

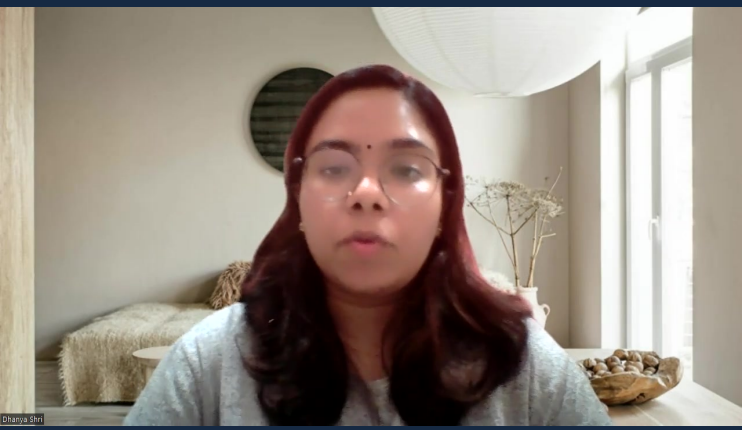
Vaccine Design for MPXV

DHANYASHRI A/P GURUPARAN
012022020020



FINAL PROJECT PRESENTATION
22/12/2022





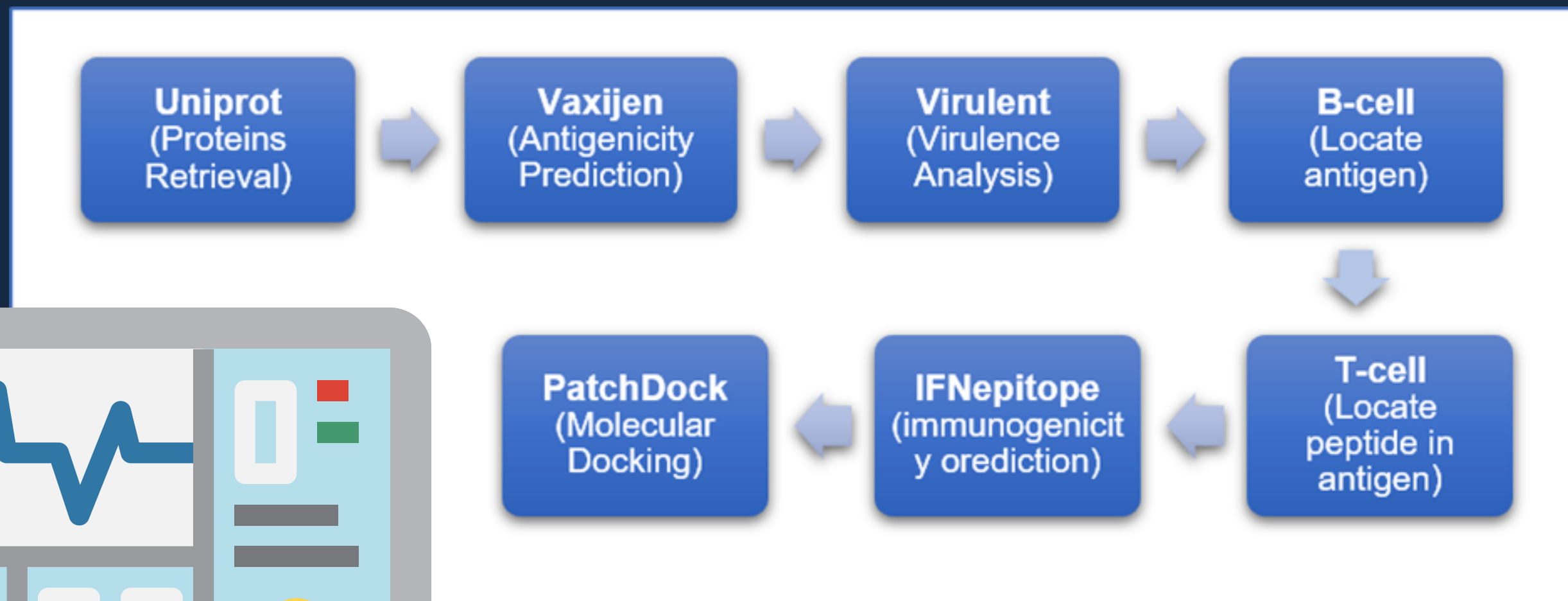
Introduction

- 01** Monkeypox is an uncommon zoonotic disease isolated to West and Central African forests in the twentieth century
- 02** The epidemic of human monkeypox in various nations since May 2022 has been exceptional in terms of the high number of cases
- 03** There is no conventional MPV vaccination available
- 04** Vaccinating individuals against MPXV is currently a critical necessity.





