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Prediction of the immunogenic properties of the VP2 protein from different variants of canine parvovirus. CPV01

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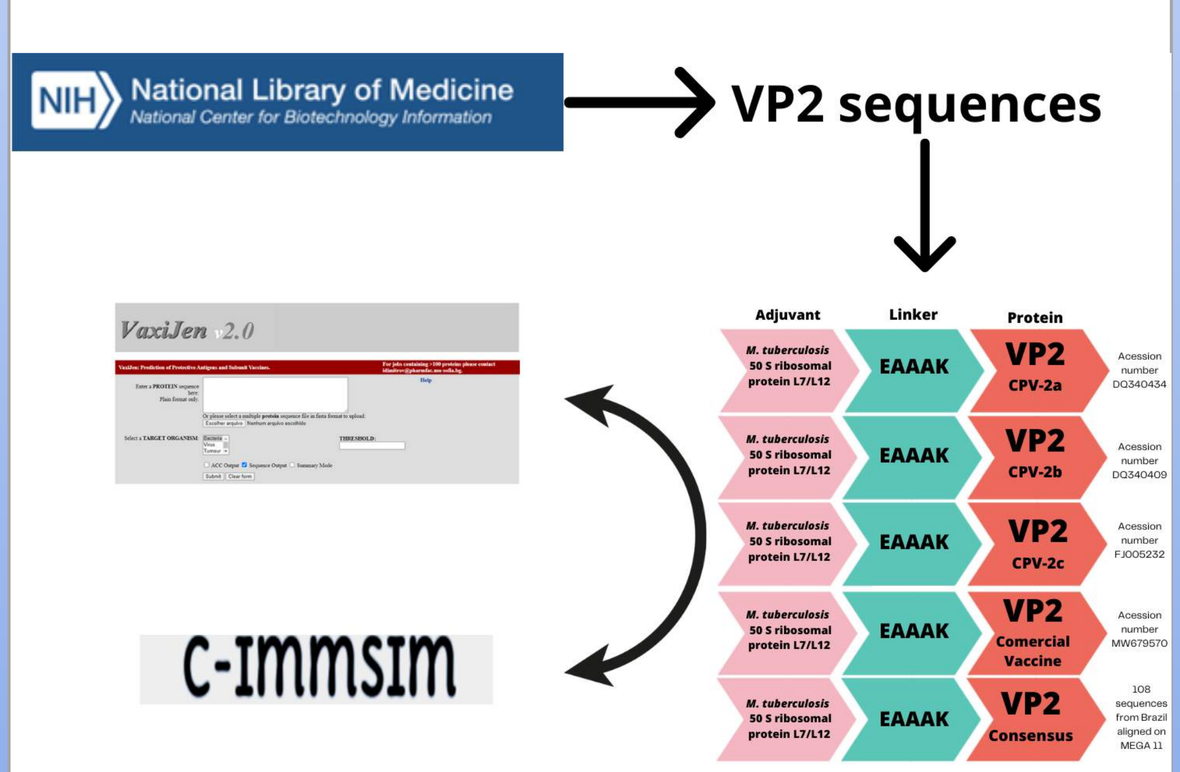
INTRODUCTION AND AIM

Canine parvovirus is a *Protoparvovirus*, from the *Parvoviridae* family, discovered in 1970 (YIP et al., 2020). It is a small, non-enveloped virus composed of non-structural and structural proteins. The VP2 protein stands out as the main structural protein, forming the majority of the capsid and playing important roles such as determining the range of hosts and interacting with receptors on susceptible cells, making it the site of viral mutations (DECARO, BUONAVOGLIA & BARRS, 2020; NELSON et al., 2007). Currently, there are three viral variants circulating in canine populations, replacing the original strain of the virus: CPV-2a, CPV-2b, and CPV-2c. Disease prevention is achieved through vaccination, as there is no specific treatment available. The disease has high mortality rates, affecting animals up to six months of age, however, there is an increasing occurrence of the disease in adult animals with a complete vaccination protocol in veterinary clinics (ZHOU et al., 2017). Therefore, the objective of this study was to perform a computational simulation of the canine immune system in order to evaluate the immune response against different strains of CPV-2.

MATERIALS AND METHODS



RESULTS AND DISCUSSION

The antigenicity was evaluated using Vaxijen. The commercial vaccine had an antigenicity score of 0.5051, the lowest result. CPV-2a and the consensus sequence had the highest values (0.5079). In silico prediction of primary immune response after vaccine injection using VP2 sequences was done in C-ImmSim server. Three injections of 1000 antigen molecules without LPS were given 4 weeks apart and immune response was recorded for 200 days (DEVI & CHAITANYA, 2021). The immunological simulation revealed a mild initial response after the first simulation of the tested VP2 applications, with an increase in IgM and IgG1+IgG2 antibodies, IgM and IgG+IgM in the subsequent simulations. The most significant increase occurred in the third simulation (figure 1)There was a significant increase in memory B cells in the second simulation, peaking in the third. After 120 days from the third simulation, there was a decrease in the population of B cells in all tested VP2. The expression of memory cells increased after the application simulation of all VP2, suggesting robust activation of the secondary immune response. The highest production of memory B cells was observed with CPV-2a and the consensus VP2. The CPV-2a variants and the consensus VP2 stood out in memory TH cells. In the CPV-2b, CPV-2c, and commercial vaccine variants, the highest levels were achieved after the third simulation. The variants also stimulated the production of cytokines in a varied manner.

