

MORPHOMETRICS AND DNA BARCODING FOR THE  
IDENTIFICATION OF WILD SILK MOTHS FROM SELECTED SITES IN KENYA

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## ABSTRACT

Wild silk moth farming is a unique eco-friendly agro-practice with the potential of raising people's standards of living. However, the species identity is poorly understood in East Africa. This undermines efforts in conservation practices. Accurate identification is important in understanding the biology and ecology of the different species. Cocoons of wild silk moths were collected from Eastern and Rift valley provinces in Kenya. The samples included *Gonometa* species, *Epiphora bauhiniae*, and *Argema besanti*. Morphometric studies of the Kenyan wild silk moth species were performed based on three morphometric characters, which included forewing length, forewing width and body length measurements. Voucher specimens of each moth species were pinned and stored appropriately. Morphometric measurements of the moth voucher specimens were then taken. DNA was extracted from the middle left leg of the moths using the CTAB DNA extraction protocol. The COI region of the mitochondrial DNA was amplified using universal primers and direct sequencing was done on the cleaned PCR product. Analysis of the COI region was initially done using the Chromas software program to edit the sequences. Clustal X software program was then used to do multiple sequence alignments to check for any polymorphism within the sequences. This was followed by drawing of a Neighbour-joining tree using Molecular Evolutionary Genetics Analysis (MEGA) software version 4.0 to observe the graphical depiction of the patterning of divergences between the species. Multiple sequence alignment of the cytochrome oxidase I gene helped discover two congeneric *Gonometa* species found in Mwingi District that had not been described before. This alignment indicated variable sites at positions 217, 412 and 542 in these sequences, which separated the two species. This approach also provided an understanding of the genetic variation that exists among these different wild silk moth species. This has now provided an avenue for investigating issues of

species distribution and abundance, which will contribute not only to the understanding of their biology and ecology, but also to their conservation and utilization for income generation in these marginal areas of Kenya.