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Clustering Analysis of Distributional Patterns of Global Terrestrial Mammal

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Abstract: In this study, the world's land (except Antarctica) is divided into 67 basic geographical units according to ecological types. Using our newly proposed MSCA (Multivariate Similarity Clustering Analysis) method, 7,591 species of modern terrestrial mammals belonging to 1,374 genera in 162 families and 2,378 species of mammals in the Wallace era before 1876 are quantitatively analyzed, and almost the same clustering results are obtained, with clear levels and reasonable clustering, which conform to the principles of geography, statistics, ecology and biology. It not only affirms and supports the reasonable kernel of Wallace's scheme, but also puts forward suggestions that should be revised and improved. The large or small differences between the clustering results and the mammalian geographical zoning schemes of contemporary scholars are caused by different analysis methods, and they are highly consistent with the analysis results of chordates, angiosperms and insects in the world analyzed by the same method. Once again, it confirms the homogeneity of the global biological distribution pattern of major groups, and the possibility of building a unified biogeographic zoning system in the world.

Key words: Terrestrial mammals, distribution, cluster analysis, geographical division.

1. Introduction

Terrestrial mammals, including humans, are the most familiar and investigated biological groups. Although species account for a small proportion of global biological species [1], most of them are studied, developed and utilized as very important groups. It is a very urgent topic to explore their distribution law, formation mechanism and geographical division. In the 19th century, British zoologist A. R. Wallace [2] formulated a zoogeographical zoning plan of 6 realms and 24 subfields based on the distribution of mammals. Wallace's line, named after him, as the boundary between the Oriental realm and the Australian realm, is his important contribution [3]. His "the geographical distribution of animals" is regarded as the foundation work of animal geography. Although some people have made some modifications [4], it is almost unchanged until now [5].

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However, people's discussion on higher zoogeography has not stopped. On the one hand, they discuss the rationality of "Wallace's line" [6-9], and on the other hand, they try to equip biogeography with quantitative analysis methods [10-20]. In the 21st century, people's attention to animal geographical zoning is rising rapidly, and various geographical zoning schemes of 7-14 boundaries are proposed for different animal groups with different methods [21-23]. S. Proches [24] conducted cluster analysis on the distribution of bats, divided the world into 10 geographical regions, and considered it suitable for animal geography and plant geography. H. Kreft and W. Jetz [25] used Simpson formula and UPGMA (Unweighted Pair Group Means Algorithm) method to gather the world into seven realms. Compared with Wallace scheme, except for the newly established Madagascar realm, the dividing line of other realms has also changed. B. G. Holt et al. [26] also used

Simpson formula and UPGMA clustering method to analyze more than 20,000 species of terrestrial mammals, amphibians and non marine birds, dividing the world into 11 realms. And M. Rueda et al. [27] also analyzed these animals and believed that it was not necessary to modify Wallace plan. In the face of such disputes, it is no wonder that Professor J. J. Morrone [28] of Mexico lamented that geographical zoning is a ghost hindering the development of biogeography.

People have gradually formed a consensus that the intervention and support of mathematics should be an important way that cannot be avoided or overstepped in the development of biogeography. If a subject does not integrate mathematics into it, it cannot be really mature [29].

There are many analysis methods used in biogeography. After extensive comparison, we propose a new clustering method to analyze the distribution pattern of global terrestrial mammals, in order to explore the reasonable core of Wallace's scheme and the places that need local correction.

2. Materials and Methods

2.1 Global Terrestrial Mammal Fauna

The data source of this study is the monograph of zoologists [30, 31]; Floristic data collated by professional biodiversity websites [32]. In addition, new species and new distribution records published by taxonomists will be supplemented at any time [33-36]. In the mammal fauna data of 20,867 species in 29 orders, excluding deep-sea species and fossil species, there are 7,591 species of terrestrial mammals in 27 orders, 162 families, 1,374 genera for analysis (Table 1).

Table 1 Global terrestrial mammal.

