

Bioinformatics designing of an mRNA vaccine for Mokolavirus (MOKV) using immunoinformatics as a secure strategy for successful vaccine development

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Introduction

The Mokola Virus belongs to the family Rhabdoviridae and is genotype 3 of the Lyssavirus genera. A small number of cases of animal and human encephalomyelitis, mainly scattered over sub-Saharan Africa, have been linked to the Mokola Virus (MOKV). Currently there is no vaccine to protect against MOKV infection in people or animals. It has been proven that rabies vaccination does not confer immunity against MOKV infection, even though MOKV and the rabies virus are related.

Methods

Using immunoinformatics approaches, this study designed an mRNA vaccine that can protect against all the five glycoproteins of the Mokola virus. NCBI was used to obtain the viral sequences, which were then screened for antigenicity, allergenicity, toxicity, B-cell epitopes, CD8+T lymphocytes

(CTL), and CD4+T lymphocytes (HTL). These epitopes were used in the construction of the vaccine. Some extra co-translational residues were added to the mRNA vaccine construct.

Results

Its molecular weight is 129.19083 kDa, and its estimated pI is 8.58. It interacts rather steadily and with limited deformability with TLR 3, among other human innate immune receptors.

Conclusion

Overall, the results show that the produced candidate vaccine is non-allergen, non-toxic, and can elicit T-cell and B-cell immune responses. These findings can further be subjected to in-vivo and in-vitro techniques for validation.