUMERICAL TAXONOMIC STUDY OF FORMOSAN LABIATAE[1,2]

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Abstract: A numerical taxonomic study was conducted on 70 taxa of Formosan Labiatae. Three clustering methods were employed using a modified Gower's generalized similarity coefficients based on 76 morphological characters. The results are drawn into three phenograms which all reveal essentially similar intra and inter-generic arrangements indicating that the phenetic relationships between the taxa at the genus level corresponds to traditional taxonomy but the groupings above the genus level are distinct.

INTRODUCTION

Numerical taxonomy is defined by Sneath and Sokal (1973) as "the grouping by numerical methods of taxonomic units into taxa on the basis of their character states." Among those who have applied the numerical techniques to plants are Rogers and Tanimoto (1960), Crovello (1965), Katz and Torres (1965), Taylor (1966), Rhodes *et al.* (1968), and El-Gazzar and Watson (1970). And this number has increased in the past few years. It is evident that numerical taxonomy provides a better taxonomic understanding of plants.

Labiatae is one of the ten largest families in Formosa and this Family has recently been revised (Huang and Cheng, 1971, 1977). The purpose of the present study is to evaluate the effects of the numerical taxonomic methods, including three clustering techniques, on 70 taxa of Formosan Labiatae by using 76 morphological characters.

MATERIALS AND METHODS

Seventy operational taxonomic units (OTU's) representing 39 genera, 61 species and 9 varieties were studied. The code number of each taxon are listed in Table 1 and will be applied in the following sections of this report. A few taxa were not included in this study because some parts of the specimens were lacking. Seventy-six morphological characters (Table 2) taken from all parts of the plant were examined for assessing the degree of over all phenetic similarity. The categories of characters and their states were assigned as follows:

(1) For dichotomous characters the presence of the character was represented by 1 and its absence by 0.

(2) Qualitative characters were divided into two classes: two state character and multistate character. The states of two state character were set by 1 and 2 and the multistate character by more than three numbers. In the present study as many as 7 states were recognized.

(3) For quantitative characters the measurements were coded into several integers and were treated as multistate characters.

All of the OTU's and characters constructed a 70×76 data matrix from which a matrix of similarity coefficients were counted. For a study with mixed characters, Gower's method

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Table 1. Code number and operational taxonomic units (OTU's) used in the present study

Code number	Operational taxonomic units (OTU's)	Code number	Operational taxonomic units (OTU's)
1	*Acrocephalus indicus*	36	*M. dianthera*
2	*Agastache rugosa*	37	*M. punctulata*
3	*Ajuga bracteosa*	38	*Ocimum basilicum*
4	*A. dictyocarpa*	39	*O. gratissimum*
5	*A. nipponensis*	40	*O. sanctum*
6	*A. pygmaea*	41	*Origanum vulgare* var. *formosana.*
7	*Anisomeles indica*	42	*Orthosiphon aristatus*
8	*Basilicum polystachyon*	43	*Paraphlomis gracilis*
9	*Chelonopsis deflexa*	44	*P. rugosa*
10	*Clinopodium gracile*	45	*P. tomentosa-capitata*
11	*C. laxiflorum*	46	*Perilla frutescence*
12	*C. umbrosum*	47	*Pogostemon auricularia*
13	*Coleus scutellarioides*	48	*P. formosana*
14	*C. scutellarioides* var. *crispipillus*	49	*Prunella vulgaris*
15	*Dysophylla verticillata*	50	*Rabdosia koroensis*
16	*Elsholtzia ciliata*	51	*R. lasiocarpa*
17	*Glechoma hederacea* var. *grandis*	52	*R. taiwanensis*
18	*Gomphostemma callicarpoides*	53	*Rubiteucris palmata*
19	*G. formosana*	54	*Salvia arisanensis*
20	*Hyptis brevipes*	55	*S. coccinea*
21	*H. rhomboides*	56	*S. hayatana*
22	*H. spicigera*	57	*S. japonica*
23	*H. sauveolens*	58	*S. japonica* var. *taipingshanensis*
24	*Keiskea macrobracteata*	59	*S. keitaoensis*
25	*Kinostemon ningponense*	60	*S. nipponica* var. *formosana*
26	*Lamium amplexicaule*	61	*S. plebeia*
27	*Lamium chinense*	62	*S. scapiformis*
28	*Leonurus sibiricus*	63	*Scutellaria indica*
29	*Leucas mollisima* var. *chinensis*	64	*S. javanica* var. *luzonica*
30	*Leucosceptrum stellipilum*	65	*S. javanica* var. *playfairi*
31	*Lycopus lucidus* var. *formosana*	66	*S. rivularia*
32	*Melissa axillaris*	67	*Sideritis lanata*
33	*Mentha haplocalyx*	68	*Stachys oblongifolia*
34	*Mesona procumbens*	69	*Suzukia shikikunensis*
35	*Mosla chinensis*	70	*Teucrium viscidum*

