

Phylogenetic Relationships of Aproaerema Simplexella (Walker) and the Groundnut Leaf Miner Aproaerema Modicella (Deventer) (Lepidoptera: Gelechiidae) Collected from Australia, India, Mozambique, and South Africa

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Abstract : Mitochondrial DNA cytochrome c oxidase I (COI) gene analyses linked the South African groundnut leaf miner (GLM) to the Australian soya bean moth *Aproaerema simplexella* (Walker) and Indian *Aproaerema modicella* (Deventer). Thus, the genetic relatedness of GLM, *A. simplexella*, and *A. modicella* was examined by performing mitochondrial and nuclear (COI, cytochrome oxidase subunit II (COII), mitochondrial cytochrome b (CYTB), nuclear ribosomal 28S (28S) and intergenic spacer elongation factor-1 alpha (EF-1 ALPHA) on 44 specimens collected from South Africa, four from Mozambique, and three each from single locations in India and Australia. Phylogenetic analyses were conducted using the Maximum Parsimony (MP) and Neighbour-Joining (NJ) methods. All of the datasets of the five DNA gene regions that were sequenced were also analyzed using the Basic Local Alignment Search Tool (BLAST) to find the closest matches for inclusion in the phylogenetic trees as outgroups and for purposes of information. In the phylogenetic trees for COI, COII, *cytb* and EF-1 ALPHA, a similar pattern was observed in the way that the sequences assembled into different groups; i.e., some sequences of *A. simplexella* from Australia were grouped separately from the others, but some Australian sequences grouped with those of the GLM from South Africa, India, and Mozambique. In the phylogenetic tree for 28S, all sequences from South Africa, Australia, India, and Mozambique grouped together and formed one group. For COI, genetic pairwise distance ranged from 0.97 to 3.60 %, for COII it ranged from 0.19% to 2.32%, for *cytb* it ranged from 0.25 to 9.77% and for EF-1 ALPHA it ranged 0.48 to 6.99%. Results of this study indicate that these populations are genetically related and presumably constitute a single species. Thus, further molecular and morphological studies need to be undertaken in order to resolve this apparent conundrum on the taxonomy of these populations.

Keywords : *aproaerema modicella*, *aproaerema simplexella*, mitochondrial DNA, nuclear DNA

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