Order	Global fauna			For analysis		
	No. of Families	No. of Genera	No. of Species	No. of Families	No. of Genera	No. of Species
1 Afrosoricida	2	29	73	2	19	55
2 Artiodactyla	50	648	1,974	21	186	572
3 Camivora	24	548	1,790	13	112	374
4 Cetacea	44	406	840			
5 Chiroptera	29	309	1,737	21	213	1,494
6 Cingulata	9	130	386	1	10	27
7 Dasyuromorphia	4	41	145	3	24	103
8 Dermoptera	1	4	13	1	4	6
9 Didelphimorphia	5	76	309	1	18	111
10 Diprotontia	23	147	497	12	41	201
11 Erinaceomorpha	9	114	275	1	17	59
12 Hyracoidea	3	24	75	1	3	5
13 Lagomorpha	3	63	257	3	13	108
14 Macroscelidea	4	27	55	1	4	18
15 Microbiotheria	2	9	17	1	1	1
16 Monothemata	3	10	27	2	3	9
17 Notoryctemorphia	1	2	3	1	1	2
18 Paucituberculata	15	75	157	1	3	9
19 Peramelemorpha	4	16	63	3	8	30
20 Perissodactyla	17	292	1,046	4	17	102
21 Pholidota	3	10	18	2	6	14
22 Pilosa	18	208	484	4	8	17
23 Primates	49	425	1,320	20	80	565
24 Proboscidea	5	32	115	1	3	10

Table 1 to be continued

25 Rodentia	76	1,367	5,397	36	519	3,236
26 Scandentia	2	8	38	2	5	20
27 Sirenia	4	48	99			
28 Soricomorpha	10	173	912	3	55	542
29 Tubulidenta	1	5	19	1	1	1
Total29	619	6,580	20,867	162	1,374	7,591

2.2 Division of Basic Geographic Units and Construction of Database

Many scholars use the grid method to divide BGU (Basic Geographic Units), and divide the world land into many grids according to longitude and latitude or geographical distance. There is nothing wrong with the grid method itself. The problem is that the number of animals in each grid is not investigated according to the grid method, but the result of long-term accumulation by taxonomists. The depth, frequency, time, collection range and recording specifications of investigations between grids are different, which inevitably form human differences, which will affect the natural differences we want to explore.

According to the ecological conditions and the details of animal distribution data, the global land (except Antarctica) is divided into 67 BGUs as the basis of cluster analysis and geographical division (Fig. 1). Among them, there are 21 BGUs based on plains, 11 BGUs based on hills, 12 BGUs based on mountains, 11 BGUs based on plateaus, 5 BGUs based on deserts, and 7 BGUs based on islands. There are 26 BGUs in the tropics, 34 BGUs in the temperate zone, and 7 BUGs in the cold zone. The names and geographical ranges of each BGU are shown in Table 2.

Fig. 1 BGUs of the world.

Table 2 The number of mammal of BGUs in the world.

BGU	Range	Number			
		Families	genera	species	Before 1876
01 Northern Europe	Norway, Sweden, Denmark, Finland, Iceland	28	71	137	130
02 Western Europe	Britain, Belgium, Ireland, Netherlands, C.N. of France	45	118	242	215
03 Central Europe	Germany, Hungary, Austria, Czech, Poland, Switzerland	52	166	242	211
04 Southern Europe	Iberian Pen., Apennine Peninsula, Balkan Pen.	52	187	240	178
05 Eastern Europe	Estonia, Latvia, Lithuania, Belarus, Ukraine, Moldova	32	88	139	125
06 European Russia	European Russia	25	77	194	160
11 Middle East	Turkey, Syria, Lebanon, Jordan, Georgia, Armenia, Azerbaijan	47	150	252	171
12 Saudi Arabia	Saudi Arabia, Iraq, Kuwait, United Arab Emirates, Qatar, Bahain	26	37	100	78
13 Yemen and Oman	Oman, Yemen, Socot Island	22	37	86	57
14 Plateau of Iran	Afghanistan, Iran, Pakistan	42	129	241	159
15 Central Asia	Kazakhstan, Turkmenistan, Uzbekistan	29	80	168	130
16 Western Siberia	Western Siberia Plain	16	33	79	71
17 Eastern Siberia	Eastern Siberia Plateau	22	66	170	126
18 Ussuri region	Ussuri region, O. Sakhalin	12	23	70	0
19 Mongolia	Mongolia	21	60	152	112
20 Plateau of Pamir	Plateau of Pamir, Tadzhikistan, Kirghizstan, Kashnir	12	23	115	92
21 N.E. of China	Heilongjiang, Jilin, Liaoning, Neimongol	24	89	128	96
22 N.W. of China	Xinjiang	23	76	78	58
23 Plateau of Q.Z.	Qinghai, Xizang (except Southeastern)	26	78	82	49
24 S.W. of China	W. Sichuan, N.W. Yunnan, S.E. Xizang	36	115	158	101
25 Southern China	S. Yunnan, Guangxi, Guangdong, Hainan	43	166	202	133
26 C.E. of China	Provinces of C.E. China	49	187	335	198
27 Taiwan of China	Taiwan region of China	28	83	120	81
28 Korea Peninsula	D.P.R. Korea, R.O. Korea	15	31	77	57
29 Japan	Japan	24	65	177	116
31 Himalayan region	Bhutan, Nepal. Sikkim, Himachal, Punjab, Assam	35	97	280	221
32 India, Sri Lanka	India, Bangladesh, Sri Lanka, Maldives	40	145	380	274
33 Myanmar	Myanmar, Andaman Is., Nicobar Is.	33	99	224	149
34 Indochina P.	Cambodia, Laos, Thailand, Vietnam	33	115	383	215
35 Philippines	Philippines	36	132	241	99
36 Indonesia	Brunei, East Timor, Malaysia, Indonesia, Singapore	41	186	704	315
37 New Guinea	New Guinea I., Papua New Guinea	23	112	282	78
38 Pacific Islands	Polynesia, Micronesia, Melanesia	24	45	182	101
41 Northern Africa	Algeria, Egypt, Libya, Morocco, Tunisia, Canary Is.	40	127	229	162
42 Western Africa	From Mauritania to Nigeria	50	193	498	266
43 Central Africa	Cameroon, Central Africa, Chad	29	96	392	231
44 Congo river basin	Congo, Equatorial Guinea, Gabon, Zaire, Sao Tome et Peincipe	45	192	578	269
45 Ethiopia region	Ethiopia, Somalia, Sudan, Djibouti, Eritrea	41	144	397	230
46 Tanzania region	Kenya, Rwanda, Tanzania, Uganda	48	195	730	306
47 Angola region	Angola, Botawana, Mozambique, Namibia, Zambia, Zimbabwe	31	120	515	276
48 South Africa	South Africa, Lesotho, Swaziland	42	160	349	245
49 Madagascar	Madagascar, Comoros, Mauritius, Reunion, Seychelles	21	60	278	105

