

Mekong schistosomiasis is more widespread than previously thought

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A new genetic analysis, published March 19th in the open-access journal *PLoS Neglected Tropical Diseases*, suggests that the parasitic worm *Schistosoma mekongi* is more widespread than previously thought. According to the study, the human population at risk of infection could be up to 10 times greater than previously estimated. Furthermore, it posits an increased possibility of the spread of the parasite across Laos and Vietnam.

Schistosomiasis, a parasitic disease which affects over 200 million people worldwide, is caused by several flatworm species of the genus *Schistosoma*. In the Mekong River basin in South-East Asia, the disease is transmitted by the species *Schistosoma mekongi*. A mass treatment program in the mid-1990s greatly reduced the prevalence of the disease and encouraged optimism regarding the control of *S. mekongi* infection. However, based on the implications of this new study, the control of Mekong schistosomiasis could be problematic.

Researchers Stephen W. Attwood of China's Sichuan University, Farrah A. Fatih of London's Natural History Museum, and E. Suchart Upatham of Thailand's Mahidol University analyzed DNA sequences of sample organisms collected from the Mekong river and its tributaries in Cambodia, Laos and Malaysia. They found, contrary to the previously held belief that *S. mekongi* is confined to a small section of the lower Mekong River, that organisms collected in its tributaries across Cambodia were also of the species *S. mekongi*. The range of the snail intermediate host and the ecological conditions for potential transmission were also shown to be much broader than once thought.

Prior to this study it was also assumed that *S. mekongi* originated in Yunnan, China, migrated southwards across Laos and into Cambodia, and later became extinct in Laos due to conditions

unsuitable for transmission. However, Attwood and colleagues' analysis suggested a more recent, and ongoing, migration northwards from Vietnam, towards Cambodia and Laos.

According to the authors, further work is required into this problem, as, if we have no reason to assume that ecological conditions in Laos are unsuitable for transmission, we may expect the future spread of this disease northwards into Laos.

Citation: Attwood SW, Fatih FA, Upatham ES (2008) DNA-Sequence Variation Among *Schistosoma mekongi* Populations and Related Taxa; Phylogeography and the Current Distribution of Asian Schistosomiasis. *PLoS Negl Trop Dis* 2(3): e200. doi:10.1371/journal.pntd.0000200

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