In-Silico Evaluation of the Capsid Proteins of FMDV as Potential Vaccine Candidates

F. M. N. Hassan¹, Md. Shaifur Rahman²*, K. M. T. Rahman³, Sharmin S. Sumi⁴, Md. F. Islam⁵, Md. Badrul Alam¹, Md. Giasuddin⁶, Khondoker M. Hossain¹

¹Biotechnology and Genetic Engineering Discipline, Life Science School, Khulna University, Khulna-9208, Bangladesh
²Tissue Banking and Biomaterial Research Unit, Atomic Energy Research Establishment, BAEC, Dhaka-1349, Bangladesh
³Research and Development Division, Incepta Vaccine Limited, Dhaka, Bangladesh
⁴Department of Biochemistry, University of Alberta, Edmonton, Alberta, Canada T6G 2H7
⁵Department of Biochemistry, University of Saskatchewan, Saskatoon, S7N 5E5 Canada
⁶Bangladesh Livestock Research Institute (BLRI), Savar, Dhaka -1341, Bangladesh

Email address: mdshaifur@gmail.com (M. S. Rahman)

To cite this article:

Abstract: In this study, the capsid proteins of four major serotypes of Foot and Mouth Disease Virus (FMDV) were assessed as the vaccine candidates. Different protein sequences regarding FMDV capsid of O, A, Asia 1 and C type were identified from NCBI Genome Database and UniprotKB. Phylogenetic tree of the four serotypes was developed using ClustalW software. HMMTOP, RANKPEP, Swiss-Model and Vaxign software were used for comparing the capsid proteins in terms of their feasibility as vaccine candidates. The virus and viral serotype were identified from the cultured disease sample using RT-PCR. Our results revealed that different capsid proteins of the four serotypes vary in their suitability to be considered as peptide vaccine components. The VP1 region of Asia 1 serotype amplified based on the result of dry lab analysis. Our findings provide a future indication of multivalent vaccine development against FMDV.

Keywords: Reverse Vaccinology, FMDV, Capsid Protein, Viral Protein 1, Vaccine Candidate

1. Introduction

Vaccines have been developed for generating effective immunogenicity to prevent diseases throughout previous decades [1-2]. Different methodologies have been exploited so far to develop vaccines against life threatening diseases of human and animals [2]. Reverse vaccinology has come out as one of the most modern system of vaccine development in recent years [3]. It takes advantages of genomic and proteomic data regarding pathogenic organisms already available in the databases. Antigenic materials of certain pathogens can be analyzed by using different computational resources and tools. Results from the computational approach can be utilized to develop vaccine within 1-2 years through further experimental approaches.

However, foot and mouth disease (FMD) is an economically important and highly contagious viral disease. The FMDV viral particle (25-30 nm) contains an icosahedral capsid consisting of proteins and no envelope [4-5]. The virus possesses a positive-sense single stranded RNA (SS RNA) (about 8.3 kb) genome that encodes a polyprotein which is subsequently processed to yield structural and non-structural proteins [8-9]. Globally, the virus exists in seven immunologically distinct serotypes; the Southern African Territories [SAT] types 1-3 and Eurasian types namely O, A, C and Asia 1, with multiple subtypes within each serotype [10]. Among these serotypes show some regionality; the O serotype is the most common while four serotypes (O, A, Asia 1, C) are available in south Asian countries [4]. The RNA genome of FMDV goes through a high rate of mutation because of error prone replication by the RNA polymerase which results in high genetic diversity [11-12]. Additionally, persistent infection, recombination, and quasi-species dynamics have also been reported as contributing factors to
the genetic variation [12-13]. One major concern is that immunity to one serotype of FMDV does not confer protection against another. The complex intra-serotypic variation coupled with the presence of multiple serotypes has complicated disease control, specifically in case of vaccination. The most common forms of vaccines against FMDV are killed or attenuated vaccines [14]. The major problems regarding such vaccination are requirement of high specificity, attainment of temporary immunity (months to years), requirement of revaccination for prophylactic control, reversal effects of vaccine components [14]. Moreover, vaccination against FMDV lacks induction of rapid protection against challenge or prevention of the development of the carrier state. Furthermore, it is evidential that the clinical protection depends upon the span of immunization and the period of exposure/challenge methods [15]. All these aspects have created great challenges in development of vaccine against FMDV. Subunit vaccine or peptide vaccine for FMDV prevention has been suggested by several authors in this regard [16]. Subunit vaccine is a vaccine that contains viral antigens made free of viral nucleic acid. It is less possibility to cause adverse reactions than a vaccine containing the whole virion.

The aim of our study was to compare and analyze the capsid proteins (VP0, VP1, VP2, VP3 and VP4) of different Eurasian serotypes (O, A, Asia 1, C; UniprotKB entry P03305 P49303, E9KMQ6, P15072 respectively) of FMDV through computational approach in order to evaluate their feasibility as vaccine candidates. In our dry lab approach, FMDV genome polyprotein sequences of different serotypes have been identified, and similarity and dissimilarity among the sequences were analyzed. Different bioinformatics tools were utilized to analyze the capsid proteins of four serotypes for their antigenic and immunogenic property. In a wet lab study, we conducted molecular characterization for particular serotypes from tissue samples of suspected FMDV infected cattle of Savar Military Firm, Dhaka Bangladesh.

2. Materials and Methods

2.1. Dry Lab Study

At first the genome polyprotein sequences of four serotypes of FMDV were identified from NCBI Genome Database. Multiple sequence alignment of the genome polyproteins of four serotypes of FMDV was done by ClustalW [17] to determine the mutations among the serotypes (Supplementary file 1). Maximum likelihood method was used for phylogenetic tree construction from MEGA software in which boot strapped value was 1000. The serotypes under study show very close phylogenetic relationship with approximately 90% sequence similarity among them and some observable point mutations (Figure:1A and 1B).

Amino acid sequence of the proteins of FMDV was identified from UniprotKB [18]. HMMTOP [19-20] was used to determine the number of transmembrane (TM) helix, topology of the antigenic proteins and feasibility of molecule cloning of the antigenic proteins. Epitope binding sites against specific MHC (major histocompatibility complex) for each antigen were determined by RANKPEP [21-22]. Determination of the adhesion probability (which denotes to binding capacity of antigen to host surface) against specific MHC molecule of each antigen was done by Vaxign [23]. The antigenic proteins were compared based on all the parameters under study (related to immunogenecity and antigenecity) to identify the better vaccine candidates. At last the structures of each antigen were also predicted based on homology modeling by SWISS-MODEL (structure not shown in this article) [24-26].
All protein ID and sequence information shown in supplementary file 1 and 2.