of ranging (Gower, 1971) is recommended (Sneath and Sokal, 1973). In this study the Gower's method was applied, but the negative matches were counted. The computation formula is shown as follows:

$$S_{ij} = \sum_{k=1}^{n} S_{ijk} / NV.$$

In the above eqation, NV is the total number of characters. S_{ij} is the sum of S_{ijk} divided by NV. S_{ijk} is a matching score of ith and jth OTU's. For dichotomous and two state character, $S_{ijk}=1$, if the ith OTU and jth OTU agree in the kth character and $S_{ijk}=0$, if they differ. For multistate character, $S_{ijk}=1-|x_i-x_j|/R_k$, x_i and x_j are the value of the kth character at the ith and the jth OTU's respectively and R_k is the range of the kth character.

Three methods of cluster analysis were performed to draw phenogram among OTU's. They were single linkage method, complete linkage method and the unweighted pair-group method using arithmetic average (UPGMA).

All the characters were examined during 1969-1972 and were revised during 1975-1976. The computations were carried out on CDC 3150 computer at the Electronic Computer Center of the

Table 2. Code number and states of characters used in the present study.

Code number	Characters	States
	Stem	
1	Habit,	1. erect; 2. both erect and procumbent; 3. procumbent.
2	Height (cm),	1. up to 20; 2. 20-40; 3. 40-60; 4. above 60.
3	Internode: eglandular hair,	1. absent; 2. sparse; 3. moderate; 4. dense.
4	glandular hair,	1. absent; 2. sparse; 3. moderate; 4. dense.
5	stellate hair,	1. absent; 2. sparse; 3. moderate; 4. dense.
6	glandular dot,	1. absent; 2. sparse; 3. moderate; 4. dense.
7	Node: eglandular hair,	1. absent; 2. sparse; 3. moderate; 4 dense.
8	glandular hair,	1. absent; 2. sparse; 3. moderate; 4. dense.
9	stellate hair,	1. absent; 2. sparse; 3. moderate; 4. dense.
10	glandular dot,	1. absent; 2. sparse; 3. moderate; 4. dense.
	Leaf	
11	Type,	1. simple; 2. compound.
12	Arrangement,	1. opposite; 2. verticillate; 3. both opposite and basal rosette; 4. basal rosette.
13	Petiol	1. petiolate; 2. both petiolate and sessile; 3. sessile.
14	Blade length (cm),	1. up to 5; 2. 5-10 3. 10-15; 4. above 15.
15	Blade width (cm),	1. up to 2; 2. 2-4; 3. 4-6; 4. above 6.
16	Blade margin,	1. entire; 2. serrate; 3. dissected; 4. pinnatifid.
17	Upper blade surface: eglandular hair,	1. absent; 2. sparse; 3. moderate; 4. dense.
18	glandular hair,	1. absent; 2. sparse; 3. moderate; 4. dense.
19	stellate hair,	1. absent; 2. sparse; 3. moderate; 4. dense.
20	glandular dot,	1. absent: 2. sparse; 3. moderate; 4. dense.
21	Lower blade surface: eglandular hair,	1. absent; 2. sparse; 3. moderate; 4. dense.
22	glandular hair,	1. absent; 2. sparse; 3. moderate; 4. dense.
23	stellate hair,	1. absent; 2. sparse; 3. moderate; 4. dense.
24	glandular dot,	1. absent; 2. sparse; 3. moderate; 4. dense.
	Inflorescence	
25	Type,	1. cymose; 2. sessile verticillate; 3. both verticillate cyme and raceme; 4. racemose; 5. both raceme and spike; 6. spike; 7. capitulate.
