

A MOLECULAR GENETIC STUDY OF BULINUS SPECIES IN LAKE ALBERT

(BUTIABA PARISH)

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Abstract

In the interest of biodiversity as well as medicine, the precise knowledge of the identity of *Bulinus* snails in Lake Albert is needed since the snails are potential vectors of schistosomes that cause urinary schistosomiasis in man and his domestic stock. The high variability at the morphological level as well as the small size and similarities between *bulinus* species complicate the correct identification of these snails. Cytochrome Oxidase Subunit I mitochondrial DNA (hereafter COI) nucleotide sequences of 105 individuals were used to examine the amount of genetic variation between two forms of *Bulinus* snails sampled from ten localities of the lake. Two genetically distinct lineages of *Bulinus forskalii* and *Bulinus truncates/tropicus* species were identified, with a sequence divergence of 12.6%. The two species are estimated to have diverged 3.2 – 6.3 million years ago. Analysis of molecular variance revealed that a large proportion of genetic variation (50%) was partitioned between populations rather than within populations. Nucleotide diversity in the total sample was 1.32% but varied within populations from 0.12% in a population sampled from Piida village to 2.09% in a population sampled from Bugoigo village. In all localities sampled, the *Bulinus truncates/tropicus* species were more abundant than the *Bulinus forskalii*

species. These results were interpreted in light of self-fertilization and low dispersal ability among snails in both the *Bulinus forskalii* species and *Bulinus truncates* species.