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MORPHOLOGICAL AND MOLECULAR ANALYSIS OF HYDATIDOSIS IN CAMELS

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ENGLISH ABSTRACT

Hydatidosis or echinococcosis is caused by *Echinococcus* spp., which infects humans and several species of wild and domestic animals including camels, cattle, equines, sheep and goats. Infection comes from the consumption of *Echinococcus granulosus* eggs with contaminated food. There are several genotypes nearly ten (from G1 to G10), which are found all over the world based on genetic diversity. Several studies are conducted on the genetic diversity of hydatid cysts in livestock animals. In view of the economic and public health threats of cystic echinococcosis, this study was designed in order to describe hydatid cysts morphology, and to determine the genotypes of *Echinococcus* cysts isolates from camels in Egypt.

Morphological analysis for hydatid cysts contents were done using eosin viability test. Histopathological study was performed on the empty dissected hydatid cyst and detecting pathological changes in neighboring tissues in different organs. Using molecular tools, the DNA extracted from cysts that had been isolated from hydatidosis slaughtered camels at Kom Hamada abattoir, Egypt, was subjected to PCR amplification, using primers, constructed to target the cytochrome oxidase subunit I gene, which is considered to be specific for *Echinococcus* genotypes. The sequenced PCR products showed homology to *E.canadensis* (G6 or camel strain genotype) and *E. granulosus* (G1 or sheep strain) .

These results can be used in future to pursue the epidemiological status of the causative strain of hydatidosis in livestock animals and humans at the study area. Moreover, it highlights the role of the camel-dog cycle in echinococcosis transmission. Such epidemiological data could help in the application of efficient control strategies against this zoonotic disease.