

## 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