2.2. Wet Lab Study

**Cell culture**

Baby hamster kidney cells (BHK-21) (American Type Culture Collection, ATCC, Rockville, MD, USA) were cultured and maintained in Dulbecco's modified Eagle's medium (DMEM) supplemented with 10% heat-inactivated fetal bovine serum (Gibco Life Technologies, USA), 100 U/ml penicillin, 2 mM L-glutamine, and 100 µg/ml streptomycin.

**Determination of cellular morphology upon FMDV infection**

BHK-21 cells (1.6 x 10^5) were grown onto 60 mm tissue culture plate. Cells were challenged with the viral sample collected from suspected FMD Virus infected cattle from Savar Military Firm, Dhaka Bangladesh. After 72 hours, images were taken under an inverted microscope with a magnification of 10X.

**Reverse transcription-polymerase chain reaction (RT-PCR) assay**

BHK-21 cells were challenged with the viral sample using established protocol of Virology Lab of Animal Health Research Division of Bangladesh Livestock Research Institute (BLRI). RNA was extracted by using Qiagen RNeasy kit and RT-PCR was done by Superscript III RT-PCR kit. The oligonucleotide primers for the detection of FMDV and FMDV serotypes were used from the 2B and VP1 (1D) regions of the viral genome as published (Table: 1) [27].

**Table 1. List of the primers, their sequences and size of PCR amplicon were used for the diagnosis of FMD virus from the field samples**

<table>
<thead>
<tr>
<th>FMDV serotype</th>
<th>Primer label</th>
<th>Sequence(5'-3')</th>
<th>Location</th>
<th>PCR products (bp)</th>
</tr>
</thead>
<tbody>
<tr>
<td>All Serotypes</td>
<td>P32</td>
<td>CAGAGTGCAGGAGGACATGTC</td>
<td>2B</td>
<td>131 bp</td>
</tr>
<tr>
<td></td>
<td>P33</td>
<td>AGCCTTGTACCAGGGTTTGGC</td>
<td>2B</td>
<td></td>
</tr>
<tr>
<td></td>
<td>P74</td>
<td>GACACCCACTCAGGGACCCCGG</td>
<td>VP1(1D)</td>
<td></td>
</tr>
<tr>
<td>Asia 1</td>
<td>P75</td>
<td>GACACCCACCAGGACCCCGG</td>
<td>VP1(1D)</td>
<td>292 bp</td>
</tr>
<tr>
<td></td>
<td>P76</td>
<td>GACACCCACACAAGGACCCCGG</td>
<td>VP1(1D)</td>
<td></td>
</tr>
<tr>
<td></td>
<td>P77</td>
<td>GACACCGACTCAGAACCACCGG</td>
<td>VP1(1D)</td>
<td></td>
</tr>
</tbody>
</table>

2.3. Results and Discussions

In the present study, the capsid proteins of four major serotypes (O, A, Asia 1, C) of Foot and Mouth Disease Virus (FMDV) were evaluated as the vaccine candidates. Using computational approach, we found no transmembrane helix of the viral proteins of the mentioned serotypes but there was an entropy variation among them. VP4 region of all the mentioned FMDV serotypes showed the lowest entropy value while VP2 exhibited highest entropy for O type FMDV serotype and VP3 showed highest entropy for Asia 1, A and C type FMDV serotypes (Table 2-5). In addition, VP1 region demonstrated moderate entropy for Asia 1 serotype (Table 2).

**Table 2. Dry lab analysis results of A type (FMDV)**

<table>
<thead>
<tr>
<th>Protein</th>
<th>HMMTOP Analysis</th>
<th>Swiss model analysis</th>
<th>RANKPEP for MHC I</th>
<th>RANKPEP for MHC II</th>
<th>Vaxign analysis</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>No. of TM helix</td>
<td>Entropy</td>
<td>QMEAN</td>
<td>Score</td>
<td>Z score</td>
</tr>
<tr>
<td>VP1</td>
<td>0</td>
<td>17.0120</td>
<td>0.63</td>
<td>-2.26</td>
<td>128.0</td>
</tr>
<tr>
<td>VP2</td>
<td>0</td>
<td>17.0135</td>
<td>0.66</td>
<td>-1.79</td>
<td>128.0</td>
</tr>
<tr>
<td>VP3</td>
<td>0</td>
<td>17.0136</td>
<td>0.67</td>
<td>-1.62</td>
<td>128.0</td>
</tr>
<tr>
<td>VP4</td>
<td>0</td>
<td>17.0079</td>
<td>0.08</td>
<td>-4.33</td>
<td>128.0</td>
</tr>
</tbody>
</table>

As entropy means disorder, it will be difficult to clone a protein with higher entropy [19] and proteins with lower entropy are more feasible for molecular cloning.

In case of O type FMDV, VP4 showed highest percentage (%) of optimal (OPT) antigenecity among these proteins (VP1, VP2, VP3 and VP4), and VP3 exhibited the lowest % OPT (Table 3).

**Table 3. Dry lab analysis results of O type (FMDV)**

<table>
<thead>
<tr>
<th>Protein</th>
<th>HMMTOP analysis</th>
<th>Swiss model analysis</th>
<th>RANKPEP for MHC I</th>
<th>RANKPEP for MHC II</th>
<th>Vaxign analysis</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>No. of TM helix</td>
<td>Entropy</td>
<td>QMEAN</td>
<td>Score</td>
<td>Z score</td>
</tr>
<tr>
<td>VP1</td>
<td>0</td>
<td>17.0119</td>
<td>0.63</td>
<td>-2.26</td>
<td>128.0</td>
</tr>
<tr>
<td>VP2</td>
<td>0</td>
<td>17.0133</td>
<td>0.66</td>
<td>-1.79</td>
<td>128.0</td>
</tr>
<tr>
<td>VP3</td>
<td>0</td>
<td>17.0125</td>
<td>0.69</td>
<td>-1.34</td>
<td>128.0</td>
</tr>
<tr>
<td>VP4</td>
<td>0</td>
<td>17.0080</td>
<td>0.08</td>
<td>-4.33</td>
<td>128.0</td>
</tr>
</tbody>
</table>
With the highest % OPT antigenicity, VP4 would show the highest epitope binding capacity with mammalian MHC I molecule. VP1 region of A type FMDV showed highest %OPT among these proteins while VP4 represented the lowest %OPT (Table 2). Consequently, VP1 would show the highest epitope binding capacity with mammalian MHC I molecule. In addition, VP2 and VP3 of Asia 1 type FMDV exhibited the same highest %OPT among these proteins (Table 4).

