

Summary

This study includes an epidemiological and molecular characterization of *Echinococcus granulosus* in intermediate hosts including humans and animals in Thi-Qar province, southern of Iraq.

The study showed the epidemiology of hydatid cyst disease in the liver and lungs of intermediate host sheep, cattle, buffaloes, and camels and knowing the extent of its spread and its risk factors over a whole year from the beginning of February 2022 until end of February 2023. This information were collected depending on the number and intensity of infections. In addition, the effect of sex, age, and infected organs on the fertility of hydated cysts in humans and other intermediate hosts. Ninety-four human infections cases were recorded among patients who were referred and treated surgically in Al-Azhar, Al-Amal, Al-Rahman and Al-Hussein Teaching hospitals in Thi-Qar province. According to questionnaire sheet that used for demographic, epidemiologic, and clinical data for each patients. The infection rates in patients were distributed as 90.43% in liver and 9.57% in lung and it had the highest infection intensity 2.67 compared to liver. The results showed the incidence of cystic echinococcosis was higher in the age group (51-60) year 27.6%. with highest fertility (73.40%), while the sterility was the lowest (26.60%).

At the same time 8847 individuals of animals that are considered intermediate hosts of the parasite were examined and they distributed as following: sheep 2792, cattle 3209, buffalo 1865, camels 980. It was found that 825 animals were infected, including hydatid cysts. The infection rate of sheep was the highest (12.29%), and the lowest prevalence of infection was in camels, (4.08%). According to the infected organ, the liver recorded the highest. In sight of the fertility status of hydatid cysts, different rates of infection were recorded among the organs and the different intermediate hosts depending on the affected organ, the age group of the host, the type and gender of the host, sheep recorded the highest fertility rate compared to the rest of the hosts.

The biochemical analysis such: Triglyceride, Cholesterol, Creatinine, Glucose, Urea and minerals (Sodium, Magnesium, Copper, Chloride, Potassium, and Calcium) were estimated by determined each element in fertile and sterile hydatid fluid of *E. granulosus* that isolated from humans and some intermediate hosts (sheep, cattle, buffalo, and camels) using diverse biochemical kits. A significant difference in biochemical constituents of the fertile and sterile hydatid cyst fluid of different hosts was observed. Cysts fluid collected from sterile hydatid cyst of buffaloes had high levels of Triglycerides (mg/dl), cholesterol, urea, glucose, magnesium, sodium and calcium, while the lowest in the sterile sheep.

Studied the genetic diversity to identify the common strains of a parasite in humans and animals intermediate hosts using the technique of the genetic characterization of the *E. granulosus* complex by using polymerase chain reaction (PCR) and DNA sequencing technology by used *Cox1* and *NADH5* genes as mitochondrial genes with *ITS1* and *ITS2* as nuclear genes and this the first study conducting in southern Iraq use both mitochondrial and nuclear genes for this purpose, and study the genetic sequences for this strain and compared it with recorded strain in global gene bank by draw the genetic tree analysis to identify the predominant strain causing *E. granulosus* in human and animal in Thi-Qar province. Thirty eight isolates were studied to determine the common strains and the diversity of individual genotypes and 20 new isolates were deposited in the National Center for Biotechnology (NCBI), under serial numbers were from LC731288-LC731292 for *mtCox1* gene, from LC733543 - LC733547 for *NADH5* gene, from LC731278 - LC731283 for *ITS2* gene and LC731284 - LC731287 for *ITS1* gene as well as, the phylogenetic analysis was mitochondrial and nucleotide loci accomplished.

The results of mitochondrial and nuclear DNA sequencing indicated that sheep strain G1 with 100% was responsible for all of the infections in Thi-Qar province. Phylogenetic trees analysis showed a close genetic relationship with isolates from other regions, indicating a high level of genetic conservation within the species. The genetic diversity study confirmed as one of the most important strategies used for controlling the disease is accurate detection of parasite genotypes in our geographical region.