

## Some considerations of evolutionary process in Fulgoromorpha

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Mitochondrial DNA sequence is generally used in recent molecular systematic studies of vertebrates and invertebrates. The genes of rDNA and cytochrome b, in particular, have been used extensively for the comparisons at the family level. Phylogenetic information from DNA sequence was well studied, however it also makes some confusion to the results of morphological characters. It is not difficult to find the conflicting phylogenetic systematics between morphological characters and DNA sequence evidence<sup>1,2</sup>; on the other hand, it was not easy to conclude which one was better than the other. Either morphological character or DNA sequence data had its supported evidence and it was just the point to cause confusion. The nature of these two types data has great difference. For examples, the concept of mutation with constant rate was unsuitable to morphological character, but it was generally used in DNA sequence data. The taxonomic category was constructed based on species numbers and morphological characters but not due to the derived time.

Three considerations are presented here to infer the possible evolutionary process in Fulgoromorpha for the conflicts between the phylogenetic results of morphological characters and that of DNA sequence evidence. First, the resulted phylogenetic relationships would be equivocal in higher categories by DNA sequence if adaptive radiation occurred (Fig. 1). It is generally accepted that the evolutionary rate of DNA sequence is not exactly constant. Therefore, there would be a confounded relationships among these high categories constructed from DNA sequence if their ancestors were derived in a short period time, i.e. adaptive radiation. Second, the evidence of DNA sequence would not provide unambiguous phylogenetic relationships in higher categories, if one clade derived from the sublineage of the other (Fig. 2). The fact that the derived time of each family is different would reveal an confounded relationships from molecular evidence due to the additive property of DNA sequence. A good example was presented in Ehinodermata by Wada<sup>3</sup>. Third, if the ancestral lineages of each clade in the higher categories are still extant (Fig. 3), it might be difficult to obtain the true phylogenetic relationships by DNA sequence evidence. Hot spot mutation of a gene would increase by time and the mutation proportion will reach the saturation level.

We obtained sequence information based on PCR method of two genes, 16S rDNA and cytochrome b, to infer the phylogenetic relationships of Fulgoromorpha. In 16S rDNA, 500bp of 3'end from 37 species in 13 families was analyzed, while in cytochrome b gene, 400bp of the middle region in 13 species of 8 families was included. Phylogenetic analyses were performed by using Neighbor-Joining method where pairwise distance estimates were based on models of Jukes and Cantor, Kimura-2-parameter, Tamura, and Tamura-Nei as implemented by the MEGA program and transversion substitution was choose only to analyze the cytochrome b gene. The phylogenetic relationships of Fulgoromorpha at family level are not clear from both 16S rDNA and cytochrome b genes. These two genes may not be suitable to resolve the relationships and some families of Fulgoromorpha may not be homogeneous. However, other considerations as we proposed earlier, which are adaptive radiation, the derived time of each category, and the saturation effect, may provide better explanations. Phylogenies derived from 16S rDNA (Fig. 4) indicated that, mostly, members of the same family were grouped together with the exceptions of the taxa Del1, Der2, Fla2. Evidences from molecular data suggest that the members of the same family were not grouped together might be due to the above considerations 2 and 3. The branching points of subfamilies of Issidae were close to each other which reflects the problem in consideration 1. Furthermore, the distance between families or family-groups was minor and the values of F-test by Tukey's multivariate analysis showed that there were successive significant differences between families. The results again suggest the existence of adaptive radiation in early divergence of Fulgoromorpha. Phylogenies derived from cytochrome b reveals the similar information, however, it needs further information of this gene to view these considerations (Fig. 5).

### References

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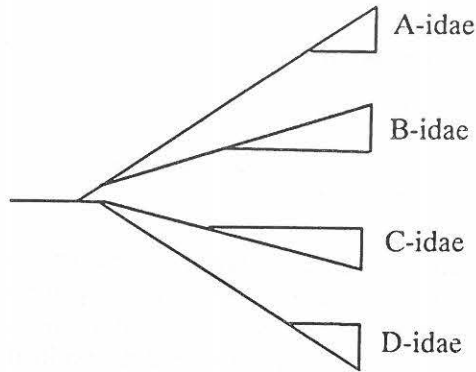


Fig. 1. There would be a ambiguous phylogenetic relationship which was constructed from DNA sequence among these hypothetical families, if their ancestors were derived in a short period of time.