Table 4. Dry lab analysis results of Asia1 type (FMDV)

<table>
<thead>
<tr>
<th>Protein</th>
<th>HMMTOP Analysis</th>
<th>Swiss model analysis</th>
<th>RANKPEP for MHC I</th>
<th>RANKPEP for MHC II</th>
<th>Vaxign analysis</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>No. of TM helix</td>
<td>Entropy</td>
<td>QMEAN Score</td>
<td>Z Score</td>
<td>Optimal score</td>
</tr>
<tr>
<td>VP1</td>
<td>0</td>
<td>17.0093</td>
<td>0.72</td>
<td>-1.04</td>
<td>128.0</td>
</tr>
<tr>
<td>VP2</td>
<td>0</td>
<td>17.0136</td>
<td>0.69</td>
<td>-1.42</td>
<td>128.0</td>
</tr>
<tr>
<td>VP3</td>
<td>0</td>
<td>17.0145</td>
<td>NA</td>
<td>NA</td>
<td>128.0</td>
</tr>
<tr>
<td>VP4</td>
<td>0</td>
<td>17.0086</td>
<td>0.08</td>
<td>-4.35</td>
<td>128.0</td>
</tr>
</tbody>
</table>

As expected, these two proteins should have highest epitope binding capacity with mammalian MHC I molecule. On the other hand, VP4 showed the lowest % OPT and VP1 showed a standard value %OPT (Table 4). VP1 region of C type FMDV, revealed the highest % of OPT among these proteins while VP4 displayed the lowest OPT (%) (Table 5). Thus, VP1 should have the highest epitope binding capacity with mammalian MHC I molecule.

Table 5. Dry lab analysis results of C type (FMDV)

<table>
<thead>
<tr>
<th>Protein</th>
<th>HMMTOP Analysis</th>
<th>Swiss model analysis</th>
<th>RANKPEP for MHC I</th>
<th>RANKPEP for MHC II</th>
<th>Vaxign analysis</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>No. of TM helix</td>
<td>Entropy</td>
<td>QMEAN Score</td>
<td>Z Score</td>
<td>Optimal score</td>
</tr>
<tr>
<td>VP1</td>
<td>0</td>
<td>17.0094</td>
<td>0.63</td>
<td>2.12</td>
<td>128.0</td>
</tr>
<tr>
<td>VP2</td>
<td>0</td>
<td>17.0136</td>
<td>0.6</td>
<td>-2.6</td>
<td>128.0</td>
</tr>
<tr>
<td>VP3</td>
<td>0</td>
<td>17.0144</td>
<td>0.61</td>
<td>-2.51</td>
<td>128.0</td>
</tr>
<tr>
<td>VP4</td>
<td>0</td>
<td>17.0079</td>
<td>0.08</td>
<td>-4.33</td>
<td>128.0</td>
</tr>
</tbody>
</table>

The study of epitope binding capacity of the viral proteins with mammalian MHC II molecule, we found that VP2 and VP4 region of O type FMDV represented the same highest OPT (%) among these proteins (Table 3). These two proteins should have highest epitope binding capacity with mammalian MHC II molecule. Additionally, VP1 of A, Asia 1, and C type FMDV demonstrated the highest OPT (%) among these proteins (Table 3-4). Consequently, VP1 should have the highest epitope binding capacity with mammalian MHC II molecule for the above mentioned three types of FMDV.

Previous studies have been suggested that the higher epitope binding capacity of particular proteins denotes to their viability as vaccine components than the proteins of lower epitope binding efficiency [21-22, 28]. Based on the binding capacity of antigenic proteins to mammalian MHC I and MHC II molecules, we concluded that VP1 region can be a novel vaccine components for A, Asia 1 and C types of FMDV. Although, the results have been based on the sequences of highest possible OPT (%) for each capsid protein, we therefore further studied the 3D structure and adhesion probability of the antigenic proteins from their sequence.

Adhesion probability represents the binding capacity of antigens to the host cell. It has been reported that highest adhesion probability corresponds to the highest binding capacity [23, 31].We found that VP4 of O and A type FMDV showed the highest adhesion probability and VP1 displayed the lowest value (Table 3, 2). In case of Asia 1 and C type FMDV, VP2 showed the highest adhesion probability and VP1 demonstrated the lowest value (Table 4-5).

Different parameters regarding the feasibility of vaccine candidates showed different results for different serotypes (in some cases HMMTOP and Vaxign analysis do not show results due to short sequence). There was no single capsid protein that showed top results in case of all studies. This actually indicates that no single capsid protein can be treated as the best vaccine component against FMDV. Different antigenic proteins can be suitable candidates from different point of view. So peptide vaccine based on a single protein for all types of FMDV will not provide the best results. So far VP1 has been regarded as the best antigen for producing peptide vaccine against FMDV [16]. Moreover, the structural protein coding region VP1 has been shown to vary significantly between strains and serotypes indicating the higher mutation rate than the structural protein coding gene of FMDV [32-33]. This reduces the suitability of VP1for being the monovalent peptide vaccine. The overall study leaves the chance to think about the production of multivalent vaccine against FMDV instead of monovalent one. This may combine the prominent capsid proteins across different serotypes of FMDV to prepare a novel
vaccine against multi-serotypes of FMDV [14].

According to the results of dry lab analysis, we tried to find out the vaccine candidate in wet-lab research. The findings of the wet-lab study confirmed that the virus infected samples contained FMDV and the serotype was Asia-1. We identified Vp1 region of Asia 1 region which showed best result in dry lab as vaccine candidate (fig:2)

![Image of gel electrophoresis with bands labeled 202bp and 131bp](image)

**Fig. 2.** Confirmation of FMDV and VP1 in tissue samples using RT-PCR. Total RNA was extracted from FMDV-infected vascular fluid of tongue epithelium tissue and reverse-transcribed using two specific primers designated as 2B and VP1 (1D) regions of the viral genome for the detection of FMDV and FMDV serotypes. Lane 1-2, VP1 region of Asia 1 serotype (292 bp); lane 3, 100 bp DNA marker; lane 4-5, B1 region of all serotypes; lane 6, 100 bp DNA marker.

We also observed the cytopathic effect of virus sample (Fig 3). Further study is needed to be done for VP1 region of different serotypes that can be assembled as a multivalent vaccine. Mainly four serotypes (O, A, Asia 1 and C type) of FMDV are predominant in Bangladesh and other countries of South Asia. Among them Asia-1 has been mostly reported in Bangladesh.

