Translation from the Chinese of the article by **Qu Fengyi** 瞿逢伊 and Qian Guozheng 錢國正, research fellows at the Parasitology Centre of the *Number Two Military Medical University* in Shanghai.

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**title: 蚊科三十八個已知屬的系統發育數值分析**

**translated title:** "Numerical phylogenetic analysis of thirty-eight already classified systems within the mosquito family" [English title on page 109: "A Numerical Phylogenetic Analysis on 38 Known Genera of Culicid Mosquitoes (Diptera: Culicidae)"; the synopsis and the Key Word list are identical to the English translation on the same page.

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Culicidae were the first of the Diptera to diversify from the Nematocera as a sophisticated group. World-wide thirty-eight known genera have up to date been registered, and 3357 species and sub-species (cf Knight & Stone 1977, Knight 1978, Ward 1984 and Qu Fengyi & Qian Guozheng 1988). The currently predominant experimental method of classification for determining genus, tribe and sub-family, using external characteristics as the main taxonomic criterion, needs to be confronted with the actual system produced by natural evolution. As fossilised evidence remains extremely scarce, research results which could be used as proof have been difficult to obtain. The authors will attempt to employ methodologies based on phylogenetic systematic theory (Hennig 1966, Chen Shixiang 1978) and on the numerical analytical method (Farris 1970, Simon & al. 1982), and will construct a Wagner Tree, utilised for the analysis of the external characteristics of the mosquito genera known to exist. They will explore the relationship in between each mosquito genus, and provide elementary materials in order to establish a system corresponding to the patterns of natural evolution.

## Source Materials and Methods

1) *Source Materials for Research*

The object of the present study are the thirty-eight mosquito genera listed in chart number one. Specimens from the collections of our institution and relevant articles from scientific publications were pre-sorted for information on the phenotypes of each mosquito genus. Sixteen unitary external characteristics of imagines and larvae were then selected as units for the operational classification necessary to carry out the numerical phylogenetic analysis.

2) *Feature Analysis and Quantification*

The quantitative analysis was conducted on the basis of the said sixteen features, consisting of twelve imago (serial numbers 1 - 12) and four larva (serial numbers 13 - 16) features. Indicating the original feature as 0 (zero), evolutionary features constitute the factor 1, whereas the above-mentioned two types of features equal 0.5 each. With the feature value for each of the genera increasing by the factor (x), the calculation for computing the evolutionary value of each genus is ($\sum x_i$, i = 1,2, ... 16). The sequential numbers and quantification criteria were allocated to the following features: 1) The curving of the mouth area (0) or its straightness (1); 2) enlargement of the mouth area (0) or normal size (1); 3) cirrus of the female being more than half longer than the ordinary mouth area (0) or less than a third of its normal length (1); 4) cirrus of the male being more than half longer than the ordinary mouth area (0) or less than a third of its normal length (1); 5) antennae which are clearly developed (0) or latent (1); 6) scale tissue of the wings being lightly coloured, white or white-with-stripes (0), or uniformly dark (1); 7) length of the wings being $V_6$ (short) (0) or surpassing $V_5$ in diameter (1); 8) rear edge of the small shield forming a circular arc (0) or having trilobal shape (0); 9) abdominal plate having few scales or being unscaled (0) or being densely covered by scales; 10) the gripping mechanism of the male tail organ being equipped with rudimentary nodes or secondary end leaves (0) or not having any (1); 11) with membranes as anal cover (0) or with fully developed antennae; 12) male stalk organ simple (0) or complex in structure (1); 13) larval jaw line undeveloped (0) or fully developed (1); 14) equipped with an oesophagus (0) or not (1); 15) oesophagus having comb-like teeth (0) or not (1); 16) the dorsal section being with VIII comb teeth [*sic*](0) or being without (1).

3) *Method of Calculation*

For the entire calculation process, the computer programme *Basic* was used, with IBM-PC/AT [hardware] equipment. Having consulted the calculation methods and programmes of Farris (1970) and Simon & al. (1982), the first step was to take the thirty-eight genera as operational taxonomic units and to construct a Primal Tree by using the law of the smallest distance. The following step was to create a Wagner Network to the basic thirty-eight genera, by adding hypothetical taxonomic units. Borrowing the mosquito with the lowest evolutionary value, the *Anopheles*, for the stem, a Wagner Tree was built up. Thereafter, an optimised Wagner tree was created out of the sketch drawings made during the course of the analytical research, by employing the method suggested by Farris (1970). In addition, using the law of the smallest distance, a chart listing all classified objects according to their numerical value was drawn up for comparison. In order to enhance the results of the comparative exercise, the Manhattan distance and not the Euclidean one was chosen for all of the methods listed above.

## Results and Discussion

*1) Systematic Phylogenetic Relationship between each of the Culicid Genera*

Culicidae are a relatively big and from an early point in their evolutionary development relatively sophisticated group within the Diptera/Nematocera (Qu Fengyi and Qian Guozheng 1988). Despite their importance, there is a dearth of research reports on the phylogenetic relationship between the different genera of the family. By means of a Wagner Tree, the current research attempts to give a preliminary presentation of the phylogenetic relationship between the thirty-eight existing genera of the Culicidae. From the illustration displaying Wagner's Tree (figure 1) the three branches and thirty-eight genera can be seen:

The first branch develops out of the genus *Anopheles*, which includes the three single-genus groups *An/Bi/Ch* - the primeval genus group with the lowest evolutionary value (5.5 - 6). In overall terms, the primeval features within this group predominate, though some features indicate a clear evolutionary tendency, for instance the complete jaw line of *An* larvae, the equally short cirri for both genders of the *Bi* imagines, and the trilobal small shield of the *Ch* imago.

