



How should veterinary medicine be studied today? - a personal vision

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Abstract

Veterinary Medicine is a fairly multifaceted discipline, according to various experiences throughout almost 30 years of professional practice. Some molecular tools have been incorporated in the study of various pathogens that cause diseases in small animals, specifically associated with the study of viral agents such as canine herpes virus and canine distemper virus, mainly.

Keywords: viral genomes, PCR, FAVET, Chile

Introduction

Virology, a dynamic discipline, has served to incorporate in several elective courses, some methodologies such as the one devised by Kary Mullis and others. In these courses, knowledge of viral genomes (RNA or DNA) is expanded in terms of their length, sequence, and other related characteristics. The existence of the Genbank®^[1] has made it possible to know the sequence of various viral species already described and, for example, to establish or design specific matches for the detection of pathogens of veterinary interest by means of Polymerase Chain Reaction (PCR). This has also made it possible to verify the nucleotide identity of the amplified fragment using some free access online programs.

Material and methods

The methodologies involved in these studies heavily incorporate the technique devised by Kary Mullis^[2] in conjunction with others such as 2% agarose gel electrophoresis, nucleic acid sequencing and determination of nucleotide identity using CLUSTAL Omega^[3] and BLAST^[4]. The samples used for the detection of viral agents include fragments of organs or fluids from which it is possible to extract the nucleic acids, both RNA and DNA. In the case of RNA, the canine distemper virus has been taken as a model and in the case of DNA, the canine herpes virus, always respecting or considering the famous phrase of André Lwoff: viruses are viruses.

The sequencing was initially carried out by Genytec Ltda., there are other companies dedicated to this mission such as Macrogen Ltd and thanks to programs such as CLUSTAL Omega it has been possible to align the delivered sequences and subsequently establish the nucleotide identity of the fragment amplified by BLAST.

Discussion and conclusion

These methodologies have allowed the initiation of the molecular study of pathogens of veterinary interest, taking the aforementioned as models^[5-17]. At the same time, these attempts have allowed our country to have at least 35 new

medical veterinarians, incorporating these techniques into their knowledge, originally known in elective courses of the Veterinary Medicine career at the University of Chile.

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