Table 2 to be continued

51 Western Australia	Western Australia	35	80	201	118
52 Northern Territory	Northern Territory	29	72	194	104
53 South Australia	South Australia	37	82	193	131
54 Queensland	Queensland	33	100	301	155
55 New South Wales	New South Wales, Australian Capital Territory, Lord Howe I.	34	94	219	152
56 Victoria	Victoria	33	81	172	133
57 Tasmania	Tasmania	28	54	96	76
58 New Zealand	New Zealand, Norfolk I.	18	28	51	50
61 Eastern Canada	Manitoba, Newfoundland, Ontario, Quebec, Northwest Territories	22	55	157	130
62 Western Canada	Alberta, British Columbia, Yukon Territory, Saskatchewan	38	116	227	175
63 Mts. Eastern US	Florida, Georgia, Maine, Virginia, New York, Carolina *et al*.	58	153	298	244
64 Plain Central US	Alabama, Arkansas, Illinois, Michigan, Missouri, Wisconsin *et al.*	54	139	244	205
65 Hills Central US	Texas, Kansas, Minnesota, Dakota, Nebraska, Iowa, Oklahoma	51	179	398	306
66 Mts. Western US	Arizona, California, Colorado, Utah, Washington, Wyoming *et al.*	78	265	602	405
67 Mexico	Mexico	60	248	616	268
68 Central America r.	Costa Rica, Salvador, Guatemala, Honduras, Nicaragua , Panama	42	162	470	217
69 Caribbean Islands	Bahamas, The Caribbean Island Countries	25	83	138	82
71 Venezuela	Venezuela, Lesser Antilles Is.	43	166	441	230
72 Plateau Guyana	Guyana, Surinam, French Guiana	37	124	283	171
73 N. Mt. Andes	Colombia, Ecuador, Peru, Arch. De Colon Is.	50	244	843	324
74 Amazon Plain	Northern Brazil	36	146	432	279
75 Plateau Brazil	Southern Brazil	44	182	452	288
76 Bolivia	Bolivia	40	158	448	266
77 Argentina	C.N. of Argentina, Paraguay, Uruguay	56	239	422	237
78 S. Mt. Andes	Chile, S. of Argentina, Is. Malvinas	30	92	176	121
BDR		2,374	7,795	18,700	11,312
BBU		162	1,374	7,591	2,378

Build the database with Microsoft Access, taking each BGU as each column and each category as each row. Convert the administrative area records of each animal distribution into BGU records, and enter them into the database. If there is a distribution record of "1", it will not be recorded if there is no distribution. These BDRs (Basic Distribution Records) will be the basic materials for quantitative analysis. Then summarize the distribution of each species in a genus and establish a "genera database". Then summarize the distribution of each genus in a family and establish a "families database". A total of 2,378 species of mammals were selected according to the named age "≤ 1876", which will be the most complete species that Wallace may have collected at that time. See Table 2 for the families, genera and species of each BGU and the number of species before 1876.

