

Discussion

1. Which data partitioning strategy has answered the questions?

Under the dataset partitioning strategy I, the phenomenon of proportion difference or not can be ascribed to the lack of colourful appearance in category A, the avoidance of including colour/pattern (termed C/P) characters in category B and D, and the insufficient data in category C and E. This calculation is opposite to that in Areekul & Quicke (2006), our result indicates that the different expression between colour/pattern and non-colour/pattern (termed non-C/P) partitions is due to the number of characters in each partition rather than the intrinsic quality of characters except in category C and E, however, these two categories own few data matrices.

The “symmetrical degree” of broken-line graph in figure 4 represents the difference between signals strength carried by C/P or non-C/P partitions, and the “degree of sharpness” represents the degree of conflict between C/P or non-C/P partitions.

The broken-line graph of category A is the most asymmetrical, which is likely due to the significant smaller number of C/P characters in their original data matrices. Except for category A, the asymmetry only happens at the 1.5x weighted comparison of category D, which indicates that the C/P characters could only mislead phylogenetic reconstruction to some degree (Table 3). Category B, C and E are statistically symmetry,

which means that these data matrices carry C/P and non-C/P partitions of approximately equal strength.

As to comparing the proportions of taxa retained in ASTs between five categories at each relative weighting scheme (Table 4), there is no significant unevenness between up-weighting C/P and non-C/P partition, again represents that the contribution of C/P partition is on a par with that of non-C/P partition. However, the post-test for relative weighting scheme which have significant difference between five categories reveals that category B behaviour significant differently from categories A, C and E; that is to say, category B (involve aposematic but not mimetic) may have some heterology between category B and the other categories.

We hereunto know that the plot of ratios of taxa remain in agreement subtrees for category A is pretty asymmetry, which indicates that the C/P characters of animals without vivid colouration do not be confided or may do not perform so well in phylogenetic reconstruction in the past studies. The plot of category B is more symmetry (Table 3) but “acute” (Fig. 4B, number of taxa remained in ASTs are between about 0.6 to 0.85), which indicates that the C/P and non-C/P partitions carry more conflicting signals and have around equal strength. The plots of category C and E is symmetry and more gradual, which indicate that the conflict between C/P and non-C/P partitions in not so drastic; The plot of category D shows similar situation as category C or E even though it is not so symmetry.

Under the dataset partitioning strategy II, we can see clear different between category B and category C+D+E, which are both symmetry (Table 3, Table 5) but the plot of category B is acute and what of category C is smoother (Fig. 5, number of taxa remained in ASTs are between about 0.7 to 0.9). Moreover, we can concentrate the comparison on “the right part of broken-line graph” of category B and category C+D+E because both of which are “symmetry”, and pay close attention correspondingly to the “up-weighted C/P partition” of the post-test for relative weighting scheme which have significant difference between 3 categories (table 6), this results again reveal that category B (involve only aposematism) is significantly different from category C+D+E (involve mimicry) (see Fig 6e).

2. Why did the test fail to detect the effect being predicted?

The data above indicates that the colour or pattern characters in semipalmate aposematic and mimetic organisms carry signals conflict to non-C/P partition to differential degree. Therefore, when talking about using coloration characters of glowing creatures in phylogeny reconstruction, we can not discuss the role of C/P characters in aposematic and mimetic organisms amalgamatively.

The clear discrepancy between aposematic (category B) and mimetic (category C, D and E) could not be obtained from our partitioning strategy I, that is, the real data is not that sensitive to our ideal partitioning to reflect different circumstances of mimicry. The reason and

explanation describe as follows; first, the colour/pattern characters in the data matrices were not necessarily involved in the biological function we predicted (for instant, the C/P characters adopted in data matrices of mimetic taxa may not involve in mimicry such as coloration of pupae, larvae or legs and abdomen of adults) and the partition betwixt categories (because there are sometimes cases not clear between categories); further more, C/P characters usually accounted for a smaller part of the whole data matrix, and did not featured largely in topology. Secondly, we can not make predictions to the distribution of the mimetic characters on a phylogenetic tree or our prediction would not occur to real data. Finally, there is significant difference while we combine all circumstances of mimicry into one category, but there is no clear significant difference while we apply detailed partition strategy, this inactive strategy indicates that the distributions of Batesian, quasi-Batesian or Müllerian mimicry could not be predicted. Therefore, the prediction of Simmons and Weller (2002) from mimetic tiger moths and wasps, which confirmed by PTP tests the mimetic type and associated traits are phylogenetic conserved as traditional Müllerian mimicry prediction, could not be inferred to other organisms.

3. Suggestion on treating colour/pattern characters in phylogenetic studies

We processed prediction to C/P characters with manifold biological function in phylogenetic reconstruction, which is more detailed and chimed better in the real situation than the partition of Areekul & Quicke

(2006), and distinguished the different behaviour of colour/pattern characters in data matrices involved in aposematism and mimicry. Areekul & Quicke (2006) considered that colour character involved in mimicry or aposematic pattern would mislead the phylogenetic relationships. However, we found that colour/pattern characters have no concern with mimicry or aposematic pattern, as category A, probably cryptic pattern or an irregular plesiomorphy, also can mislead the phylogeny reconstruction; and the C/P characters involved in mimicry are not so bad as their conclusion.

In the consequence, we suggest that it is unnecessarily to give peculiar judgments to C/P characters before reconstruct phylogenetic trees, and the other non-C/P characters also have similar risks such as convergence or random appearance.

To estimate the effect of a dataset to the phylogenetic reconstruction, we suggest that there should be two independent partitions (for example, one consisted of C/P characters and the other consisted of non-C/P characters, or one consisted of adult characters and the other consisted of immature characters) in one data matrix to test the influence on topology construction caused by such a character subset while processing phylogenetic analysis by morphological characters. The better resolution scheme is to reconstruct phylogenetic relationship by characters independent of morphological characters, for instance, molecular (or chemical) characters, then regard the molecular topology as a framework and map the colour and pattern characters onto the tree for further

discussion.