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STUDY OF GENETIC VARIATION OF NADH DEHYDROGENASE SUBUNIT 5 (NAD5) GENE FOR *HYMENOLEPIS NANA* ISOLATED FROM DIFFERENT HOST (MICE AND RATS) IN DIYALA PROVINCE, IRAQ

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ABSTRACT : *Hymenolepis nana* (*H. nana*), the dwarf tapeworm, is the smaller and widespread tapeworm among humans people all over the world. Current study aimed to detect the genetic variation of *nad5* gene for *H. nana* between isolated samples from different hosts (mice and rats) and phylogenetic relationships between sequences them. Using polymerase chain reaction (PCR) and parts of *nad5* gene was amplified by PCR and sequenced directly. Data were analysed by using (bioedit v 7.0 Software) for alignment of sequences and (MEGA6 software) for UPGMA analysis and dendrograms phylogenetic tree to isolates of *H. nana* from different hosts compared with Genbank published isolates of *H. nana*; (KT589891.1; KT589905.1; KT951722.1; AP017666.1, KT589901.1). Results showed nucleotide substitutions in positions 261 from G- A in sample 9, 10 of *H. nana* isolates from rat and nucleotide substitutions in positions 280 from G-A in all sample of *H. nana* isolates from rat and mice compare with reference sequence of GeneBank *nad5*. Regarding in phylogenetic analysis, our data similarity with 100% with Genbank published excepted minimum similarity (99.9%) with (KT589901.1). However, there is not obvious differences between of *H. nana* mice and rat isolates are seen in cluster of phylogenetic tree.

Key words : *Hymenolepis nana,* genetic variation, nad5, mice, rats.

INTRODUCTION

Hymenolepis nana (*H. nana*), the dwarf tapeworm, is the smaller and widespread tapeworm among people all over the world. *H. nana* infection occurs more frequently in warm climates and temperate regions such as South and Central America, Asia and Eastern Europe (Kim *et al*, 2014). This tapeworm is found in the small intestine of mice, rats and humans (Mohammadzadeh *et al*, 2007). The wide-spreading of *H. nana* is variable in the world. In northwestern Australia is very high 55% (Sadaf *et al*, 2013), in Pakistan was 1.81% (Tasawar *et al*, 2004), while Saudi Arabia prevalence rate of *H. nana* was 3.0% (Omar *et al*, 1991). In regard, local studies of *H. nana*, study indicated in Najaf province was prevalence rate of *H. nana* about 1.79% from 24.800 samples (Taher, 2017) and Baghdad province, infection rate of *H. nana* was 1.8% for both gender (Yakoob and Hadi, 2009), whereas, recorded Babylon Province higher rates of prevalence of *H. nana*, the ratio reached 7.2% (Al-Kahfaji, 2014). Traditionally, protein electrophoresis was used classify species, whereas after the discovery of Polymerase Chain Reaction (PCR) technique the genetic was used to differentiate the species (Faddagh *et al*, 2012), with the advancement of biological science, used of different sequences of genes to study the evolutionary molecular. Mitochondrial DNA (mtDNA) is one of the best neutral signs to detect evolutionary relationships between the relevant groups, due to mtDNA is maternally inherited. It is evolving rapidly to some extent, most of the variation nucleotide occur at neutral sites (Okamoto *et al*, 1997). In the current study, we used partial sequence from the mitochondrial DNA NADH dehydrogenase subunit 5 (*nad5*) gene to detect the genetic variation of *H. nana* between isolated samples from different hosts (mice and rats), in addition, found phylogenetic relationships between sequences of isolated samples from different hosts (mice and rats) and comparison with NCBI-GeneBank accession numbers.

MATERIALS AND METHODS

Collection of parasites

A total of 20 adult worms of *H. nana* was collected from intestine of wild rats and small intestine of house mice from different regions of Diyala Province. The specimens were washed repeatedly in PBS followed by