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Biogeography of Medically Important Insects using Quantitative Analysis

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Abstract

We summarized distributional information of medically important insects from 76 families and 4531 genera occurring worldwide. The continents were divided into 67 basic geographical units. Using a new similarity formula and a new clustering method for quantitative analysis, 67 basic geographical units were clustered into 7 large unit groups and 20 small unit groups. The results were superior to the traditional single linkage method, average group linkage method, or sum of squares method. The cluster results were similar with the result of mainly phytophagous insects 104,344 genera in the world, but were different from the Wallace?s mammal geographical division scheme. Based on these seemingly contradictory results, we infer that animals, insect and plants may have the same distribution pattern and that it is necessary to conduct precise quantitative analysis for animals and plants worldwide.

Index terms— biogeography; medical important insect; similarity general formula; multivariate similarity clustering analysis.

1 Introduction

here are three categories of medically important insects: insects that feed on the blood of warm blooded animals (humans, mammals, and birds) and can transmit disease; insects that feed on the fur, feathers, and skin secretions of animals and birds, irritating the host; insects that live in the habitats of humans, mammals and birds, causing irritation and sometimes transmitting diseases. Since these insects have a close relationship with mammals and birds, they may have the same geographical distribution pattern with the mammals described by Wallace (1876). Computer and Internet technology has made it possible to collect and analyze large data sets and re-evaluate previous Wallace's scheme which are based on qualitative analysis **??**Olson et Different geographical division schemes for some insect orders and families have been proposed (Herman et al., 2001;Evans, 2007; **??**alianet al., 2008;Moor et al., 2008;Morse et al., 2011; **??**aegeret al., 2010). The results of most of these studies did not support the "Wallace line", that is Wallace's great contribution to the field. Among them, as medical important insects, Culinidae and Siphonaptera geographic division settings are also proposed the same questions **??**Siver, 2004; **??**ashchonovet al., 2013). The extensive attention and indepth discussion in biogeography interpretation provides an exciting opportunity for evaluating insect distributions and geographical division plans.

We used the similarity general formula (SGF) proposed by Shenet al. (2008a) and multivariate similarity clustering analysis (MSCA) **??**Shenet al., 2008b) for quantitative analysis of the medically important insects in China (Shen, 2014). The results were unexpectedly similar to the results of all (93661) insect species in China **??**Shenet al., 2013a;2013b;2015), but different from the results of a Chinese mammalian species geographical division, made using qualitative analysis (Zhang, 2011). To study the relationship between the global distributions of medically important insects, phytophagous insects, and mammals, we used a variety of quantitative methods for this analysis.

2 II.

3 Materials and Methods

4 a) Global medically important insect species

We used medically important insect distribution data from four resources: (1) World species and distribution data collected and summarized by entomologists, e.g. **??**night et al., 1977, Durden et 1). This was 4.3% of the total number of insect genera and 6.1% of the total insect species in the world. Because insects have small bodies, their species distribution is narrower compared with higher animals and plants **??**Shenet al., 2018). To improve the data utilization ratio and accuracy of the analysis, the genus was used as the basic biological unit (BBU).

5 b) Division of basic geographical units (BGU) and building the databank

According to the terrain, climate, and other ecological conditions, we have divided the continents (except Antarctica) into 67 basic geographical units (BGU) (Fig. 1). Of these BGUs, 21 BGUs were mainly plain, 11 were mainly hills, 12 were mainly mountain, 11 were mainly plateau, five were mainly desert and seven were mainly islands. A total of 27 BGUs were in tropical zone, 34 were in temperate zones and six were extended to the frigid zone. The names and geographical ranges of the BGUs are listed in Table 2.

We used Microsoft Access as our database software. Each BGU was listed as the column and BBU was listed as the row. The distribution of different species belonging to the same genus was transferred to the BGU and summarized as the genus distribution. During the data entry, when there was a distribution, it was marked as 1; if there was no distribution, no record was entered. These basic distributional records (BDR) were the basis of quantitative analysis. Each BGU insect genus number is listed in Table 2. SI n = ?H i /nS n = ?(S i ?T i)/nS n

In this formula, SI n is the similarity coefficient of n BGUs: S i , H i and T i are i BGU species number, common species number and unique species number, respectively, and H i = S i ?T i : S n is the total species number in n BGUs. For calculation, all values were obtained from the database search page. This was convenient for both manual and computer calculations.

