The phylogenetic analysis of tribe troidini and preliminary study of comparative phylogeography of Atrophaneura horishan

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ABSTRACT

Phylogenetic relationships among the Troidini butterflies in Taiwan were analyzed by comparing 830 nucleotide sequence of mitochondrial gene encoding cytochrome oxidase I (COI). The phylogenetic analysis reconstructed by neighbor-joining (NJ) and maximum-parsimony (MP) method suggested that the genera Byasa and Atrophaneura were closely related. The Atrophaneura horishana is the conservative butterflly in Taiwan, The Atrophaneura spp. is predominantly tropical, distribured in the low latitude area in South-East Asia, and the low altitude area in temperate Asia. Atrophaneura horishana is an endemic species in Taiwan, distributing at an altitude from 1500 to 2500 meters, mainly at mountains in central Taiwan. Atrophaneura horishana in Taiwnan must be suffered from the environmental changes during glacial periods. It is unknown that the implication of conservation of Atrophaneura horishana though such the evolutionary process. For understanding the post-glacial recolonization history of Atrophaneura horishana, it might be possible to study comparative phylogeography of Atrophaneura horishana the sympatric species Byasa polyeuctes termessus. The results show that the gene flow of low altitude populations of Byasa polyeuctes termessus is very frequently. The population differentiation of Byasa polyeuctes termessus distributed at high altitudeis not significant because of flying abilities. Comparatively, the populstions of Atrophaneura horishana in high alititude mountain area are more differentiated, but gene flow is still frequently. From the results, we suggest that the populations of Atrophaneura horishana in Taiwan is an Evolutionary Significant Unit (ESU), and it will be very important for the conserevation strategy of Atrophaneura horishana to monitor population dynamics and population genetic structure campared with Byasa polyeuctes termessus.

Keywords : Triodini、Atrophaneura horishan、Byasa polyeuctes termessu、mitochondrial DNA、phylogeographic

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