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Genetic Variability Patterns of Haemonchus Species Affecting Small Ruminants in Egypt and Bulgaria

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The current study was carried out to study the impact of disparate geographical regions on genetic structures variability of *Haemonchus* species populations among small ruminants from Egypt and Bulgaria using mtDNA markers and to diagnose the predominant *Haemonchus* species isolated from the naturally infected sheep and goats through studying the genetic characterization and the phylogenetic relationships of such isolates. This study disclosed that the nucleotide sequences of PCR products belonged to the Cytochrome Oxidase subunit 1 gene of *H. contortus*. The dendrogram elucidated a close relation between Egyptian and Bulgarian goat isolates where they were located in the same sub genotype group. Thus goats' nucleotide sequences from Egypt and Bulgaria showed little variations among all published sequences with one substitution. Contrariwise, the Egyptian and Bulgarian sheep isolates are in two varied sub genotypes where sheep nucleotide sequences from Egypt and Bulgaria demonstrated great variation with others including five substitutions. The data obtained bring out the level of genetic variability among populations of *H. contortus* isolates of small ruminants in Egypt and Bulgaria. Thus, the current results could be a starting point for applying potent diagnosis and control measures and assaying the consequences of altering environment and management conditions.

Key words: Haemonchus, genetic variability, PCR, COI, small ruminants, Egypt, Bulgaria.

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