2.3 Clustering Method

The hierarchical clustering method used in biogeography research has more than 40 similarity formulas and more than 10 clustering methods [37]. The commonly used formulas include Jaccard (1901) formula, Szymkiewicz (1934) formula (= Simpson (1947) formula), Czekanowski (1913) formula (= Sørensen (1948) formula), and the commonly used clustering methods include single linkage method (= nearest neighbor method), average group linkage method (= UPGMA (Unweighted Pair Group Means Algorithm) method), sum of squares method (= Ward's method).

After extensive comparison, we adopt the simulation general formula, SGF and multivariable simulation clustering analysis method, MSCA (Multivariate Similarity Clustering Analysis) newly proposed by Shen Xiaocheng and others [19, 20]. SGF is defined as: the similarity coefficient between multiple regions is the ratio of the average number of common species in each region participating in the analysis to the total species:

$$SI_n = \sum H_i/nS_n = \sum(S_i\text{-}T_i)/nS_n$$

In the formula, SI_n is the similarity coefficient of n geographical units, S_i, H_i and T_i are the number of species, common species and unique species of i geographical units respectively, and meet the requirements of $H_i = S_i\text{-}T_i$, and S_n is the total number of species of n geographical units. Each value required for calculation can be easily obtained from the query page of the database. Both manual calculation and computer software analysis are very convenient and fast.

The MSCA used with SGF is that the similarity coefficient of any group is calculated directly with the original number of BUGs involved in the analysis, which is not affected by the similarity coefficient of the previous analysis, and is not limited by the clustering order. It can even first calculate the GSC (General Similarity Coefficient) of 67 BUGs, which is a concept that other clustering methods do not have and an index that cannot be calculated. Finally, the clustering diagram is arranged according to the similarity coefficient. This method has been verified and applied in different biological groups and different geographical regions [38-53].

3. Analysis Results

The clustering results of 162 families, 1,374 genera and 7,591 species, three different taxonomic levels of terrestrial mammals in the world are shown in Figs. 2-4. The GSC of 67 BGUs are 0.227, 0.086 and 0.036 respectively. At the similarity levels of 0.420, 0.240 and 0.140 respectively, 67 BUGs are clustered into A~G, a total of 7 UCs (Unit Crowds). The composition BGU of each UC is adjacent and connected, which conforms to the principle of geography; all crowds occupy continental blocks with ecological differences, which conforms to ecological principles; the similarity level within each UC is higher than that between UC, which conforms to the statistical principle. The difference is that the higher the classification level is, the higher the similarity level is, and the higher the clustering level is. Although the location of individual geographical units has changed, they all move in the middle of the adjacent two UCs, which does not violate the principles of geography.

The clustering results of 2,378 terrestrial mammal species known before 1876 in the world are shown in Fig. 5, with a GSC of 0.073. When the similarity level is 0.220, 67 BUGs are also clustered into 7 UCs. The composition of each UC is almost the same as that of Fig. 4, except that unit 18 has no distribution record and does not participate in the analysis.

Each UC fauna has a considerable proportion of unique endemic groups (Table 3), and each group has its own core area. The core area relies on its own more

Table 3 Mammal fauna of every UC.

UC	Families	Endemic Families	%	Genera	Endemic genera	%	Species	Endemic species	%
A	78	5	6.41	305	25	8.19	852	243	28.52
B	57	4	7.02	276	29	10.51	699	274	39.20
C	61	3	4.92	383	154	40.21	1,340	839	62.61
D	69	9	13.04	394	181	45.94	1,625	1,291	79.63
E	48	8	16.67	163	42	25.77	690	525	76.09
F	99	11	11.11	476	85	17.86	1,316	626	47.57
G	69	4	5.80	367	140	38.15	1,504	1,087	72.27
Total	162	44		1,374	673		7,591	4,885	