![Image of cytopathic effects of FMDV](image)

**Fig. 3.** Cytopathic effects of FMDV in BHK-21 cells. About 1.6 × 10⁵ BHK-21 cells were grown onto 60 mm cell culture plate and infected with FMDV at multiplicity of infection (MOI) of 1. After 72 hrs cells were rinsed with 1 ml of 1X PBS buffer and the cellular morphological appearance was observed using inverted microscopy (Olympus, Canada) with a magnification of 10X. (A) Mock. (B) Infection with FMDV.

In conclusion, the present study mainly focused on genomic based approach of vaccine development known as reverse vaccinology. In the dry lab study, the capsid proteins of different serotypes of FMDV showed different levels of feasibility that are to be considered as peptide vaccine components. Since the idea of producing single peptide vaccine can be replaced by the concept of multivalent vaccine. The wet lab study identified the Asia 1 serotype of FMDV in the samples of suspected animals. The results can be further validated in the laboratory. Our study enhances our knowledge for the possibility of producing novel vaccine based on VP1 sequence of multiple serotypes.

**Author Contributions**

FMNH has contributed to idea development, wet lab and dry lab experimentation, and data generation. KMTR, SSS, MSR, MFI and MBA have contributed to data analysis, literature mining and interpretation of results. MSR and MFI has contributed to data maintenance and handling. KMH and MG have supervised the whole work. All the authors have contributed equally to the writing of the paper.
Acknowledgements

The authors like to acknowledge Dr. Md. Abu Hadi Noor Ali Khan, Professor, Pathology Department of Bangladesh Agriculture University; Dr. Asadul Ghan, Biosafety officer, International Center for Diarrhoeal Diseases Research, Bangladesh (ICDDR, B); Dr. Mohammed Ahasan Habib, Veterinary Surgeon, Department of Livestock Services, Dhaka for their endless inspiration, support and guidance throughout the work. We are also grateful to Md. Firoj Mortuza, IFRB, AERE, Bangladesh for his help in some data analysis.

References

In-Silico Evaluation of the Capsid Proteins of FMDV as Potential Vaccine Candidates

12 F. M. N. Hassan et al.

Genome Polyprotein Sequences of Different Serotypes of FMDV

<table>
<thead>
<tr>
<th>Serotype</th>
<th>Polyprotein Accession</th>
<th>OS</th>
<th>PE</th>
<th>SV</th>
<th>Sequence (partial)</th>
</tr>
</thead>
<tbody>
<tr>
<td>O Type</td>
<td>sp</td>
<td>P30305</td>
<td>POLG_FMDVO Genome polyprotein</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>OS=Foot-and-mouth disease virus (isolate Bovine/Germany/O1Kaufbeuren/1966 serotype O)</td>
<td>PE=1</td>
<td>SV=1</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>MNNTDCIFIALVQAIREIKALFLSRTGKMLTNGEKKTF</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>YSRPNHNDINLALQ</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>RYVEEFFPDVYSSPENLLEAIKQLEDILGHEGGPPA</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>LVNINHKLHITGTA</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>PSEVCMDVDTMCLUDHAGIFLKGQHEAVFACVTSNGWYA</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>IDDEDFYPWTPDPSDVLVF</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>VPYDQEPLNGEKFVKVA</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>INNYMQLQNYQNSMTDG</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>DNAIGSGNEDSTDTSTHTTNTDNAFSL</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>DOLLKTEETTEDLD</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>LTRRNHTTSTTSQSVGTGVTAYATDAEVFSFSPNTSLEN</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>VQAERFFKTHDLWNTZS</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>FGRCHLLELPITDKHGYSILLSYARNMGDWEVTVAQNG</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>FNNGCCVLNMVFPEISYQK</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>RELYQRTLPFQINFRTNMTAHITPFGVNYRQDK</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>PWTLVVVMVAPLTNTEGA</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>PQQKYVYANIAPNVHVAGEPSKEGGFVACSDYGGLVT</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>DKTPADTPVYKSFNPFRQ</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>LPGFRTNLNDVVEACCPFPFEGGGYVPTTKTSNDRVAQF</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>DMSLAAQKSMTFGLAQ</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>YTTYQSTGINLHMFPTGDPAKARYMAYAPAEMEPKTE</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>AAHAHIAWDETLGNSKFT</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>FSIPYLSADAYATSAEVNTVQWCLFQITHKGADG</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>ALVVLASAGKDFEELRPLVPD</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>ARAETTSAEADSVPTVTENYGETPIQRRQHTDVSFIMD</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>RFVKTQFPQINILDMOQ</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>PSHTLVARGSRYSTFSDLTAVKHEGDLWTPVNGAPEAKA</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>LDNNTNPTAYKAPLTRL</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>LPTYATPRHLATVYNGCVRNNAVPNRGDLQVLAQVKVAR</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>TLTPSFGYAIKATRVTLE</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>LYMKRERAETYCFRPLLAIIHPTEARHOKKIVAPVQLNTNL</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>KLAGDVESEIPFPPFSDF</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>A Type</td>
<td>sp</td>
<td>P49303</td>
<td>POLG_FMDVZ Genome polyprotein</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>OS=Foot-and-mouth disease virus (isolate /Azerbaijan/A22-550/1965 serotype A)</td>
<td>PE=1</td>
<td>SV=1</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>MNNTDCIFIALVQAIREIKALFLSRTGKMLTNGEKKTF</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>YSRPNHNDINLALQ</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>RYVEEFFPDVYSSPENLLEAIKQLEDILGHEGGPPA</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>LVNINHKLHITGTA</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>PSEVCMDVDTMCLUDHAGIFLKGQHEAVFACVTSNGWYA</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>IDDEDFYPWTPDPSDVLVF</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>VPYDQEPLNGEKFVKVA</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>INNYMQLQNYQNSMTDG</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>DNAIGSGNEDSTDTSTHTTNTDNAFSL</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>DOLLKTEETTEDLD</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>LTRRNHTTSTTSQSVGTGVTAYATDAEVFSFSPNTSLEN</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>VQAERFFKTHDLWNTZS</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>FGRCHLLELPITDKHGYSILLSYARNMGDWEVTVAQNG</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>FNNGCCVLNMVFPEISYQK</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>RELYQRTLPFQINFRTNMTAHITPFGVNYRQDK</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>PWTLVVVMVAPLTNTEGA</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>PQQKYVYANIAPNVHVAGEPSKEGGFVACSDYGGLVT</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>DKTPADTPVYKSFNPFRQ</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>LPGFRTNLNDVVEACCPFPFEGGGYVPTTKTSNDRVAQF</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>DMSLAAQKSMTFGLAQ</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>YTTYQSTGINLHMFPTGDPAKARYMAYAPAEMEPKTE</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>AAHAHIAWDETLGNSKFT</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>FSIPYLSADAYATSAEVNTVQWCLFQITHKGADG</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>ALVVLASAGKDFEELRPLVPD</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>ARAETTSAEADSVPTVTENYGETPIQRRQHTDVSFIMD</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>RFVKTQFPQINILDMOQ</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>PSHTLVARGSRYSTFSDLTAVKHEGDLWTPVNGAPEAKA</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>LDNNTNPTAYKAPLTRL</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>LPTYATPRHLATVYNGCVRNNAVPNRGDLQVLAQVKVAR</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>TLTPSFGYAIKATRVTLE</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>LYMKRERAETYCFRPLLAIIHPTEARHOKKIVAPVQLNTNL</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>KLAGDVESEIPFPPFSDF</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
In-Silico Evaluation of the Capsid Proteins of FMDV as Potential Vaccine Candidates

