Two new species of *Anopheles (Anopheles)* Hyrcanus Group (Diptera: Culicidae) from the Republic of South Korea

LEOPOLDO M. RUEDA

*Department of Entomology, Walter Reed Army Institute of Research, 503 Robert Grant Avenue, Silver Spring, MD 20910-7500, U.S.A. (Mailing address: Walter Reed Biosystematics Unit, Museum Support Center, Smithsonian Institution, 4210 Silver Hill Road, Suitland, MD 20746); email: ruedapol@si.edu*

**Abstract**

Two new mosquito species belonging to the Hyrcanus Group, *Anopheles (Anopheles) belenrae* Rueda and *An. (Ano.) kleini* Rueda, are described from the Republic of South Korea, with illustrations of the larvae, pupae, adults, and male genitalia.

**Key words:** *Anopheles belenrae*, *kleini*, Culicidae, taxonomy, description, mosquitoes, Hyrcanus Group

**Introduction**

The recent increase of human malaria cases in South Korea (Feighner *et al.* 1998, Lee *et al.* 1998, Wilkerson *et al.* 2003) necessitates a serious urgency to clarify the identity of the possible mosquito vectors. Misidentifications of vector species often lead to poor understanding of the epidemiology of disease transmission and inadvertently affect control measures. Integrated systematic research, combining both morphology and molecular biology, for the *Anopheles (Anopheles)* Hyrcanus Group is underway in the Walter Reed Biosystematics Unit, in collaboration with other laboratories, to clearly define the relationships among the species and to revise the taxonomy of the group.

The known and potential vectors of malarial parasites in South Korea belong to the *An. (Ano.)* Hyrcanus Group (Wilkerson *et al.* 2003). Previously, there were 27 species listed under the group (Harbach 2004), with a wide distribution from the Oriental Region to eastern and western Palearctic Regions (Ramsdale 2001, Water Reed Biosystematics Unit 2001, A. Lee, L. M. Rueda, R. C. Wilkerson and Y. M. Litton, unpublished data). Recently, Wilkerson *et al.* (2003) and Li *et al.* (2005) recognized two unnamed species closely related to *An. sinensis*, using rDNA ITS2 sequence.