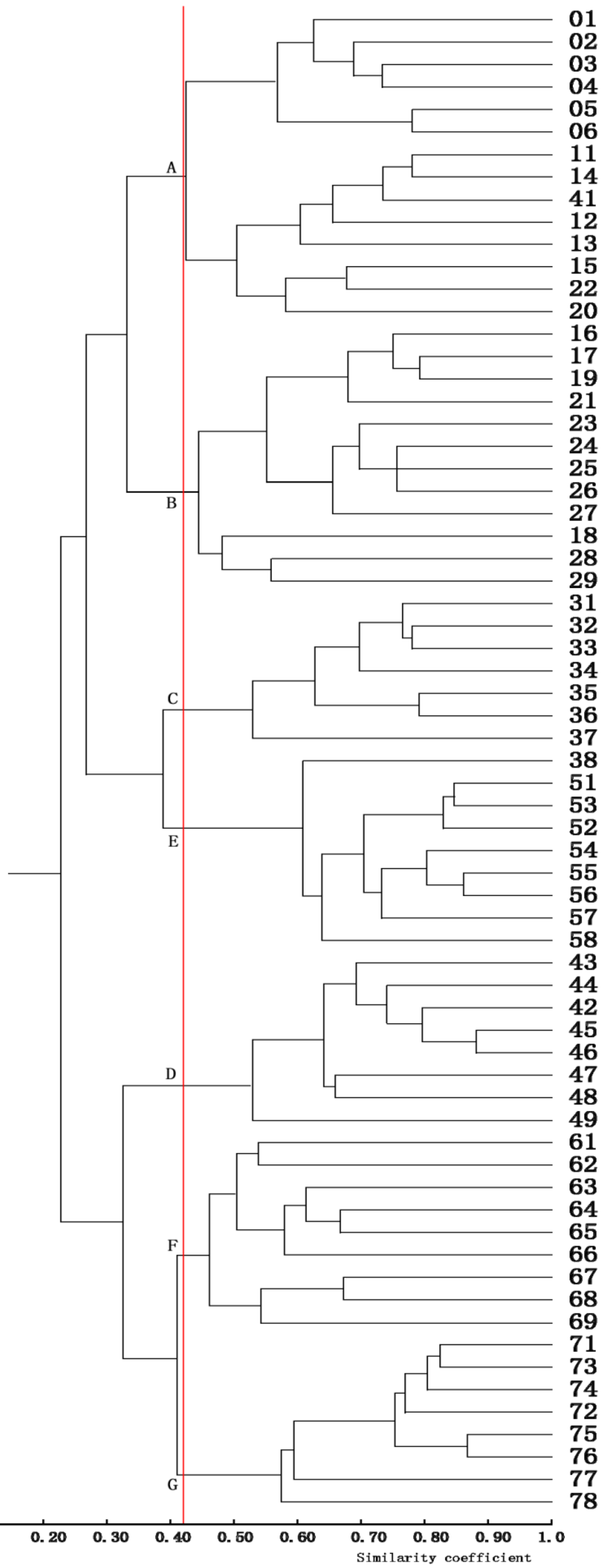

Fig. 2 Clustering tree of 162 families of global terrestrial mammal.