**C Type**

>&sp;|P15072|POLG_FMDVT Genome polyprotein
OS=Foot-and-mouth disease virus (isolate /Germany/C1Oberbayen/1960 serotype C)
PE=1

| MVCDPALNRFHDFIDVSAKGDYKNICKLDIKALEDHTTHFVMAPFQDCALLNGMAMVEMMKRQMQDFMPPQFLPQNYQLVQEVIRDELHKVSSHPFQIKSIFSQSKSVLYFLIQEQGKREHPHLPQHQYAMFQYDCALLNGMAVMKREEUPQGQPMPSQFPLQNYQLVQEVUNILQFDFILXNYLQYLVIRESKYFVIFVGYFEVEEAIKLMKEREYEKFKACQTFVLIDIRFRKPDVRLLQYVEHILLTRMIMGRFCAPMQHSNMPQGSAVCNPIDMQRFQATHLYVRQVWNYDWDVFSAHACKSDANMAIMFEEFVTFEFEGPHFNAEHWLTLTNTVEHAVNKRVVEHFMPSGCSTESITLNNYLYLVRHYEVGELITMTISYGGDDIVSAASYDLPEALKPHFSGAQITPADSDKGKVPFGHGHSLTIDTVFLKRRHMHDYGTGFYPKVKKAPTLEALSFARRGTVIQLEKLSVAGLVASHSGDEYRLEPFEQFQGFEIPSYSRLYRIVNAVCGDA

C Type

MVCDPALNRFHDFIDVSAKGDYKNICKLDIKALEDHTTHFVMAPFQDCALLNGMAMVEMMKRQMQDFMPPQFLPQNYQLVQEVIRDELHKVSSHPFQIKSIFSQSKSVLYFLIQEQGKREHPHLPQHQYAMFQYDCALLNGMAVMKREEUPQGQPMPSQFPLQNYQLVQEVUNILQFDFILXNYLQYLVIRESKYFVIFVGYFEVEEAIKLMKEREYEKFKACQTFVLIDIRFRKPDVRLLQYVEHILLTRMIMGRFCAPMQHSNMPQGSAVCNPIDMQRFQATHLYVRQVWNYDWDVFSAHACKSDANMAIMFEEFVTFEFEGPHFNAEHWLTLTNTVEHAVNKRVVEHFMPSGCSTESITLNNYLYLVRHYEVGELITMTISYGGDDIVSAASYDLPEALKPHFSGAQITPADSDKGKVPFGHGHSLTIDTVFLKRRHMHDYGTGFYPKVKKAPTLEALSFARRGTVIQLEKLSVAGLVASHSGDEYRLEPFEQFQGFEIPSYSRLYRIVNAVCGDA

C Type

MVCDPALNRFHDFIDVSAKGDYKNICKLDIKALEDHTTHFVMAPFQDCALLNGMAMVEMMKRQMQDFMPPQFLPQNYQLVQEVIRDELHKVSSHPFQIKSIFSQSKSVLYFLIQEQGKREHPHLPQHQYAMFQYDCALLNGMAVMKREEUPQGQPMPSQFPLQNYQLVQEVUNILQFDFILXNYLQYLVIRESKYFVIFVGYFEVEEAIKLMKEREYEKFKACQTFVLIDIRFRKPDVRLLQYVEHILLTRMIMGRFCAPMQHSNMPQGSAVCNPIDMQRFQATHLYVRQVWNYDWDVFSAHACKSDANMAIMFEEFVTFEFEGPHFNAEHWLTLTNTVEHAVNKRVVEHFMPSGCSTESITLNNYLYLVRHYEVGELITMTISYGGDDIVSAASYDLPEALKPHFSGAQITPADSDKGKVPFGHGHSLTIDTVFLKRRHMHDYGTGFYPKVKKAPTLEALSFARRGTVIQLEKLSVAGLVASHSGDEYRLEPFEQFQGFEIPSYSRLYRIVNAVCGDA

C Type

MVCDPALNRFHDFIDVSAKGDYKNICKLDIKALEDHTTHFVMAPFQDCALLNGMAMVEMMKRQMQDFMPPQFLPQNYQLVQEVIRDELHKVSSHPFQIKSIFSQSKSVLYFLIQEQGKREHPHLPQHQYAMFQYDCALLNGMAVMKREEUPQGQPMPSQFPLQNYQLVQEVUNILQFDFILXNYLQYLVIRESKYFVIFVGYFEVEEAIKLMKEREYEKFKACQTFVLIDIRFRKPDVRLLQYVEHILLTRMIMGRFCAPMQHSNMPQGSAVCNPIDMQRFQATHLYVRQVWNYDWDVFSAHACKSDANMAIMFEEFVTFEFEGPHFNAEHWLTLTNTVEHAVNKRVVEHFMPSGCSTESITLNNYLYLVRHYEVGELITMTISYGGDDIVSAASYDLPEALKPHFSGAQITPADSDKGKVPFGHGHSLTIDTVFLKRRHMHDYGTGFYPKVKKAPTLEALSFARRGTVIQLEKLSVAGLVASHSGDEYRLEPFEQFQGFEIPSYSRLYRIVNAVCGDA