26	Congestion,	1. opeen; 2. both open and dense; 3. dense.
27	No. of flowers per bract,	1. one; 2. two; 3. more than two.
28	Bract shape,	1. linear; 2. triangular; 3. lanceolate to ovate; 4. ovate to cordate: 5. fan-shaped.
29	Pedicel,	0. absent; 1. present.
	Calyx	
30	Type (1),	1. campanulate; 2. intermediate between campanulate and tubular; 3. tubular.
31	Type (2),	1 slightly bilabiate; 2. moderate bilabiate; 3. distinctly bilabiate.
32	Length (mm),	1. up to 3; 2. 3-6; 3. 6-9; 4. above 9.
33	Coverings: eglandular hair,	1. absent; 2. sparse; 3. moderate; 4. dense.
34	glandular hair,	1. absent; 2. sparse; 3. moderate; 4. dense.
35	stellate hair,	1. absent; 2. sparse; 3. moderate; 4. dense.
36	glandular dot.	1. absent; 2. sparse; 3. moderate; 4. dense
37	Puberulent at throat,	0. absent; 1. present.

Table 2. Code number and states of characters used in the present study. (continued)

Code number	Characters	States
38	Scutellum,	0. absent; 1. present.
39	No. of teeth,	1. 5; 2. 10; 3. neither 5 nor 10.
40	Teeth spine-like,	1. no; 2. yes.
41	Teeth of upper lip,	1. equal; 2. unequal.
42	Teeth of lower lip,	1. equal; 2. unequal.
	Corolla	
43	Type (1),	1. campanulate; 2. intermediate between campanulate and tubular; 3. tubular.
44	Type (2),	1. slightly bilabiate; 2. moderate bilabiate; 3. distinct bilabiate; 4. 1-lipped.
45	Length (mm),	1. up to 3; 2. 3–6; 3. 6–9; 4. 9–12 5. above 12.
46	Coverings: eglandular hair,	1. absent; 2. sparse; 3. moderate; 4. dense.
47	glandular hair,	1. absent; 2. sparse; 3. moderate; 4. dense.
48	stellate hair,	1. absent; 2. sparse; 3. moderate; 4. dense.
49	glandular dot,	1. absent; 2. sparse; 3. moderate; 4. dense.
50	Minutely hairy at throat,	0. absent; 1. present.
51	Gibbosed at base,	0. no; 1. yes.
52	Tube/limb ratio,	1. <1; 2. =1; 3. >1.
	Androecium	
53	Stamens,	1. exserted; 2. inserted.
54	No. of fertile stamens.	1. 4; 2. 2.
55	No. of fertile cell per anther for lower pair of stamen,	1. 2; 2. 1; 3. 0.
56	No. of fertile cell per anther for upper pair of stamen,	1. 2; 2. 1; 3. 0.
57	Minutely hairy throughout the anther,	0. no; 1. yes.
58	Puberulent at the end of anther,	0. no; 1. yes.
59	Puberulent at the aperture	0. no; 1. yes.
60	Anthers confluent,	0. no; 1. yes.
61	Filaments connate,	0. no; 1. yes.
62	Filaments appendaged,	0. no; 1. yes.
63	Filaments villous,	0. no; 1. yes.
64	Filaments minutely hairy,	0. no; 1. yes.
	Gynoecium	
65	Style (1),	1. gynobasic; 2. terminal.
66	Style (2),	0. glabrous; 1. hairy.
67	Ovary wall,	0. glabrous; 1. hairy.
	Nutlets	
68	Length (mm),	1. up to 1; 2. 1–2; 3. 2–3; 4. 3–4; 5. above 4.
69	Width (mm),	1. up to 1; 2. 1–2; 3. 2–3; 4. 3–4; 5. above 4.
70	Shape: compressed,	1. no: 2. slight: 3. moderate; 4. distinct.
71	trigonous,	1. no; 2. slight; 3. moderate; 4. distinct.
72	Apex: truncate,	1. no; 2. slight; 3. moderate; 4. distinct.
73	hairy,	0. no; 1. yes.
74	Surface: muricate,	0. no; 1. yes.
75	glandular dotted,	0. no; 1. yes.
76	reticulate	0. no; 1. yes.