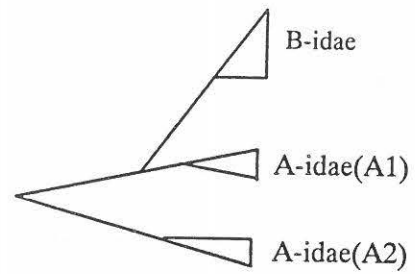


Fig. 2. From DNA sequence, B-idae should be grouped with A1 if B-idae was derived from the sublineage(A1) of A-idae.

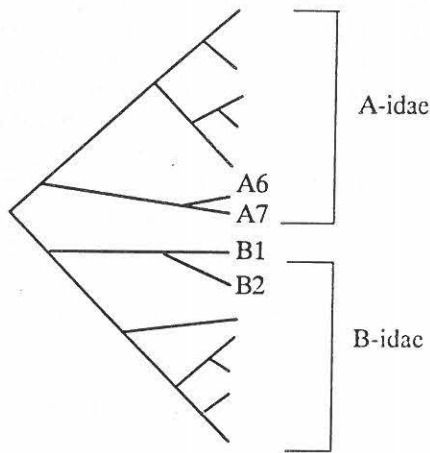


Fig. 3. If A-idae and B-idae were two distinctly families from morphological data, whereas the taxonomic location of A6-A7 and B1-B2 would be equivocal from molecular data.

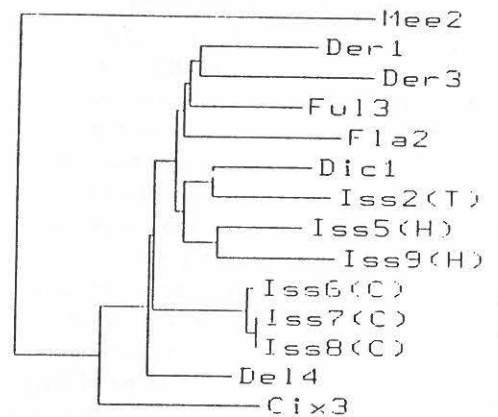


Fig. 5. The phylogenetic tree was inferred from partial cytochrome b sequence by Neighbor-Joining method based on transversion substitution.

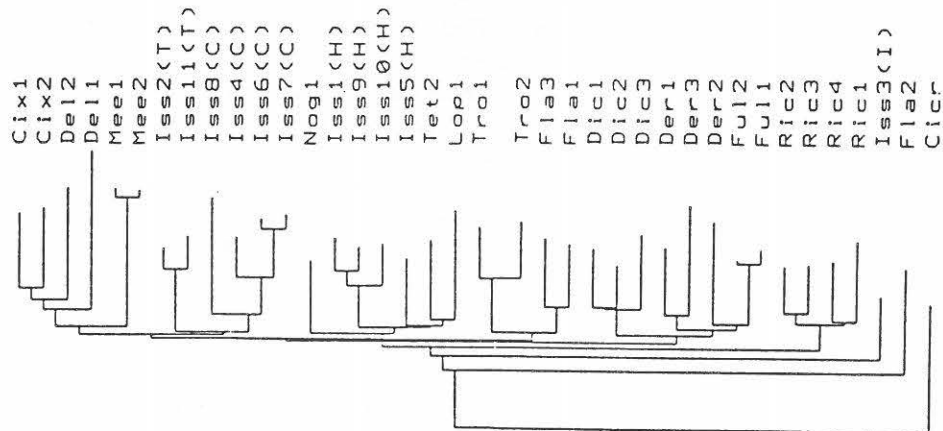


Fig. 4. The phologenetic tree was inferred from partial 16S rDNA sequence by Neighbor-Joining method.



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