C Type

MVCDPALNRFHDFIDVSAKGDYKNICKLDIKALEDHTTHFVMAPFQDCALLNGMAMVEMMKRQMQDFMPPQFLPQNYQLVQEVIRDELHKVSSHPFQIKSIFSQSKSVLYFLIQEQGKREHPHLPQHQYAMFQYDCALLNGMAVMKREEUPQGQPMPSQFPLQNYQLVQEVUNILQFDFILXNYLQYLVIRESKYFVIFVGYFEVEEAIKLMKEREYEKFKACQTFVLIDIRFRKPDVRLLQYVEHILLTRMIMGRFCAPMQHSNMPQGSAVCNPIDMQRFQATHLYVRQVWNYDWDVFSAHACKSDANMAIMFEEFVTFEFEGPHFNAEHWLTLTNTVEHAVNKRVVEHFMPSGCSTESITLNNYLYLVRHYEVGELITMTISYGGDDIVSAASYDLPEALKPHFSGAQITPADSDKGKVPFGHGHSLTIDTVFLKRRHMHDYGTGFYPKVKKAPTLEALSFARRGTVIQLEKLSVAGLVASHSGDEYRLEPFEQFQGFEIPSYSRLYRIVNAVCGDA

C Type

MVCDPALNRFHDFIDVSAKGDYKNICKLDIKALEDHTTHFVMAPFQDCALLNGMAMVEMMKRQMQDFMPPQFLPQNYQLVQEVIRDELHKVSSHPFQIKSIFSQSKSVLYFLIQEQGKREHPHLPQHQYAMFQYDCALLNGMAVMKREEUPQGQPMPSQFPLQNYQLVQEVUNILQFDFILXNYLQYLVIRESKYFVIFVGYFEVEEAIKLMKEREYEKFKACQTFVLIDIRFRKPDVRLLQYVEHILLTRMIMGRFCAPMQHSNMPQGSAVCNPIDMQRFQATHLYVRQVWNYDWDVFSAHACKSDANMAIMFEEFVTFEFEGPHFNAEHWLTLTNTVEHAVNKRVVEHFMPSGCSTESITLNNYLYLVRHYEVGELITMTISYGGDDIVSAASYDLPEALKPHFSGAQITPADSDKGKVPFGHGHSLTIDTVFLKRRHMHDYGTGFYPKVKKAPTLEALSFARRGTVIQLEKLSVAGLVASHSGDEYRLEPFEQFQGFEIPSYSRLYRIVNAVCGDA

C Type

MVCDPALNRFHDFIDVSAKGDYKNICKLDIKALEDHTTHFVMAPFQDCALLNGMAMVEMMKRQMQDFMPPQFLPQNYQLVQEVIRDELHKVSSHPFQIKSIFSQSKSVLYFLIQEQGKREHPHLPQHQYAMFQYDCALLNGMAVMKREEUPQGQPMPSQFPLQNYQLVQEVUNILQFDFILXNYLQYLVIRESKYFVIFVGYFEVEEAIKLMKEREYEKFKACQTFVLIDIRFRKPDVRLLQYVEHILLTRMIMGRFCAPMQHSNMPQGSAVCNPIDMQRFQATHLYVRQVWNYDWDVFSAHACKSDANMAIMFEEFVTFEFEGPHFNAEHWLTLTNTVEHAVNKRVVEHFMPSGCSTESITLNNYLYLVRHYEVGELITMTISYGGDDIVSAASYDLPEALKPHFSGAQITPADSDKGKVPFGHGHSLTIDTVFLKRRHMHDYGTGFYPKVKKAPTLEALSFARRGTVIQLEKLSVAGLVASHSGDEYRLEPFEQFQGFEIPSYSRLYRIVNAVCGDA
Capsid Protein Sequences of Different Serotypes of FMDV

**O Type**

vp0

>sp|P03305|202-504

GAQQSSPATGSQNSGNSTSIINNYMYQQYQNSMTDQLGDN AIGSSNEGSSSTTTSTHT NTQNDWFKSLASSAFSLGFALLA DKKTEETTLEDRLT RNHTTTTSTTQSSVGVTGY TAYATDVFSGNPSLELTVQVQAERRFKTHLDFWTSDFGS RCHLLELPTDHHKVGYSGLT DSYAMRNGWDVDVTAQNVFGNGCQLVVAMVPEVLISYKRE LYLQLTFHQQFQINPRNTMT AHTIVPFVGVNRYSQYKVKWPTLVMVVAPELTVNTEFAPQ IKVYANIAPTNVHVAGEFSSKE

vp1

>sp|P03305|725-935

GAGQSSPATGSQNSGNSTSIINNYMYQQYQNSMTDQLGDN AIGSSNEGSSSTTTSTHT NTQNDWFKSLASSAFSLGFALLA DKKTEETTLEDRLT RNHTTTTSTTQSSVGVTGY TAYATDVFSGNPSLELTVQVQAERRFKTHLDFWTSDFGS RCHLLELPTDHHKVGYSGLT DSYAMRNGWDVDVTAQNVFGNGCQLVVAMVPEVLISYKRE LYLQLTFHQQFQINPRNTMT AHTIVPFVGVNRYSQYKVKWPTLVMVVAPELTVNTEFAPQ IKVYANIAPTNVHVAGEFSSKE

vp2

>sp|P03305|287-504

GAGQSSPATGSQNSGNSTSIINNYMYQQYQNSMTDQLGDN AIGSSNEGSSSTTTSTHT NTQNDWFKSLASSAFSLGFALLA DKKTEETTLEDRLT RNHTTTTSTTQSSVGVTGY TAYATDVFSGNPSLELTVQVQAERRFKTHLDFWTSDFGS RCHLLELPTDHHKVGYSGLT DSYAMRNGWDVDVTAQNVFGNGCQLVVAMVPEVLISYKRE LYLQLTFHQQFQINPRNTMT AHTIVPFVGVNRYSQYKVKWPTLVMVVAPELTVNTEFAPQ IKVYANIAPTNVHVAGEFSSKE

vp3

>sp|P03305|505-724

GIFPVACSDGYGGLVTTDPKTADPVYGMVYNPPRTNYPGRF TNLDDLVAEACPFLCFFDGD KPYVVVTRTEDQRLLAKDFLSLAHKMSNTYLSGIAQYQYAQ SGTINHLHMTGTSDDSKAR YMAYVPGVPETPDTPAAKCIHAEDTGLNKSTFSEP YVAADyAYTASDVAETTNY VQQWCVQCYQHTKGKAEQDTVSVSAGKDFELRLPDSRPSA IKVYANIAPTNVHVAGEFSSKE