Materials & Methods





Results & Discussions




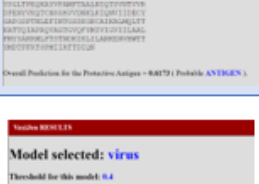
MPXV Sequence	Antigen Score	Antigen/Non-Antigen	Results
MPXV A33R	0.4775	Antigen	
MPXV H3L	0.4684	Antigen	
MPXV M1R	0.6173	Antigen	
MPXV L1R	0.4085	Antigen	

Table 1.0: VaxiJen prediction results of 4 different monkeypox sequence analyses.

conserved portions reveals that all of the antigenic regions satisfied VaxiJen's standard criteria of 0.4.

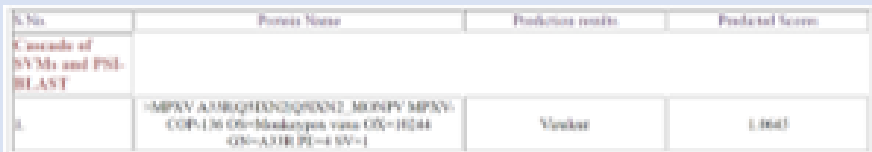
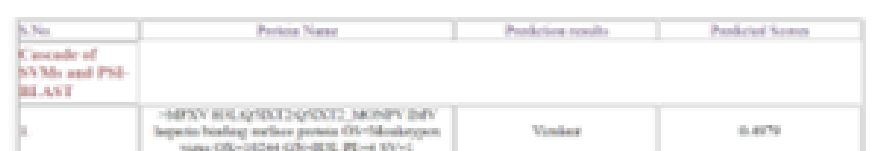
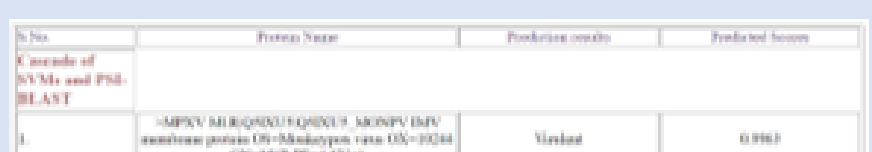
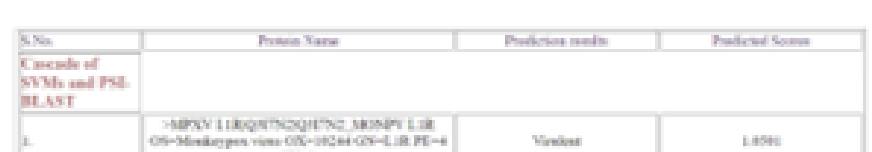
MPXV Sequence	Virulent Result	Virulent Score	Results
MPXV A33R	Virulent	1.0645	
MPXV H3L	Virulent	0.4979	
MPXV M1R	Virulent	0.9963	
MPXV L1R	Virulent	1.0501	

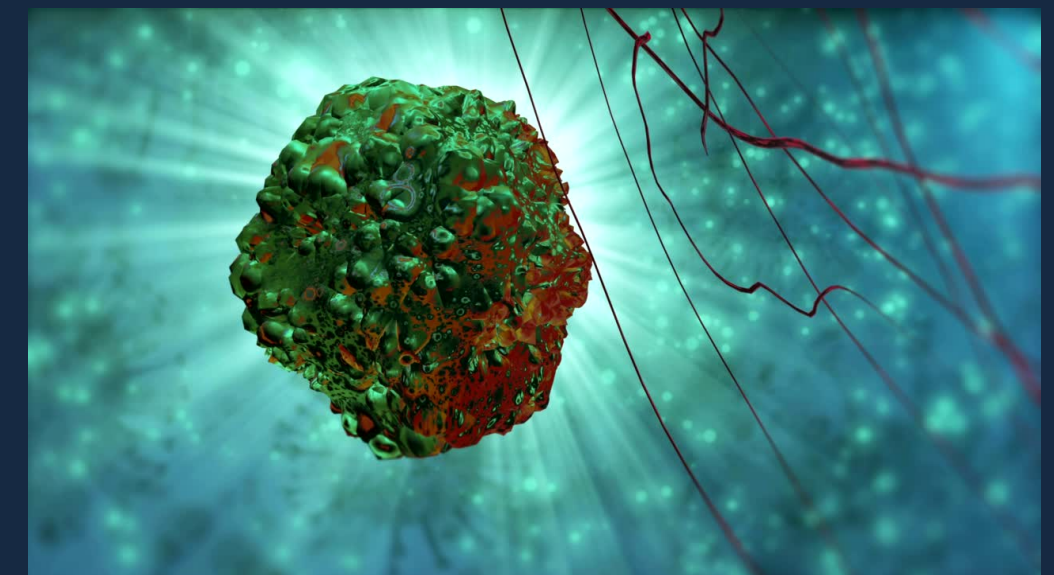
Table 2.0: Virulent prediction results of 4 different monkeypox sequence analyses.

