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THE VIROLOGY IN SMALL ANIMALS OR HOW TO GET OUT OF COMPLICATED QUESTIONS

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Abstract: Classical or traditional virology has been greatly complemented by some molecular techniques such as the Polymerase Chain Reaction (PCR) and the way in which precise molecules can be detected in an unambiguous way. The design of specific primers has also left behind any pretext to attempt the detection of a pathogen of human or animal interest. Veterinary medicine students are incorporated through the development of their title memories on topics such as those mentioned, taking as a basis the pathogens that mainly affect dogs and cats. Among the agents already studied, the canine distemper virus and the canine and feline herpes virus stand out. However, others have also been studied: Canine parvovirus, Feline panleukopenia and other non-viral agents such as *Bordetella canis*, *Brucella canis* or *Leptospira interrogans*, for example.

Keywords: *viral pathogen, Polimerase Chain Reaction, questions*

BACKGROUND

This story begins in early 2000 with studies of canine herpes virus, the agent that causes hemorrhagic syndrome in puppies under four weeks of age and is almost 100% fatal. The virus has been isolated in Chile, its biological characterization has been published (Navarro *et al*., 2003, 2005) and molecular studies have been carried out very later that demonstrate its presence in our country (*Fuentes et al*., 2018).

However, one of the questions that best defines our work together with Veterinary Medicine students is: why do dogs vaccinated against canine distemper get sick and die? The canine distemper virus is an RNA virus that causes a highly infectious disease not only in the *Canidae* family (Frisk *et al*., 1999). Its genome has been studied previously (Mochizuki *et al*., 1999) and precisely in that study the first evidence of changes in the genome were given, which have an impact on the generation of amino acid changes in Hemagglutinin, the crucial protein in the generation of antibodies. protectors. In other words, the virus has a different hemagglutinin in each change of the viral genome, and this is how in 2021 at least 14 different genotypes have been described (Ke *et al*., 2015; Piewbang *et al*., 2019)

In our country, the six different CDV genes (N, P, M, F, H, L) have been used by RT-PCR to visualize the best of them as a detection target. Of all, the L gene and the M gene have shared the laurels with the N gene, as shown by other annexed studies. Thus, today veterinary medicine students can learn about and propose a method for detecting CDV using the best detection target (Jara *et al*., 2018; Pincheira *et al.*, 2018; Mateo *et al.*, 2019; Navarro *et al.*, 2019, Gallegos *et al.*, 2018; Salas *et al.*, 2018)

In a report (Salas *et al.*, 2018), were able to know that, in Chile, at least two of the fourteen existing CDV genotypes coexist: America-1 and European-1. The above is excellent news, since it is known that the CDV vaccine is still made with one of the old genotypes: America -1, however the news is eclipsed when considering that a vaccinated dog can theoretically die when facing another of the thirteen possible genotypes to exist in that geographic location.

Undoubtedly, the H gene has been the most studied and at this time we have made several successful attempts to distinguish between the American-1 and European genotypes existing in Chile (Bolívar *et al.,* 2019; Correa *et al.,* 2019), which has allowed to leave the lure in place for the detection of another existing genotype in our country, since when both protocols are negative, the sample is sent to be sequenced and that's it ...!

Other viruses such as canine parvovirus, canine and feline herpes viruses, feline calicivirus and other non-viral agents such as *Bordetella canis*, *Brucella canis* or *Leptospira interrogans*, have already been involved in the degree of several veterinarians to date. In all of them, PCR has been used both to initiate the diagnosis of the agent involved and to incorporate new trained personnel into the scientific ambit sphere. However, the financing has not been the typical one since the mentioned animal species are not of economic importance for our country. Thus, almost all the research carried out has been thanks to the personal contribution, of the veterinarians involved and recently the Wolf Foundation, of the city of Michigan, USA. (Sepúlveda *et al*., 2019; Macías *et al*., 2018; Cisternas *et al*., 2019; Bravo & Navarro, 2018; Tamayo *et al*., 2018; Yáñez *et al*., 2018).

Apparently and being a virus that affects species in possible danger of extinction, CDV has been a subject of extensive research and interest (Hidalgo-Hermoso *et al*., 2020; Vergara-Wilson *et al.,* 2021)

The interest in viral agents detection has currently been increasing when considering the pathogen called SARS-CoV-2, which causes COVID19, the current pandemic. The detection method for this agent is like that used in the preceding paragraphs: PCR with a previous stage: retro transcription by an enzyme that synthesizes DNA from RNA, which is called RT-PCR (Bwire *et al.,* 2021).

Yes, the virus that causes COVID19 is a ribovirus, a virus after all, and animal viruses are similar to viruses that affect other species. Research carried out in animals and the pathogens that produce their diseases have been used for a long time for the knowledge and strategies to be carried out in human beings.

In particular, the canine distemper virus, which initially affected only dogs, is now known to have crossed the species barrier and one question must be responsibly answered: why do dogs vaccinated against VDC get sick and die? In general, what causes the new SARS-CoV-2 variants then?

The answers point directly to changes in the viral genome and will be obtained quickly if some research is maintained and others are funded.

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