RESULTS AND DISCUSSION

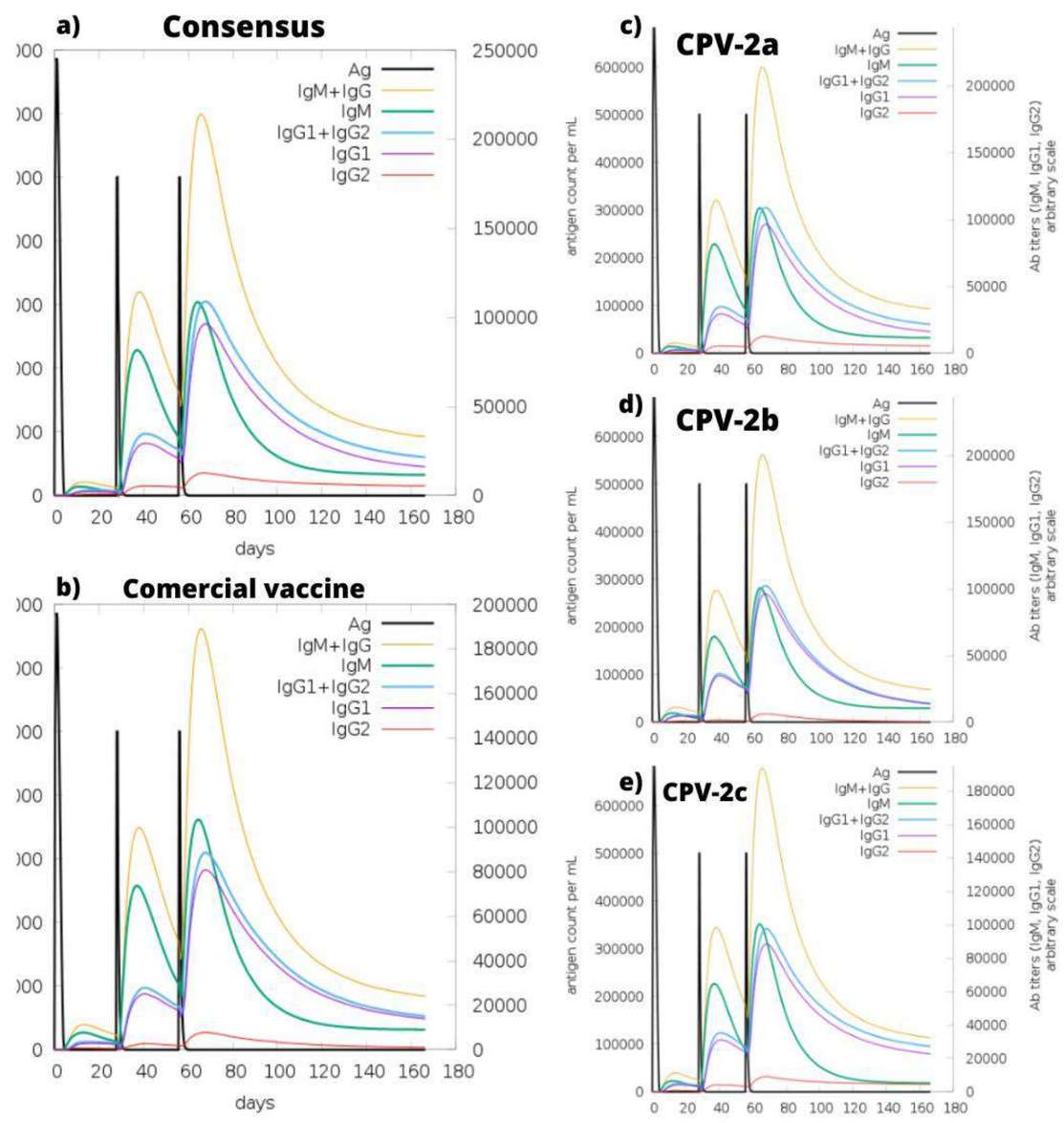


Figure 1. Graphics representing the variantions of IgM, IgG1+ IgG2, IgG+IgM in each simulation.

FINAL CONSIDERATIONS

Overall, the computational analyses suggest that the VP2 from different strains of CPV-2 are good immunogens. The VP2 protein is predicted to trigger mostly IgG, IgM, B-cell, T-cell, and cytokines (IFN-γ and IL2). It can be concluded that the VP2 protein from different strains of parvovirus is a promising protective antigen for the development of subunit vaccines against CPV-2.

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