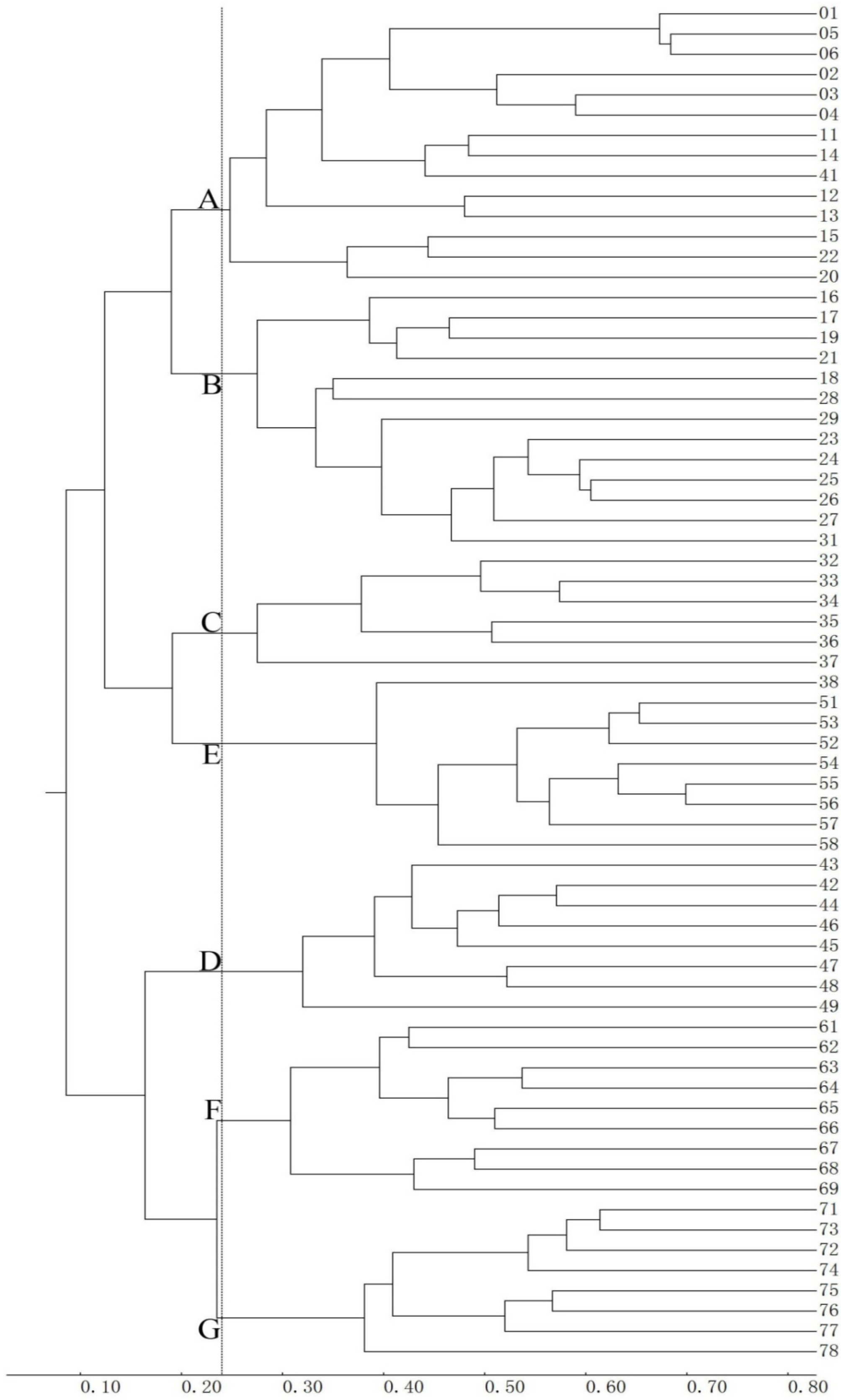

Fig. 3 Clustering tree of 1,374 genera of global terrestrial mammal.

