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Phylogeographies of *Angiostrongylus cantonensis* and its host *Achatina fulica* in China

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The giant African snail *Achatina fulica* and its nematode *Angiostrongylus cantonensis* are mainly found in Southern China areas including Taiwan. In the present study, the phylogeographies of *A. fulica* and its nematode *A. cantonensis* in South China (including Taiwan) were investigated. Based on the mt Cytb and ND2 sequences, phylogeographical pattern of the giant African snail (*Achatina fulica*) in the South China (including Taiwan) showed that all local populations vary in the genetic diversity, the Kaohsiung (KH) population in Taiwan exhibited relatively high level of genetic diversity based on both Cytb and ND2 sequences. Analyses of both molecular variance (AMOVA) and pairwise *F*_{ST} detected no significant population genetic structure among populations. Neutrality tests revealed that *A. fulica* might have undergone population expansion. The results of the median joining network (MJN) showed two not distinct lineages, the greater one contained the haplotypes from all populations, the other merely included haplotypes from Taiwan, which is different from the topology of the neighbor-joining trees. We suggested that the original populations invading Taiwan was a mixture of two or more different populations, but only one of them was afterwards brought to Mainland China.

Based on whole sequences of the mitochondrial cytochrome b (Cytb) of 496 individuals and NADH dehydrogenase subunit 2 (ND2) of 498 individuals of *Angiostrongylus cantonensis* obtained from 12 localities in South China, relatively low genetic diversities were detected for all local populations except for that from Hekou (HK) in Yunnan Province. The analyses of molecular variance (AMOVA) and *F*_{ST} detected distinct population genetic structure between Hekou (HK) population and each of other populations, which consists with the result of exact test of differentiation. The phylogenetic trees based on the sequences of ND2 and Cytb showed 2 (based on ND2) or 3 (based on Cytb) major lineages respectively, with obvious geographical relevance (HK and HKW). Among other populations than HK, there also existed a certain degree of genetic differentiation between those from south China and Taiwan. Both neutrality tests and mismatch distribution revealed that *A. cantonensis* did not undergo population expansion. We suggested that southwest border regions of China is the origin or one of the origins of *A. cantonensis* in China.

Biography

Tingbao Yang completed his Ph.D from Sun Yat-sen University in 1991. He has been working on fish parasitology for more than 25 years and published more than 80 relevant papers, mainly international peer-reviewed journals. He is now professor and Vice-Director of the Institute of Aquatic Economic Animals in the School of Sun Yat-sen University, China.

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