**Asia 1 Type**

vp1

>tr|E9KMQ6|724-932

TTTGESADPVTTTVENYGETQTARRLHTDVFVLDREVK LTQPKTSQTDDLMQSPHT LVLARRASATYFSDLELVHTGPVTWVNPGAPKTLNMM TNPTAYQKQPITRPLPRTY AHPYLSTYQKTYGEESSRSSGDRLAARVSNRLEPSF YVGAOKAADTEILLMRK AEYTCRPCRLALADTDDQRKQIEEIPKQ

vp2

>tr|E9KMQ6|287-504

GAGQSSPATGSQNSGNSTSIINNYMYQQYQNSMTDQLGDN AIGSSNEGSSSTTTSTHT NTQNDWFKSLASSAFSLGFALLA DKKTEETTLEDRLT RNHTTTTSTTQSSVGVTGY TAYATDVFSGNPSLELTVQVQAERRFKTHLDFWTSDFGS RCHLLELPTDHHKVGYSGLT DSYAMRNGWDVDVTAQNVFGNGCQLVVAMVPEVLISYKRE LYLQLTFHQQFQINPRNTMT AHTIVPFVGVNRYSQYKVKWPTLVMVVAPELTVNTEFAPQ IKVYANIAPTNVHVAGEFSSKE

vp3

>tr|E9KMQ6|505-723

DSFAYMRNGWDVEVSAVNGQFNGCQLVVAMVPEWKEFTPRE KYQLTLFHPHQFISPRNTMT AHIIVPVLGVRNRYSQYKVKWPTLVMVVAPELTVNTEFAPQ IKVYANIAPTNVHVAGEFSSKE

vp4

>tr|E9KMQ6|202-286

GAGQSSPATGSQNSGNSTSIINNYMYQQYQNSMTDQLGDN AIGSSNEGSSSTTTSTHT NTQNDWFKSLASSAFSLGFALLA DKKTEETTLEDRLT RNHTTTTSTTQSSVGVTGY TAYATDVFSGNPSLELTVQVQAERRFKTHLDFWTSDFGS RCHLLELPTDHHKVGYSGLT DSYAMRNGWDVDVTAQNVFGNGCQLVVAMVPEVLISYKRE LYLQLTFHQQFQINPRNTMT AHTIVPFVGVNRYSQYKVKWPTLVMVVAPELTVNTEFAPQ IKVYANIAPTNVHVAGEFSSKE
In-Silico Evaluation of the Capsid Proteins of FMDV as Potential Vaccine Candidates

Genome Polyprotein Sequences of Different Serotypes of FMDV

O Type

>sp|P03305|POLG_FMDVO Genome polyprotein
OS=Foot-and-mouth disease virus (isolate Bovine/Germany/O1Kaufbeuren/1966 serotype O) PE=1 SV=1

MNTTDCFIALVQAIREIKALFLSRTTGKMLTNYNGETK
YRSPNNHDCLWNALIQFL
RYEEPPFDFWYVSPEELNLTLEAIKQLEDLTLGELHLEGFFPA
LVWNKILHLLHTIGTAR
PSECVCMGDTCMCLAFLHAGIFLQKEHAFVACVTSGNYWA
IDDEFYPWTDPFSDLVYL
VYPYDQPLNMTKLVKQKRLGAKQSSPAGSNQQSNSTGNS
IINNYMQYQYMQNSDQLG
DMSAIAGSNESQDTSTTTSTHTNTQNNNDWFKSLASSAFSGF
GALLA

C Type

vp0

>sp|P15072|202-504
GAGQSSPAGSNQQSNSTGNSIINNYMQYQYMQNSDQLG
DMSAIAGSNESQDTSTTTSTHTNTQNNNDWFKSLASSAFSGFL
GALLA

vp1

>sp|P15072|724-930
GIFPVACSDGYGNMVTTDPKTADPVYGKVFSNQPSFSGF
GFLNLDAVCACFPFLRGEV
GFLVTVNSGDRLLAKFDDVSLLAGHMSNTYLAGLAATQY
GT
MVAYIPGMDTFDFEERAAHCISWEEDTLGNSKFTFSIPYL
SNAADDYSATDSVATTSQV
GWCY1QTHGKAEGDGLVSVSAGKDFERFRLPVDAarroQ

vp2

>sp|P15072|287-504
GIFPVACSDGYGNMVTTDPKTADPVYGKVFSNQPSFSGF
GFLNLDAVCACFPFLRGEV
GFLVTVNSGDRLLAKFDDVSLLAGHMSNTYLAGLAATQY
GT
MVAYIPGMDTFDFEERAAHCISWEEDTLGNSKFTFSIPYL
SNAADDYSATDSVATTSQV
GWCY1QTHGKAEGDGLVSVSAGKDFERFRLPVDAarroQ

vp3

>sp|P15072|505-723
GIFPVACSDGYGNMVTTDPKTADPVYGKVFSNQPSFSGF
GFLNLDAVCACFPFLRGEV
GFLVTVNSGDRLLAKFDDVSLLAGHMSNTYLAGLAATQY
GT
MVAYIPGMDTFDFEERAAHCISWEEDTLGNSKFTFSIPYL
SNAADDYSATDSVATTSQV
GWCY1QTHGKAEGDGLVSVSAGKDFERFRLPVDAarroQ

vp4

>sp|P15072|202-286
GAGQSSPAGSNQQSNSTGNSIINNYMQYQYMQNSDQLG
DMSAIAGSNESQDTSTTTSTHTNTQNNNDWFKSLASSAFSGFL
GALLA

 Genome Polyprotein Sequences of Different Serotypes of FMDV

O Type

>sp|P03305|POLG_FMDVO Genome polyprotein
OS=Foot-and-mouth disease virus (isolate Bovine/Germany/O1Kaufbeuren/1966 serotype O) PE=1 SV=1

MNTTDCFIALVQAIREIKALFLSRTTGKMLTNYNGETK
YRSPNNHDCLWNALIQFL
RYEEPPFDFWYVSPEELNLTLEAIKQLEDLTLGELHLEGFFPA
LVWNKILHLLHTIGTAR
PSECVCMGDTCMCLAFLHAGIFLQKEHAFVACVTSGNYWA
IDDEFYPWTDPFSDLVYL
VYPYDQPLNMTKLVKQKRLGAKQSSPAGSNQQSNSTGNS
IINNYMQYQYMQNSDQLG
DMSAIAGSNESQDTSTTTSTHTNTQNNNDWFKSLASSAFSGFL
GALLA