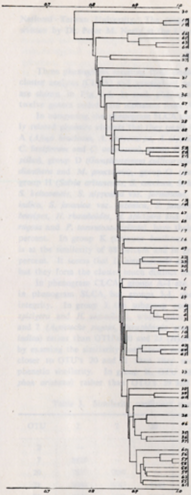

Fig. 1. Phenogram resulting from Single Linkage Clustering Analysis (SLCA). Details see the text.

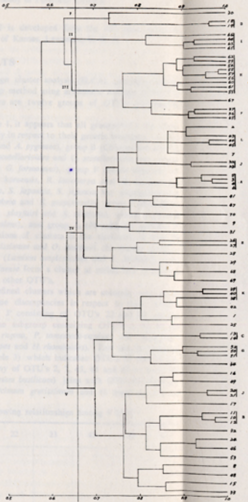

Fig. 2. Phenogram resulting from Complete Linkage Clustering Analysis (CLCA). Details see the text.

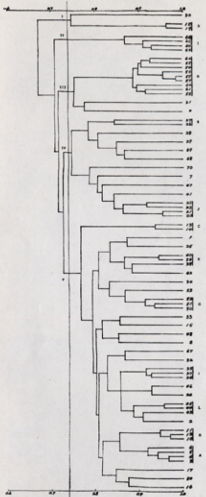

Fig. 3. Phenogram resulting from Unweighted Pair-group Method Using Arithmetic Average (UPGMA). Details see the text.

National Taiwan University. The program used is developed from the NT class program written by Dr. Peter M. Neely at the University of Kansas, Lawrence, U. S. A.

RESULTS

Three phenograms resulting from single linkage cluster analysis (SLCA), complete linkage cluster analysis (CLCA) and unweighted pair-group method using arithmetic average (UPGMA) are shown in Fig. 1–3. In each phenogram there are twelve groups of OTU's representing twelve genera coded with alphabets from A to L.

In comparing the phenogram SLCA and Table 1, it appears that all groups(A–L) are closely related phenetic clusters that they retain integrity in respect to their generic boundary. Group A (*Ajuga bracteosa, A. dictyocarpa, A. nipponensis* and *A. pygmaea*), group B (*Clinopodium gracile, C. laxiflorum* and *C. umbrosum*), group C (*Coleus scutellarioides* and *C. scutellarioides* var. *crispipillus*), group D (*Gomphostemma callicarpoides* and *G. formosana*), group F (*Mosla chinensis, M. dianthera* and *M. punctulata*), group G (*Rabdosia koroensis, R. lasiocarpa* and *R. taiwanensis*), group H (*Salvia arisanensis, S. coccinea, S. hayatana, S. japonica, S. japonica* var. *taipingshanensis, S. keitaoensis, S. nipponica* var. *formosana, S. plebeia* and *S. scapiformis*), group I (*Scutellaria indica, S. javanica* var. *luzonica, S. javanica* var. *playfairi* and *S. rivularia*), group J (*Hyptis brevipes, H. rhomboides, H. spicigera* and *H. suaveolens*), and group L (*Paraphlomis gracilis, P. rugosa* and *P. tomentosa-capitata*) have their junctions of clusters at the similarity of over 90 percent. In group K (*Ocimum basilicum, O. gratissimum* and *O. sanctum*) the cluster junction is at the similarity of 88 percent and in group E (*Lamium amplexicaule* and *L. chinense*) at 83 percent. It seems that *L. amplexicaule* and *L. chinense* form a cluster at rather low similarity, but they form the cluster much distinct from the other OTU's.

