Molecular confirmation of *Anopheles (Anopheles) lesteri* from the Republic of South Korea and its genetic identity with *An. (Ano.) anthropophagus* from China (Diptera: Culicidae)

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Abstract

Recent malaria transmission in The Republic of Korea led to a search for the identity of the possible vectors. The Anopheles fauna of South Korea is presently considered to consist of six species: Anopheles (Anopheles) sinensis, An. (Ano.) lesteri, An. (Ano.) pullus, An. (Ano.) sineroides, An. (Ano.) lindesayi japonicus, and An. (Ano.) koreicus, of which only the former three are considered potential vectors. Based on a combination of published and newly generated rDNA ITS2 sequence we found that An. lesteri from South Korea, An. anthropophagus from Jiangsu Province, China, and An. lesteri from near the type locality in Laguna Province, in the Philippines, are indistinguishable. Also, a species reported in GenBank as An. lesteri from Shandong Province, China, is the same as an unnamed species also discovered by us in South Korea. The above are compared to An. sinensis from South Korea and the type locality in China. These data indicate that An. anthropophagus, an important malaria vector in China, is actually An. lesteri. We therefore place An. anthropophagus in synonymy with An. lesteri. In addition, based on Korean specimens, An. yatsushiroensis was recently synonymized under An. pullus. We are in agreement with the conclusion that Korean specimens that have morphological attributes previously thought to differentiate these two species are actually just highly variable characters of a single species. However, genetic comparison to specimens from the type locality of An. yatsushiroensis, Yatsushiro City, Japan, is still needed to rule out the possibility that this is a valid species.

Key words: malaria, *Anopheles lesteri*, South Korea, taxonomy, Hyrcanus Group

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