The MSCA indicated that the similarity coefficient of any group could be calculated directly and not restrained by the clustering order. It even was possible the first to calculate the total similarity coefficient of the 67 BGUs.

For example, we calculated the similarity coefficient of four BGU from Europe (Fig. 2). The 4066 in the first column of the first row was the number of genera that have not distribution by all four BGUs. The first number in other each column was the unique species number of every BGU. The number 465, which was the total genus number 4531 minus 4066, was the total species number of all five BGUs. The genus numbers of four BGUs were 253, 316, 245, and 271 as shown in Table 2. Using a calculator for these steps 253+316+245+271?30?59?7?68=921, dividing by 4, then dividing by 465, produced a similarity coefficient 0.495. The process was simple compared to the processes of other clustering methods. 1) The single linkage method, also called nearest neighbor method, using the Jaccard (1901) similarity formula: SI=C/(A+B ?C), which was the most basic clustering method; 2) Average group linkage method, which was also called unweighted pair group means algorithm (UPGMA) method, using the Szymkiewicz (1934) similarity formula, also called the **??**impson (1947) formula: SI=C/min(A,B), which is the most popular clustering method. 3) Sum of squares method (Ward's method), using the Czekanowski (1913) similarity formula (also called Sørensen (1948) formula): SI=2C/(A+B). Using this method, better results can be obtained, but the calculation process is complicated.

The three similarity formulas were subjected to pairwise comparisons. A and B were species numbers in two regions and C was the species number shared by two regions.

6 III.

7 Results

MSCA clustering results (Fig. **??**) showed that the 67 BGUs total similarity coefficient was 0.089. At 0.370 similarity coefficient level, 67 BGUs were clustered as at 20 small unit groups, at 0.250 similarity coefficient level, 20 small unit groups were clustered as A-G 7 big unit groups. Unit of each group was neighbor and connected to each other, corresponding to the geographical principles. The similarity level was greater within the group than among different groups and the ecological condition of each group was independent, corresponding to the principles of statistics and ecology.

Clustering results showed high consistency with world insects clustering results **??**Shenet al., 2018). The numbers of big and small unit groups were the same, components of each big and small group were almost the same, and the structures between the groups were consistent. One difference was that the total similarity coefficient and similarity level of large and small unit groups of medically important insects were higher than all insects. This may be because medically important insects have generated more attention and research. The clustering location of individual units had moved: Unit 25# moved from the g small unit group to the f small unit group. Unit 37# moved from the h small unit group to the i small unit group. Unit 74# moved from the r

small unit group to the s small unit group. These movements were between neighboring groups, consistent with geographical principles.

We compared mammalian division scheme (Wallace, 1876) and except for the D big unit group that was the same in the Ethiopian realm, all other groups were different. A and B big unit groups divided the Palearctic realm into east and west sections. C and E big groups incorporated New Guinea and Pacific islands from the Australian realm into the Oriental realm. F and G big groups incorporated Central America in the Neotropic realm into the Nearctic realm.

Compared with current world plant division proposed by Cox (Cox, 2001), the C, D, E big unit groups were the same as the India-Pacific kingdom, Afritropic kingdom, and Australian kingdom. The difference was that the A, B and F big unit groups divided the Holarctic realm into three parts. F and G big groups categorized Central America in the Neotropic kingdom into the Nearctic kingdom.

Compared with the current several insect groups division, our results support the following: the Palearctic realm is divided into two parts by Trichoptera and Aleyrodidae (Morse et al., 2011;Evans, 2007). The Siphonaptera and Trichopteracategorize New Guinea and the Pacific Islands into the Oriental realm **??**Vashchonoket al., 2013;Moor et al., 2008). The results also support separating Pacific Islands from the Australia realm by Staphylinidae, Aleyrodidaeand aquatic insects (Herman et al., 2001;Evans, 2007; **??**alianet al., 2008); incorporation of Yemen and Oman into the Palearctic realm by Symphyta and Culicidae **??**Taegeret al., 2010;Silver, 2004); And incorporation of Mexico into Nearctic realm by the Culicidae (Silver, 2004). However, the results did not support assigning New Zealand, Madagascar and Antarctic as separate realms.