The second branch consists of three groups and has its origin in the *Tr* genus, incorporating the *Tr Tx Cq, Sh, In, Jb, Mi, Ru* as well as eight other genera. In evolutionary terms, this branch has reached the middle level (evolutionary value 8 - 12). The single-genus groups *Tr* and *Tx* constitute ancestral types which ceased to progress from an early stage onwards. The former is located in the tropical zones of our earth, whereas the latter can be found all over the world. The mouth area of the adult *Tx* is bent, the rear edge of its small shield round in shape. The larva's jaw line is undeveloped, retaining clear evidence of primeval features. Within the system of experimental classification, the *Tx* represents a single-genus sub-family. The feature patterns within the six genera of the *Cq* group are unclear, making diversity the main characteristic of this group. Whereas earlier literature incorporated *Tr* into the same category as *Sh, Ru, Jb, Tr,* etc, the genus *Tr (s.lat.)* is now treated separately (Zavotink 1979, Ward 1984). All evidence suggests, that *Tr (s.lat)* and *Tr (s.str.)* in reality have very different characteristics. The result of our research not only clearly indicates the group into which this genus belongs, but also sheds light on the correlation between dissimilar phylogenetic systems. On this basis, it enables us to adapt the existing classifications to the one determined by the natural development of the Culicidae.

The third branch arises from the straight-legged genus *Or*, containing twenty-seven genera (*Or Ma/Ad, Ur, Ze, Mg/Wy, Ph, Sa, Fri, Li/Ar, Er, Hg/Ps, Ud/Ae, Hz, Cx/Cs, Op, Tp, De, Ga, To, Mi, Ho*, etc) in eight groups. Representing the majority of all Culicid genera, this branch has the highest evolutionary value of 10 - 16. The two genera *Or* and *Ma* form two groups with very similar evolutionary value and features. They can be regarded as the ancestors of the third branch, interrupted in their development. The branch contains a great number of genera with complex interrelation.

*2) Classification Systems for the Culicid Mosquito*

The result of the phylogenetic analysis of the thirty-eight genera of the Culicidae can be summarised in the observation that there are three branches with fourteen groups. As detailed in Table 2, additional research has provided a possible classification for three sub-families and fourteen tribes. Current research divides the families of the Anophelinae, the Culicinae and the Toxorhynchitinae, their three subfamilies and thirty-eight genera (including one of these sub-families, which is again divided into ten tribes) into unmistakable categories. This current classification model, however, contains a great number of subjective factors, leading to shortcomings from the evolutionary perspective, from which we have clearly distanced ourselves in this article. Despite the many theoretical disputes which dominate the field of present day taxonomy, virtually everybody agrees that any taxonomic system based on evolutionary facts would overcome the current divisions. Based on morphological, ecological and other related features used as evidence for taxonomic classifications, and by enhancing the findings of previous phylogenetic and numerical analyses, we conclude that it is very well possible to establish a new, unified ... classification system which corresponds to the natural evolutionary development. Reaching such a point of systematic unification would also indicate an important development in the systematic study of the Culicidae.

*3) Comparison of Methods for the Analysis of Natural Correlational Systems*

This article used the illustrative techniques of the Primal Tree, the Wagner Network and Wagner Tree, numerical taxonomies and other methods for a comparative study, and has come to the following conclusions: The Primal Tree method can differentiate a system of thirty-eight genera and of three branches which can be discerned by analysing the development during their early stages. It cannot, however, deliver a solid picture representing the components within each of the three branches. The Wagner Network corrected the relationship between the genera; Wagner's Tree clearly illustrates the composition of each of the branches. Comparatively speaking, there is a high degree of disorder in between the various constituents within any numerical taxonomy, reducing the distinctive meaning of any model. For the sake of saving space, only Wagner's Tree was reprinted in this article.

## Reference Literature
## (Chinese titles)


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- Qu Fengyi & Qian Guozheng, *Wenke deng bage jinyuanke de xitong fayu guanxi chubu yanjiu* (A tentative study for a phylogenetic taxonomy for the Culicidae and eight related families), in *Dongwu fenleixuebao* (Bulletin for Zoological Taxonomy) 13 / 4 (1988), pp. 373-377.
- Qu Fengyi & Qian Guozheng, *Wenke de quxi fenbu jiqi yanbiande chubu tantao* (A first study of interrelations within the Culicidae and their development), in *Dongwu fenleixuebao* (Bulletin for Zoological Taxonomy) 14 / 4 (1989), pp. 468-474.


## Tables and Illustrations

*table one* (pages 104 and 105) : Results of the analysis of features, the evolutionary value and of the geographical location* of the Culicidae
*(P = Prehistoric North; O = Pacific; A = Australia; E = Africa; N = new North; NT = New Tropics)

*table two* (page 106) : Comparison of features between each of the groups and branches of the Culicidae

(n.b. + : signifies evolutionary features throughout; - : signifies primeval features throughout; 0 : interaction between evolutionary and primeval features)

*illustration one* (page 107): Diagram of the Wagner Tree for the thirty-eight genera of the Culicidae