

Phylogenetic Relationship of *Anopheles* Species Based on Internal Transcribed Spacer 2

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We sequenced internal transcribed spacer 2 (ITS2) region of 6 *Anopheles* species (*A. lindesayi japonicus*, *A. yatsushiroensis*, *A. sinensis*, *A. pullus*, and *A. sineroides* and *A. anthropophagus*). They were aligned with those of other *Anopheles* species retrieved from the EMBL databank. Subsequently, phylogenetic analysis was performed using three different tree making methods, maximum likelihood (ML), neighbor joining (NJ), and maximum parsimony (MP), within PAUP 4.0*. Interestingly, ITS2 of *A. lindesayi japonicus* was far shorter than those of the other five *Anopheles* species. The dramatic deletion event is also observed from those of palaeartic *Anopheles* mosquitoes (ex. *A. melanoon* and *A. martinius* etc). Phylogenetic analysis indicated that *A. lindesayi japonicus* was separated from the other five *Anopheles* species and rather closely related with the palaeartic members of *Anopheles* mosquitoes.