proteins are non-allergenic, non-toxic, and is virulent implying that host cell-induced immunogenic responses target only the virus rather than the host



Results & Discussions

Eight conserved peptides with a length of more than 14 amino acids were selected from the server's results to execute the antigenicity test again.











MPXV Sequence	Peptide	Length	Antigen Score	Antigen/ Non-Antigen	Results
MPXV A33R	FLEKTSFYNCN DSITKEKIKI	21	0.2106	Non-Antigen	
	KVNNNNYNNN YNCYNNYNCYNYDDTFF	28	0.8273	Antigen	
MPXV H3L	PPSETFPNVHEHINDQ KFDDVKDNEVMQEKR DVIVNDPDPHY	43	0.4473	Antigen	
	ALWDSKFFTELENKN	15	0.8294	Antigen	
	ITGNKVKTTELVIDKDH	16	0.2125	Non-Antigen	
MPXV M1R	AALNIQTSVNTVVRDF ENYVKQTCN	25	0.2174	Non-Antigen	
	KATTQIAPRQVAGT	14	0.6627	Antigen	
MPXV L1R	KLEAVGHCOYESLSE EYRQLTKFTDSQDFKK LFNKVPIVTD	40	0.0919	Non-Antigen	

Table 3.5: Summary table of filtered B-cell epitope prediction results of 4 different monkeypox sequences with lengths 14 and above.



Results & Discussion

- T-cell Epitope

the MHC class-I T cell epitope predictions based on the percentile rank of $\leq 0.05\%$ for each MHC allele and length combination to cover most of the immune responses. Meanwhile, for MCH-II-related peptides, each peptide was correlated to the alleles it was associated with where selections were based on a consensus percentile rank of 99% and above.

- IFNEpitope

The projected ability of the submitted monkeypox peptides to trigger IFN-gamma was used to rank and order them and only positive results were selected

- Overlapping residues

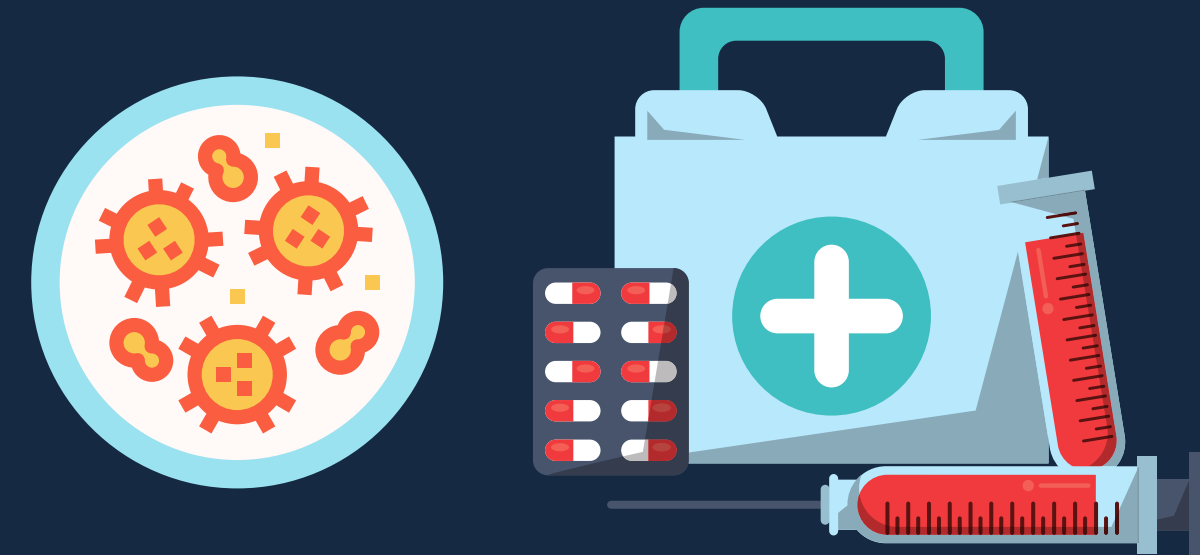
Manual comparison and cut-off values were used to choose overlapped B-cell, T-cell, and IFN epitopes to verify that the developed vaccine might elicit both host immune and cytotoxic immunogenicity

