

DEVELOPMENT OF MOLECULAR TESTS FOR IDENTIFICATION AND STUDY OF GENETIC DIVERSITY OF *Eimeria* spp. IN RABBITS FROM THE SOUTH EAST OF THE MEXICO STATE

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ABSTRACT

Poverty is one of the great challenges to be solved by the State, the 47 % of the Mexican population is in some degree of food poverty, capacity or equity, SEDESOL (2008) mentions that more than 86% of the poor are in rural areas. The rabbit is a livestock activity has been shown to be important in the last four decades, has established itself as an alternative to solve problems of food and poverty in rural and suburban society. Production of rabbit noted for its easy productive and reproductive management, quality of derivative products and the beneficial characteristics of meat. However, there are significant economic losses in the rabbit production, due to the presence of infectious agents causing a great number of diseases, one of the most important, Coccidiosis are infections caused by obligatory intracellular protozoan parasites belonging to the genus *Eimeria* and considered as major causes of significant morbidity and mortality in rabbits. The eimeriosis has two presentations; hepatic and intestinal infections caused by eleven species of *Eimeria*, of which only *E. stiedae* is causing liver eimeriosis which causes stunted growth and loss of weight, the other species are causing the eimeriosis in the intestinal manifestation, causing mortality even with a low level of infestation. The identification of each *Eimeria* species is characterized by morphological characters and micrometer, however the implementation of more sensitive diagnostic methods that allow us to timely and accurate identification of the agent

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is necessary, therefore, the objective of this studied was to identify the species of *Eimeria* spp. present in the stool samples of rabbits with enteric signology on the south east of the Mexico State, sampling was performed in rabbits from one to three months old, that had not been treated with coccidiostats, regardless of race, sex or type of unit rabbit production, a total of 72 samples were collected and analyzed by microscopy, was obtained a 8.66 % of samples positive for *Eimeria* spp , the collected samples were analyzed by means of chain reaction (PCR) using primers ITSF 5 ' GGGAAGTTGCGTAAATAGA 3' , ITS R 5 ' CTGCGTCCTTCATCGAT 3' (Oliveira et al. , 2010) that amplify a fragment of 400-600 bp of the ITS1 region of *Eimeria* spp, whereby the percentage increase at 16.6 % , the molecular identification of *Eimeria*, identified the species found in positive samples, finding *E. stiedai*, *E. performans*, *E. magna*, *E. coecicola*, *E. flavescens* and *E. exigua*, the results obtained are of great importance because the literature reports to *E. stiedai* as the most pathogenic species that affects rabbits. It is noteworthy that the phylogenetic analysis of the sequences obtained in this study show genetic diversity of *Eimeria* species reported here as described worldwide.

Keywords: *Eimeria* spp , enteropathy , molecular diagnostics , genetic diversity.

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