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Short Communication

How To Detect a Pathogen of Human or Veterinary Interest?

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Abstract

Molecular Medicine is a fairly multifaceted activity and according to various experiences of almost 30 years of professional practice, it has been possible to incorporate some molecular biotools in the study of disease-causing pathogens in both humans and small animals and in relation to the latter, associated with canine herpes virus or canine distemper virus. However, according to André Lwoff: Viruses are viruses, so their detection does not very much.

Keywords: Virus, Detection, Biotools, Data base

Introduction

Molecular virology, in addition to being a dynamic discipline, has had to incorporate various methodologies that have appeared lately, such as the fantastic idea of Kary Mullis and other scientists. Although this has made it possible to expand the knowledge of viral genomes (RNA or DNA) in terms of size, length or nucleotide sequence thanks to the existence of the Genbank® [1] and some computer programs that allow both the design of primers for a reaction of PCR, the alignment of nucleotide sequences or the determination of the identity of the pathogen of interest. To anyone within this area, the existence of these programs should be unknown, even online and for free. The molecular detection of the pathogenic agent, therefore, is today a task without pretexts, that is, there is no pretext for its implantation anywhere on our planet.

Material and Methods

Today, the existence of the Genbank® has allowed access to many of the nucleotide sequences of various viral agents that affect both humans and other animals. With this valuable information and the famous invention of Kary Mullis [2], a conventional Polymerase Chain Reaction is formed when complemented with 2% agarose gel electrophoresis. Subsequently, by sending the amplified fragment for sequencing and determining the nucleotide identity using other internet platforms such as CLUSTAL Omega [3] and BLAST [4], the detection of the suspected agent can be validated. In the context of the samples to be used for the detection of the agent (human or animal), we have been able to access fragments of organs or fluids from which the nucleic acid involved is extracted. Subsequently, the PCR can be developed by designing the primers and subsequent sequencing in companies dedicated to this mission such as Macrogen Ltd. Finally, thanks to CLUSTAL Omega and BLAST it is possible to align the delivered sequences and subsequently establish the nucleotide identity of the amplified fragment.

Discussion

The indicated methodologies and the existence of free access computer programs have been mentioned in various publications in mainstream journals [5,6].and in others of equal importance and it has been possible to magnify the importance of the molecular study of pathogens of interest and in our case, taking as models those mentioned [7-17].

Conclusion

Thanks to the use of these methodology, at least 35 new veterinarians have graduated in our country, who have incorporated these techniques into their professional knowledge, which are here to stay.

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Conflict of Interest

No conflict of interest.

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