The traditional methods did not produce accurate, sensitive, and precise results. The results of the single linkage method (Fig. **??**) were chaotic with no distinct layers. Many geographical units could not be clustered, such as units 20, 31, 49, 58, 69, 78, that were called "noise". The average group linkage method (Fig. **??**) was better than the single linkage method and removed most of the "noise". At the distant level of 0.63 the BGUs could be clustered into six unit groups, five of which had significant geographical meaning. The letters corresponding to the areas in Fig. **??**, the largest group which was composed of 26 BGUs, were chaotic and lacked geographical values. More precise division did not improve this. The sum of squares method (Fig. **??**) had better clustering results. At the distance of 1.2, the BGUs could be clustered into eight groups and the first seven had geographical meaning. The last group did not conform to the principle of geography and it was difficult to achieve precise clustering.

8 Discussion

This study demonstrated that the distribution pattern of medically important insects is consistent with that of phytophagous insects. However it is indisputable fact that the medical insects have a close relationship of food chain with higher animals. Therefore, we can speculated that most insects are phytophagous and the distribution pattern is the same as for plants. Although of them are carnivorous, the final food sources are plants. Their distribution pattern should be the same as plants. Thus, medical important insects belong to the bidirection food chain of animals ? plants ? phytophagous insects and showed the same results as the total insect distribution. Without doubt this hypothesis requires confirmation from quantitative analysis of plants and mammals and the first step would be to select and standardize the different methods. The comparisons made in this study showed that MSCA method can be useful. We look forward to establishing a consistent model of the distribution patterns of plants, mammals, and insects across the world. [1]

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1

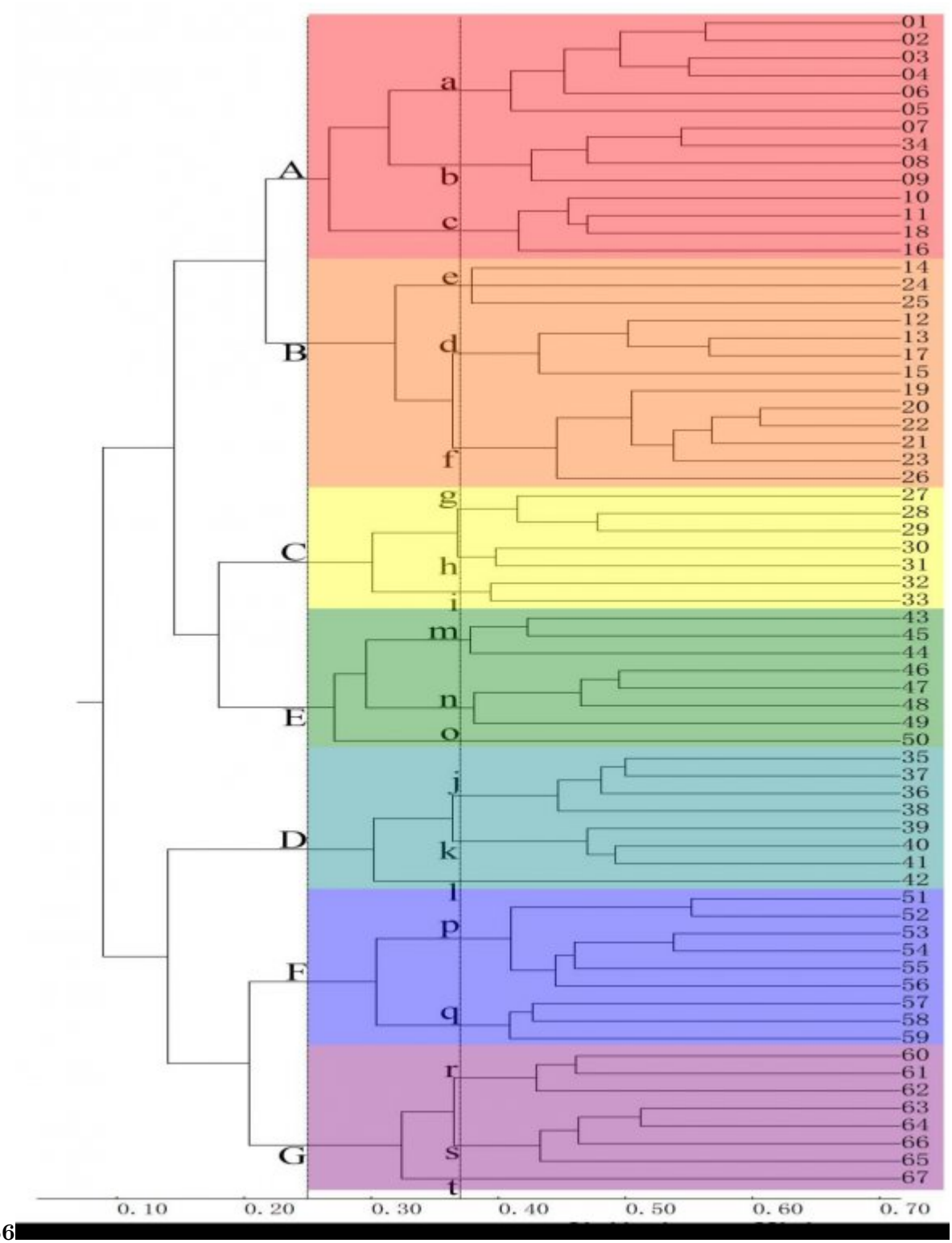
Figure 1: Fig. 1 :

