Infestation Levels and Molecular Identification Based on Mitochondrial COI Barcode Region of Five Invasive Gelechiidae Pest Species in Kenya

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Abstract

Invasive Gelechiidae pest species, namely Tuta absoluta, Phthorimaea operculella, Aproaerema simplixella, Sitotroga cerealella, and Pectinophora gossypiella are among the major constraints hampering agricultural economy in Kenya. Infestation levels were determined on respective host crops sampled from different localities and P. operculella recorded the highest infestation of 68.00 \pm 4.92% on stored potato. Aproaerema simplixella and T. absoluta accounted for 61.33 \pm 5.35% and 51.56 ± 5.22% maximal infestation on groundnuts and tomato leaves, respectively. Stored maize was significantly infested by S. cerealella (54.33 \pm 5.31%) while no infestation was observed on the freshly harvested grains. Infestation on open bolls by P. gossypiella was relatively low (6.11 \pm 3.46%) compared to Anatrachyntis simplex (45.67 \pm 7.84%) that emerged as the key pest of cotton. The species were discriminated based on sequence similarities, evolutionary divergences, and phylogenetic analyses. Α 658-bp fragment mitochondrial cytochrome c oxidase subunit I (COI) gene was obtained from 302 specimens. Generally, genetic variations were low within and between Gelechiid populations, with an average of 0.02% and all intraspecific divergences were less than 2% except for S. cerealella. The Gelechiids data set generated eight Barcode Index Numbers (BINs), five of which were concordant and three belonging to S. cerealella were singleton. All species were separated into distinct clusters on a maximum likelihood tree. Data on infestation levels will be useful in defining the pest status of these Gelechiids in Kenya. DNA barcoding is also presented as a valuable tool to complement traditional taxonomy for rapid and accurate identification of these species of agronomic interest.

Keywords: invasive Gelechiidae species, infestation levels, species identification, DNA barcoding