PHYLOGENETICS OF *EIMERIA SPP.* IN SHEEP

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ABSTRACT

This study was conducted for 150 faecal samples taken from sheep from different areas of Baghdad governorate for the year 2020, in which the parasite was identified by the usual method, which is the method of microscopy and also by staining with iodine dye, which was the positive result of 150 samples were 90 samples (60%).This study showed that the rate of infection and the presence of this parasite in sheep increases in cold months (66) 44% more than in hot months (24)16%. The results of this research showed us that young animals are more susceptible to infection than adult animals, as in these results 70 (46.66%) and 20 (13.33%). Making a gene tree for this parasite and comparing it to the rest of the countries and for the same parasite, a program Mega 6 that shows the convergence of the genetic sequence found in Iraq with other countries. Genetic sequence with the gene sequences of a parasite in other countries to look for the presence of any gene mutations.

Key words: Eimeria, sheep, Iraq, molecular diagnosis

Introduction

This parasite is one of the parasites that belong to the family of protozoa that is widespread among sheep, which infects the intestines of sheep and causes disease symptoms, the most important of which is diarrhoea and also affects the economy of livestock and causes great economic losses due to the loss of this type of animals (Davies *et al.,* 1963; Karaer and Nalbantoðlu, 2005; Levine and Ivens, 1986 and Berriatua *et al*., 1994)

There are 14 types of coccidiosis that infect the intestines of sheep (Reginsson and Richter, 1997).

The oocysts of this parasite can remain for a not short time in the environment and remain capable of infecting, and this increases the rate of parasite spread among sheep significantly (Abebe *et al*., 2008).

Materials and Methods

One hundred fifty faecal samples were collected from sheep from different areas and were examined by microscopy in the direct method and also by the method of iodine staining.

After making sure of this parasite, a molecular diagnosis was made by the researcher (Zaid and Haider, 2019), who then sent the sample in order to perform the genetic analysis, and later gene tree was made.

Results and Discussion

The result showed that 90 samples out of 150 samples were infected with this parasite, and the results indicated that the infection rate was higher in the hot months than the cold months as in Table 1. The results also showed that young sheep are more susceptible to infection than large sheep and Table 2 showed the differences infection between young and adult sheep.

Table 1: Coccidian infection in Bagdad city.

Total number of samples	Number of infection	Cold month	Hot month
150	90 (60%)	66(44%)	24 (16%)

Table 2: Differences infection between young and adult sheep

Total number	Young animal (1-18 month)	Adult animal (18-30 month)	Total infection
150	70 (46.66%)	20 (13.33%)	90 (60%)

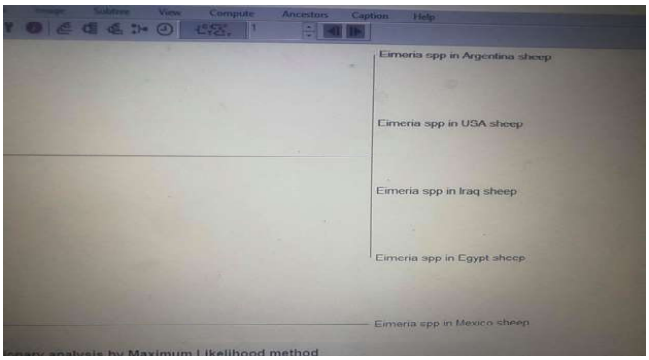

Fig. 1: Phylogenetics of *Eimeria spp.* in sheep

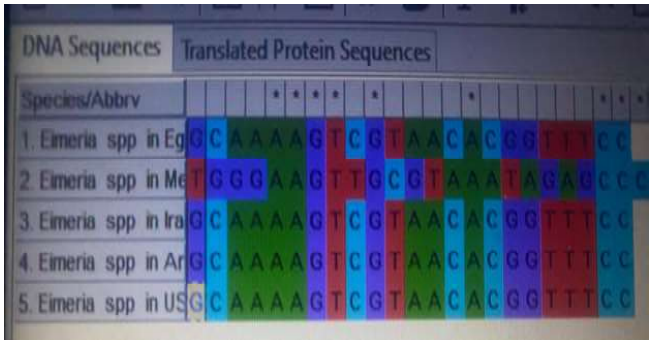

Fig. 2: DNA sequences of *Eimeria spp.* in sheep

The prevalence of this parasite in this way is due to the climatic conditions in this city, which provide the prevalence rate and also the percentage of survival of these eggs in the feces, which are a source of parasite propagation among animals in a large way, and this percentage also coincided

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with the researcher(Manal , 2012; Keeton and Navarre, 2017).

The reason for the spread of this parasite in the summer more than the preference of winter is due to the low temperature, which the eggs cannot survive in this conditions for a long time and have the ability to infect other hosts and spread the disease, unlike what happens in the summer(Parker and Jones, 1990) and, which has temperatures suitable for the survival of these eggs by this environmental and their ability to infect (Taylor 2012; Foreyt, 1987).

This parasite is considered one of the important parasites that infect the intestines of animals and cause severe diarrhea and thus, cause high economic losses in livestock, and among the most important causes of the parasite's spread is due to the environment surrounding the animal, the animal's immunity and the stress factors of the animal such as malnutrition, physiology and others (Christophe and Carine, 2012; Zachary, 2017; Cox, 1998 and Gul, 2007).

The cause of the parasite's spread in young animals is due to several reasons, including the immune system, which occurs antibodies after the first infection of the parasite (Silva *et al*., 2011; Lillehoj, 1998; Smith *et al*.,1994).

The work of the gene tree for this parasite and the comparison with this parasite became evident with the countries that showed the existence of a difference in the genetic sequence of this parasite present in the state of Mexico, unlike the rest of the countries with which there is a rapprochement with them, such as America, Argentina and Egypt (Fig.1 and 2).

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