In phenogram CLCA, groups A–I are well-defined clusters which are coincide with those in phenogram SLCA, but groups J–L show some discrepancies in respect to their generic integrity. In group J, the subgroup coded with J' consisting of OTU's 22 and 23 (*Hyptis spicigera* and *H. suaveolens*), which joins with the subgroup containing OTU's 2, 43, 44, 45 and 7 (*Agastache rugosa, Paraphlomis gracile, P. rugosa, P. tomentosa-capitata* and *Anisomeles indica*) rather than OTU's 20 and 21 (*Hyptis brevipes* and *H. rhomboides*). This can be resolved by examing the similarity coefficients matrix (Table 3) which indicates OTU's 22 and 23 are closer to OTU's 20 and 21 than they are to any of OTU's 2, 7, 43, 44 and 45 in terms of phenetic similarity. In group K, OTU 38 (*Ocimum basilicum*) joins with OTU 42 (*Orthosiphon aristatus*) rather than OTU's 39 and 40 (*Ocimum gratissimum* and *O. sanctum*), and in

Table 3. Similarity coefficient matrix showing relationships among 9 OTU's.

OTU	2	7	20	21	22	23	43	44	45
2	—								
7	.8610	—							
20	.7877	.7897	—						
21	.8082	.8103	.9543	—					
22	.7959	.7979	.8845	.9119	—				
23	.7710	.7913	.8185	.8390	.9180	—			
43	.9062	.8603	.8281	.8486	.8180	.8140	—		
44	.8603	.8011	.7826	.8123	.7863	.7829	.9158	—	
45	.8603	.7966	.7781	.8169	.7871	.7783	.8929	.9589	—

group L, OTU 43 (*Paraphlomis gracile*) joins with OTU 2 (*Agastache rugosa*) rather than OTU's 44 and 45 (*Paraphlomis rugosa* and *P. tomentosa-capitata*). It is indicated in Table 4, the similarity coefficient between OTU 38 and OTU 42 (.8820) is higher than that between OTU 38 and the cluster consisting of OTU's 39 and 40(.8553) with complete linkage clustering method. The same case in group L can also be explained by checking the similarity coefficient in Table 3, where OTU 43 joins with OTU 2 at .9062 rather OTU's 44 and 45 at .8929. In phenogram UPGMA. groups A–J are concordant with those in the phenogram SLCA, and group K–L have the same distortions as those in the phenogram CLCA. A summary of groups A–L in all three phenograms are given in Table 5.

Table 4. Similarity coefficient matrix showing relationships among OTU's 38–40 and OTU 42.

OTU	38	39	40	42
38	—			
39	.8847	—		
40	.8553	.9432	—	
42	.8820	.8671	.8559	—

Tabie 5. Groups of OTU's representing 12 genera defined in the phenograms

Group	OTU's	Genus	Phenograms SLCA	CLCA	UPGMA
A	3–6	Ajuga	+	+	+
B	10–12	Clinopodium	+	+	+
C	13–14	Coleus	+	+	+
D	18–19	Gomphostemma	+	+	+
E	26–27	Lamium	+	+	+
F	35–37	Mosla	+	+	+
G	50–52	Rabdosia	+	+	+
H	54–62	Salvia	+	+	+
I	63–66	Scutellaria	+	+	+
J	20–23	Hyptis	+	−	+
K	38–40	Ocimum	+	−	−
L	43–45	Paraphlomis	+	−	−