- Docking

Ligand	Receptor	Solution Number	Global Energy	Attractive VdW	Repulsive VdW	ACE	HB
MPXV A33R	TLR4	6	-10.65	-10.67	1.40	8.02	-1.72
MPXV H3L	TLR4	7	-7.58	-17.97	5.87	7.69	-2.08
MPXV M1R	TLR4	7	-23.79	-32.18	11.34	-1.24	-1.66

Table 3.19: Docking results of each MPXV vaccine target with TLR4 after refinement using Patchdock Webserver.

Based on its minimum global energy, MPXV M1R was chosen as the most suitable vaccine design



Results & Discussion

a) MCH-I

Peptide	Alleles	Percentile Rank
SLNRTIVTK	HLA-A*03:01	0.01
	HLA-A*11:01	0.03
VTSSGAIYK	HLA-A*11:01	0.01
	HLA-A*03:01	0.05
MTSILNTRL	HLA-A*08:01	0.04
KVNNNNYNNY	HLA-A*30:02	0.01
GVTSSGAIYK	HLA-A*11:01	0.03
RFLEKTSFY	HLA-A*30:02	0.02
FYKPKHSTV	HLA-B*08:01	0.03
IYHDDLVL	HLA-A*24:02	0.05

Table 3.6: Table of B-cell epitope prediction results (MHC-I Binding Predictions) of MPXV A33R monkeypox sequence.

b) MCH-II

Allele	Method	Peptide	Percentile Rank	Adjusted Rank
HLA-DRB3*01:01	Consensus (comb.lib./smp/aa)	YNCYNYDDTFFDDDD	0.52	0.52
HLA-DRB3*01:01	Consensus (comb.lib./smp/aa)	NYNCYNYDDTFFDDDD	0.59	0.59
HLA-DRB3*01:01	Consensus (comb.lib./smp/aa)	NNYNCYNYDDTFFDD	0.76	0.76
HLA-DRB1*03:01	Consensus (smp/aa/stunipola)	GKVTINDLKMMLFYM	0.88	0.88
HLA-DRB1*03:01	Consensus (smp/aa/stunipola)	KVTINDLKMMLFYMD	0.88	0.88
HLA-DRB1*03:01	Consensus (smp/aa/stunipola)	LGKVTINDLKMMLFY	0.88	0.88
HLA-DRB1*03:01	Consensus (smp/aa/stunipola)	VLGKVTINDLKMMLF	0.91	0.91
HLA-DRB1*03:01	Consensus (smp/aa/stunipola)	VVLGKVTINDLKMMML	0.94	0.94
HLA-DRB3*01:01	Consensus (comb.lib./smp/aa)	YNNYNCYNYDDTFFD	1.30	1.30
HLA-DRB1*15:01	Consensus (smp/aa/stunipola)	KGMLFVYKPKHSTV	1.40	1.40

Table 3.9: Table of B-cell epitope prediction (MHC-II Binding Predictions) results of MPXV A33R monkeypox sequence.

a) MPXV A33R

B-Cell Epitope	MCH-I Epitope	MCH-II Epitope	IFN Gamma Positive Score
FLEKTSFYNCN DSITKEKIK	RFLEKTSFY	YNCYNYDDTFFDDDD	0.57338052
KVNNNNYNNY CYNNYNCYNYDDTFF	KVNNNNYNNY	NNYNCYNYDDTFFDD	0.36477612

Table 3.15: Table of epitopes with overlapping residues after IFNepitope prediction for MPXV A33R.

a) MPXV A33R

Epitope Name	Sequence	Method	Result	Score
Epitope1_A33R_	YNCYNYDDTFFDDDD	SVM based	Positive	0.57338052
Epitope2_A33R_	NYNCYNYDDTFFDDDD	SVM based	Positive	0.36477612
Epitope3_A33R_	NNYNCYNYDDTFFDD	SVM based	Positive	0.15087603
Epitope9_A33R_	YNNYNCYNYDDTFFD	SVM based	Positive	0.34938794

Table 3.14: Table of IFNepitope prediction results of MPXV A33R monkeypox sequence.





Conclusion

- The MPXV M1R vaccine design was shown to have the minimum global energy and ligand binding for the TLR4 receptor in all of the analyses carried out in this paper.
- It is understood that the MPXV M1R vaccination has the capacity to elicit immune cellular and humoral reactions against the MPXV.