]1

序号之计数	01	02	03	04
4066				
68				1
7			1	
26			1	1
59		1		
11		1		1
11		1	1	
30		1	1	1
30	1			
2	1			1
7	1		1	
9	1		1	1
43	1	1		
7	1	1		1
37	1	1	1	
118	1	1	1	1

2

Figure 2: Fig. 2 :



3456

Figure 3: Fig. 3 :Fig. 4 :Fig. 5 :Fig. 6 :

Figure 4:

1

Orders	No. of families	No. of genera	No. of species	Main data sources
Blattodea	8	490	4428	Roth, 2003, Vidli?ka, 2013, 2017, Beccdloni, 20 Vrsansky, 2010, 2012, 2013
Mallophaga	9	485	4565	Mey, 2004, Pickering, 2014, Gustafsson, et 2015
Anoplura	14	46	553	Durden et al., 1994, Sánchez-Montes et al., 20
Hemiptera	1	22	74	Usinger, 1966,Iorio, 2012, GBIF, 2019c
Coleoptera	1	126	2480	GBIF, 2019a
Diptera	16	2337	36594	
Siphonaptera	20	241	2099	Acosta, 2003, Hastriteret al., 2006, Lewis al., 2013,Vashchonoket al., 2013,Beaucournuet 2014
Lepidoptera	2	544	5969	GBIF, 2019e
Hymenoptera	5	440	6708	GBIF, 2019d
Total	76	4531	63470	

Figure 5: Table 1 :

2

BGU	Number of genera	BGU	Number of genera	BGU	Number of genera	BGU	Number of genera
01	253	19	310	37	207	55	242
02	316	20	457	38	131	56	323
03	245	21	474	39	241	57	325
04	271	22	614	40	251	58	459
05	99	23	419	41	292	59	133
06	143	24	125	42	180	60	179
07	208	25	300	43	116	61	173
08	81	26	161	44	101	62	376
09	75	27	310	45	79	63	263
10	211	28	214	46	239	64	239
11	246	29	284	47	232	65	150
12	165	30	201	47	135	66	235
13	315	31	343	49	151	67	74
14	124	32	179	50	71	BBU	4531
15	103	33	168	51	205	BGU	67
16	127	34	209	52	256	BDR	15450
17	446	35	222	53	299	AR *	231
18	314	36	139	54	233	ADT **	3.41

*[Note: *AR (average richness): BDR/BGU: **ADT (average distributional territory): BDR/BBU c) Clustering methods]*

Figure 6: Table 2 :

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