+: desirable cluster, −: questional cluster,

There is an undersirable case that OTU 47 (*Pogostemon auricularia*) and OTU 48 (*P. formosana*) did not join together in the three phenograms. It is interesting to note that in the similarity coefficient matrix (Table 6), OTU 47 has the closest similarity to OTU 16 (*Elsholtzia ciliata*) with 83 percent and OTU 48 has the closest similarity to OTU 33 (*Mentha haplocalyx*) with 85 percent, but the similarity between OTU's 47 and 48 is 80 percent. *Pogostemon auricularia* was transfered from the genus *Dysophylla* (El-Gazzar and Watson, 1967), but it appears a little closer to *Dysophylla verticillata* than to *Pogostemon formosana* in their over all phenetic similarity (Table 6).

Table 6. Similarity coefficient matrix showing relationships among OTU's 15 and 16, 33, and 47–48.

OTU	15	16	33	47	48
15	—				
16	.8000	—			
33	.8598	.8507	—		
47	.8075	.8329	.8123	—	
48	.8192	.8064	.8525	.8000	—

The intercluster relationships in the three phenograms show various arrangements. However, OTU's 1 and 25 (*Acrocephalus indicus* and *Kinostemon ningponense*), OTU's 16 and 49 (*Elsholtzia ciliata* and *Prunella vulgaris*) and OTU's 24 and 46 (*Keiskea macrobracteata* and *Perilla frutescence*) form three clusters respectively in all three phenograms. OTU's 9 and 31 (*Chelonopsis deflexa* and *Lycopus lucidus* var. *formosana*) form clusters in phenograms CLCA and UPGMA, and show close relationships in phenogram SLCA. Two distinctive clusters, one consisting of OTU's 8, 48, 15 and 33 (*Basilicum polystachyon, Pogostemon formosana, Dysophylla verticillata* and *Mentha haplocalyx*) and another of OTU's 26–29 (*Lamium amplexicaule, L. chinense, Leonurus sibiricus, Leucas mollisima* var. *chinense, Stachys oblongifolia*, and *Suzukia shikikuensis*) appear both in phenograms CLCA and UPGMA.

An isolated group containing OTU's 18–19 (*Gomphostemma callicarpoides* and *G. formosana*) and OTU 30 (*Leucosceptrum stellipilum*) forms a cluster at low similarity in three phenograms and joins with all other OTU's very distinctly. These three species are characterized by having stellate hairs different from the other taxa.

No suitable stopping-level could be found in phenogram SLCA to group the clusters into categories between the genus and family, because the over all arrangements of OTU's appears as so-called chaining (Sneath and Sokal, 1973). But a stopping-level was set at the fiven group level in phenograms CLCA and UPGMA. A summary of the five groups in terms of genera is shown in Table 7.

DISCUSSIONS AND CONCLUSION

The intrageneric affinities expressed in the three phenograms resulting from different clustering techniques coincide with the priori relationships of conventional taxonomic study (Huang and Cheng, 1971, 1977). The grouping of taxa within a genus by traditional taxonomic methods is based on intuitive decision from an abstract analysis of the resemblance between the taxa, but the clustering of taxa into hierarchical arrangements by numerical methods is obtained by a measurable and operative approach on the over all similarity between taxa. Especially when there is a large genus with many characters to be treated, numerical taxonomic study gives advantages in dealing with the ambuiguity and complexity among taxa (Bemis *et al.* 1970; Crawford and Reynold, 1974; Rhodes *et al.* 1968 and Taylor, 1966). In this study, the genus Salvia, which has the same subgrouping patterns in the nine taxa through the three phenograms, show not only an inter-taxa relationship corresponding with the results of previous biosystematic study (Wu and Huang, 1975) and revision work (Huang and Wu, 1975), but also presents an objective scheme. In some genera the position of the taxa in the phenogram also provides interesting relationships corresponding with the information of their geographical distribution. For example, in the phenograms, *Ajuga pygmaea*, which only grows