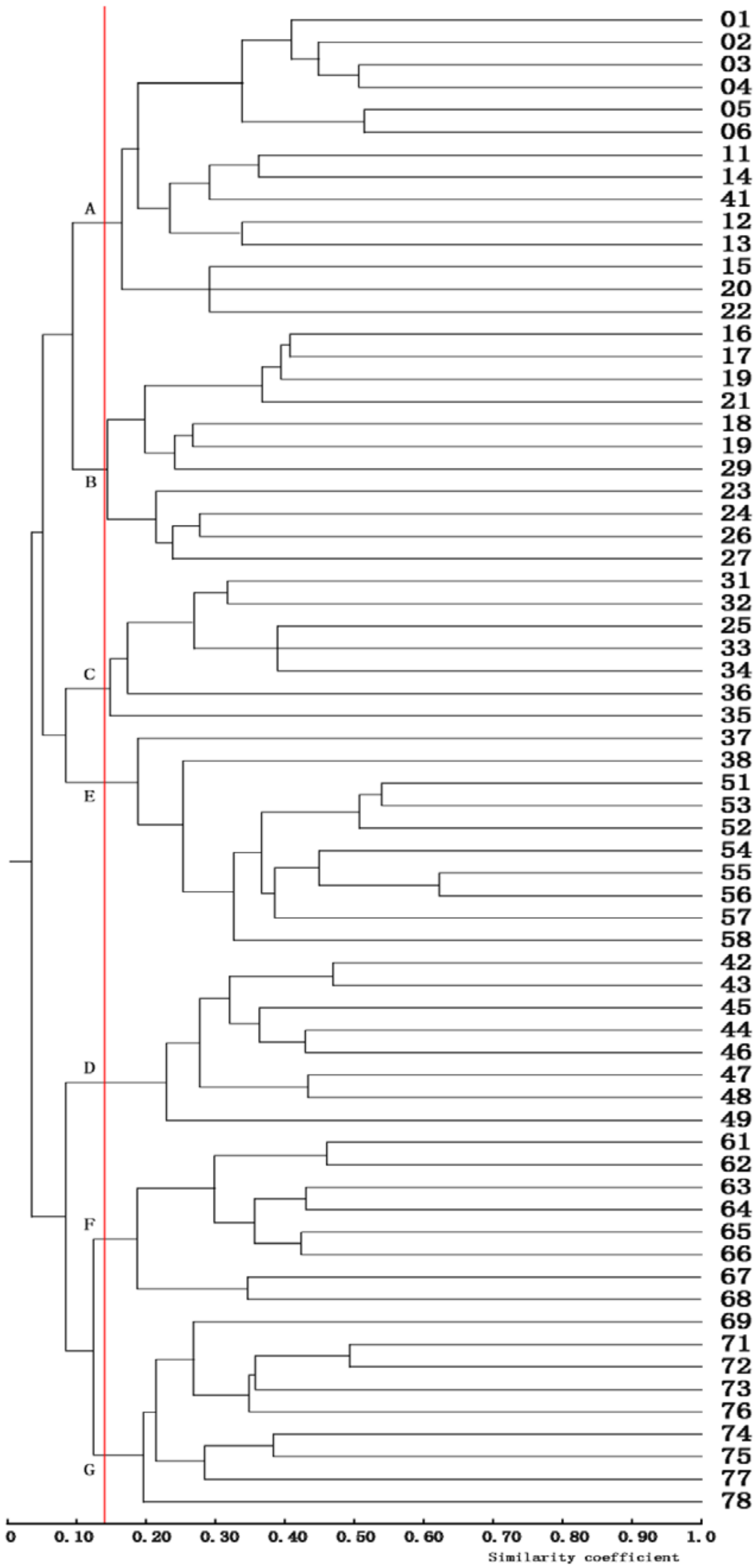

Fig. 4 **Clustering tree of 7,591 species of terrestrial mammal before 1876.**

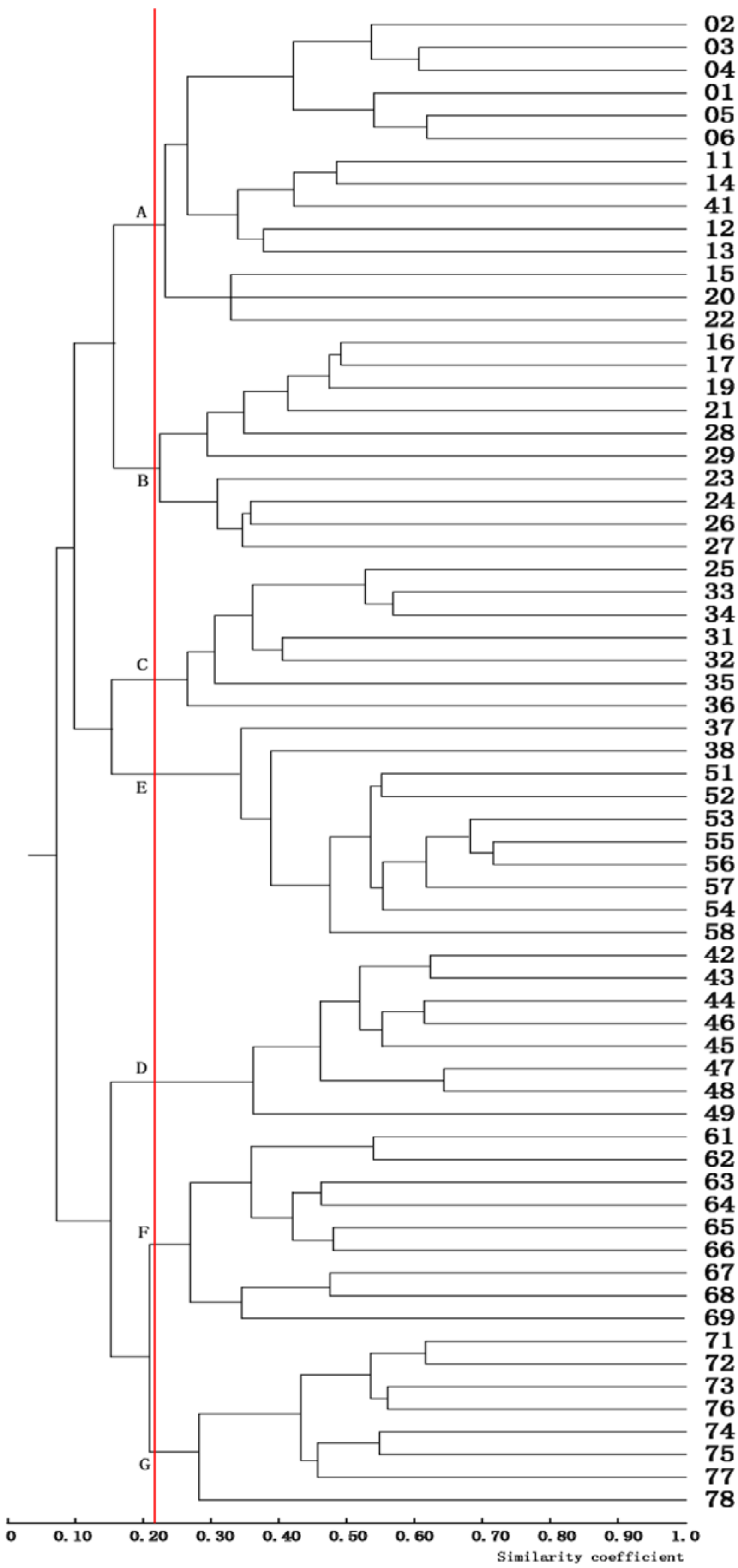

Fig. 5 **Clustering tree of 2,378 species of terrestrial mammal before 1876.**

common species to exert its gathering power, builds its own unit group, and also depends on the difference between its own unique species and other groups.

4. Discussion

Mammals are biological groups that have received great attention, and the prevalence and detail of the investigation are far from that of other biological groups. Its distribution characteristics are also prominent. The diversity of developed regions is poorer than that of developing regions. Unlike other biological groups, Europe, North America and Australia are richer than other regions. This obvious difference does not affect the clustering results. Mammals flourished in the Cenozoic era, and the world continental pattern has been formed. Although mammals are warm blooded animals, which are less affected by the environment and have strong diffusion ability, they are obviously blocked by the ocean, that is, they are widely distributed in continents and have significant differences between continents. Although this feature does not have an impact on the large pattern, it has an obvious impact on the crowd. Within crowds C, D, and E, the differences of BGU between continents become smaller, and the independence of islands increases, such as BGU 35, 36, 37, 38, 49, 58 and 69.

Compared with Wallace's scheme, the clustering results have a relatively consistent general pattern and obvious specific differences. Crowd A and crowd B are equivalent to Palaearctic realm, crowd C and crowd E are equivalent to Oriental realm and Australian realm, crowd D is equivalent to Afrotropical realm, and crowd F and crowd G are equivalent to Nearctic realm and Neotropical realm. The difference is that the Palaearctic realm is divided into two parts: the East and the West with kingdom level; The island of New Guinea broke away from Australia and gathered in the Oriental realm, and Wallace's line no longer existed; Central American region left the Neotropical realm and gathered in the Nearctic realm; Yemen, Oman, etc. left the Afrotropical realm and gathered in the west Palaearctic realm; Taiwan left the Oriental realm and gathered in the east Palaearctic realm. This shows that the division of Wallace's scheme based on continental blocks has a reasonable scientific core. Due