

A newly recognized species in the *Anopheles* Hyrcanus Group and molecular identification of related species from the Republic of South Korea (Diptera: Culicidae)

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Abstract

We report here a previously unrecognized mosquito species from the Republic of South Korea that is closely related to *Anopheles* (*Anopheles*) *sinensis*. We also present an rDNA ITS2-based method for identification of this and the other morphologically similar *Anopheles* from the country. The PCR assay is a multiplex of seven primers in a single reaction that unambiguously identifies all included species. The other species include *An. sinensis*, *An. lesteri*, *An. pullus*, and a previously reported unknown *Anopheles*. Based on the ITS2 sequence, the two unnamed species have genetic distances from *An. sinensis* of 9.1% (unknown 1) and 10.7% (unknown 2), and are 10.6% different from each other. Adult females of *An. sinensis* and unknown 2 are morphologically indistinguishable, while unknown 1, *An. lesteri* and *An. pullus* can usually be separated from each other and from *An. sinensis* using available keys and descriptions. This PCR identification tool offers vector biologists and malaria epidemiologists a means to identify the potential vectors of malaria parasites in South Korea.

Key words: malaria, *Anopheles*, PCR identification, Hyrcanus Group, South Korea

Introduction

Recent malaria transmission in the Republic of South Korea has resulted in an increased effort to incriminate the vector or vectors of this disease (reviewed in Wilkerson et al. 2003). Reported in the above study was the existence of an unknown species (“unknown