Table 7. Summary of five groups consisting of genera in phenograms CLCA and UPGMA.

phenogram	Group I	Group II	Group III	Group IV	Group V
CLCA	Gomphostemma Leucosceptrum	Scutellaria	Mosla Salvia Sideritis	Agastache Ajuga Anisomeles Chelonopsis Hyptis Lamium Leonurus Leucas Lycopus Origanum Paraphlomis Pogostemon Stachys Suzukia Teucrium	Acrocephalus Basilicum Clinopodium Coleus Dysophylla Elsholtzia Glechoma Hyptis Keiskea Kinostemon Melissa Mentha Mesona Ocimum Orthosiphon Perilla Pogostemon Prunella Rabdosia Rubiteucris
UPGMA	Gomphostemma Leucosceptrum	Scutellaria	Chelonopsis Lycopus Salvia	Anisomeles Hyptis Lamium Leonurus Leucas Origanum Pogostemon Stachys Suzukia Teucrium	Acrocephalus Agastache Ajuga Basilicum Clinopodium Coleus Dysophylla Elsholtzia Glechoma Keiskea Kinostemon Melissa Mentha Mesona Mosla Ocimum Orthosiphon Paraphlomis Perilla Pogostemon Prunella Rabdosia Rubiteucris Sideritis

on rock at sea shores, is connected last to three other species of *Ajuga*. Another example, *Clinopodium laxiflorum*, an alpine plant, joins two other species last.

In a few cases, distortions are found in one or two phenograms. Since phenogram shows simplified relationships between taxa based on similarity coefficients, a combination of necessary similarity coefficient matrix with phenogram would explain the distortions. As measuring the raw data for a numerical analysis is a time consuming work, a few distortions may be due to man-made errors. But checking the original data will reduce the problem.

There is no stopping-level applied in defining the cluster at the genus level, the delimitation of generic boundary in terms of similarity is different from genus to genus in each phenogram. Subgrouping above the genus level is set by two stopping-levels: one in phenogram CLCA at the similarity of 66 percent and another in phenogram UPGMA of 74 percent. Both stopping-levels yield five groups in either phenogram CLCA and UPGMA.

To compare the five groups in both phenograms CLCA and UPGMA in terms of the genera contained (Table 7), groups I and II are identical in both phenograms, group III contain the large genus *Salvia*, the 10 genera contained in group IV of phenogram UPGMA are included in group IV of phenogram CLCA, and 19 of the 20 genera contained in group V of phenogram CLCA are included in group V of UPGMA. In general view, two phenograms show essentially similar generic schems. It was not attempted to compare these five groups to the eight tribes classified by Bentham (1848) or the eight subfamilies by Briquet (1897), because these two systems differ in various heirarchical levels and, as stated by El-Gazzar and Watson (1970), they "make no appreciable contribution towards a better understanding of the arrangement of genera" in Labiatae. Traditional taxonomists subdivide classes of individuals into subclasses based on a character or characters which may vary from one class to another, while the distinct feature of numerical taxonomy is that it classifies operational taxonomic units into clusters at various clustering cycles by using the same set of characters. However, a report from Crovello (1968) stated that changes in characters in numerical taxonomy brings different clusters which reveal a significant information to the problem of the discrepancies in the arrangement of genera in this family.

In conclusion, the numerical taxonomic study of Formosan taxa of Labiate has provided a precise evaluation of the phenetic relationship among taxa in terms of degree of similarity which can not be satisfactorily revealed by traditional taxonomy. The results are objective, when compared with the intuitive methods, though some degree of subjectivity may be introduced during the numerical prosesses as suggested by Katz and Torres (1965).

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