to the limitations of the scientific level at that time, there are areas that need to be improved and perfected. The consistency between the analysis results of 7,591 modern species and 2,378 mammal species in the Wallace era shows that the stability of the nature of the fauna in various regions of the world does not affect the overall distribution pattern because of the in-depth investigation and the improvement of species richness.

There are big or small differences between the clustering results and the analysis results of contemporary scholars [21-27], obviously due to different analysis methods.

The clustering results are highly consistent with the analysis of chordates, angiosperms and insects in the world [44, 46, 48, 50, 52, 53], which not only shows the homogeneity of the impact of environmental conditions on the distribution of various organisms, but also shows that it is convincing to modify and improve Wallace's scheme in this way.

Medical insects that feed on mammals should have the same distribution pattern as mammals. The analysis results of Shen et al. [42, 47, 49] on medical insects are the same as those of phytophagous insects, but different from Wallace's scheme. This seemingly contradictory result is answered in this study. The distribution pattern of mammals and medical insects is the same, the same in the new clustering results, rather than the same in Wallace's scheme.

Insects (except medical insects) have little direct relationship with mammals, and their evolution is more than 300 million years earlier than that of mammals. There seems to be no basis for entomological circles to borrow or apply Wallace's scheme for a long time, so an insect geographical division system of 7 kingdoms and 20 subkingdoms has been established [1]. In this study, mammals and insects are unified in the new clustering results, rather than Wallace's scheme.

The geographical division of mammals and flowering plants has been carried out independently. Although people expect it to be similar or similar [5], it seems to be getting farther and farther [26]. The results of this study once again confirm the homogeneity of the world's biological distribution pattern [53], which provides the possibility and feasibility for establishing a unified biogeographic zoning scheme in the world. In this way, people's understanding and understanding of the complex biological distribution pattern will be easy and clear.

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