C Type

vp0

>sp|P15072|202-504
GAGQSSPAGSNQQSNSTGNSIINNYMQYQYMQNSDQLG
DMSAIAGSNESQDTSTTTSTHTNTQNNNDWFKSLASSAFSGFL
GALLA

vp1

>sp|P15072|724-930
GIFPVACSDGYGNMVTTDPKTADPVYGKVFSNQPSFSGF
GFLNLDAVCACFPFLRGEV
GFLVTVNSGDRLLAKFDDVSLLAGHMSNTYLAGLAATQY
GT
MVAYIPGMDTFDFEERAAHCISWEEDTLGNSKFTFSIPYL
SNAADDYSATDSVATTSQV
GWCY1QTHGKAEGDGLVSVSAGKDFERFRLPVDAarroQ

vp2

>sp|P15072|287-504
GIFPVACSDGYGNMVTTDPKTADPVYGKVFSNQPSFSGF
GFLNLDAVCACFPFLRGEV
GFLVTVNSGDRLLAKFDDVSLLAGHMSNTYLAGLAATQY
GT
MVAYIPGMDTFDFEERAAHCISWEEDTLGNSKFTFSIPYL
SNAADDYSATDSVATTSQV
GWCY1QTHGKAEGDGLVSVSAGKDFERFRLPVDAarroQ

vp3

>sp|P15072|505-723
GIFPVACSDGYGNMVTTDPKTADPVYGKVFSNQPSFSGF
GFLNLDAVCACFPFLRGEV
GFLVTVNSGDRLLAKFDDVSLLAGHMSNTYLAGLAATQY
GT
MVAYIPGMDTFDFEERAAHCISWEEDTLGNSKFTFSIPYL
SNAADDYSATDSVATTSQV
GWCY1QTHGKAEGDGLVSVSAGKDFERFRLPVDAarroQ

vp4

>sp|P15072|202-286
GAGQSSPAGSNQQSNSTGNSIINNYMQYQYMQNSDQLG
DMSAIAGSNESQDTSTTTSTHTNTQNNNDWFKSLASSAFSGFL
GALLA
A type

>sp|P49303|POLG_FMDVZ Genome polyprotein

OS=Foot-and-mouth disease virus (isolate A22-550/1965 serotype A)

PE=1 SV=1

MTNTDCFIALLYALREIKALPSLRQGTKMELTLYNEKTF

>tr|E9KMQ6|E9KMQ6_9PICO Polyprotein

OS=Foot-and-mouth disease virus - type Asia 1

PE=3 SV=1
In-Silico Evaluation of the Capsid Proteins of FMDV as Potential Vaccine Candidates

C Type

OS=Foot-and-mouth disease virus (isolate /Germany/C1Oberbayen/1960 serotype C)
Capsid Protein Sequences of Different Serotypes of FMDV

**O Type**

vp0

>sp|P03305|202-504
GAGQSSPAGSNSQNSNRSISINNYMQQYQNSMDTQLGDN AISGGSNAGSTTSTTSTHT NTQNNDFSKLASASFLGALLA

vp1

>sp|P03305|1725-935
TTSGAESADPVVTMTVENYGETQIQRRQHDTVDSDFIMDVFK

vp2

>sp|P03305|202-504
GAGQSSPAGSNSQNSNRSISINNYMQQYQNSMDTQLGDN AISGGSNEGGTSTTSTHT NTQNNDFSKLASASFLGALLA

vp3

>sp|P03305|202-504
GAGQSSPAGSNSQNSNRSISINNYMQQYQNSMDTQLGDN AISGGSNAGSTTSTTSTHT NTQNNDFSKLASASFLGALLA

**A Type**

vp0

>sp|P49303|202-504
GAGQSSPAGSNSQNSNRSISINNYMQQYQNSMDTQLGDN AISGGSNAGSTTSTTSTHT NTQNNDFSKLASASFLGALLA

vp1

>sp|P49303|1725-935
TTSGAESADPVVTMTVENYGETQIQRRQHDTVDSDFIMDVFK

vp2

>sp|P49303|202-504
GAGQSSPAGSNSQNSNRSISINNYMQQYQNSMDTQLGDN AISGGSNAGSTTSTTSTHT NTQNNDFSKLASASFLGALLA
In-Silico Evaluation of the Capsid Proteins of FMDV as Potential Vaccine Candidates

Asia 1 Type

vp3
>sp|P49303|505-725
YLGVNRYDQKHKPWTLV
VMVSVPLTNTVSAGQYIQVKYANIAPTHVHVAGELPSKE

vp4
>sp|P49303|202-286
GAGQSSPAGSNGQGNTSGIINNYMQQYQSMTDQLGDN
AISGSNGESESTTTTSTHT
NTQNNDDWFKLSASSAFSLFGALLA

vp1
>tr|E9KMQ6|724-932
TTTTGESADPVTTVTENYGETQTARRLHDTADVFALDFRVK
LTQKSTQTLDDLQIPSH
LVGALLRSATYYFSDLEIALVTGPVTPVNPAGKNTAHL
TNPASYKQITPITRLAYTP
APHRVLSTVNYKGGTEAASSRGLAALARRSVNRLSFTSF
NYVAGKATIDTELNRKKRAME
AETYCPRLAPPLELLTLTQDRRQKEIIAEFKQ

vp2
>tr|E9KMQ6|287-504
DQKTEETTLEDRLRTLTRHHTTSTTTQSSVGVTYGAYAED
AVSGNPCSTLGRVTQAOER
FFKHEFDTWPDSLGFHCYELPESEHKVGFGSLMSYAM
RNGWDETVAVNOQIPNGGC
LHVAVELKEDLRKQYLTLHFQINFRTNMTAHINVP
YVGVRNYQYELKHPWTLV
VMVAPLTVKTGSSQIKYVMNAAPTYNVHVAGELPSKE

vp3
>tr|E9KMQ6|505-723
GIPVACDGYGMVTDIDTPKATAPDYGVKNPFRTPSFQGRF
TNNLDVAAECPTLPFGEV
FYYKVTNSGDRLLAFKFDVSLAAHMSNTLYALAGYQYTS
GMTNIFHPMTGFDKARY
MVAYIPPMGTPTDPERAACHISDNTGLNKSTEFISIPY
SAADYATASDVAETTSVQ
GWCVYIQTHKGAEKDVALVSAGKDIFEFRLPVDAQRQQ

vp4
>tr|E9KMQ6|202-286
GAGQSSPAGSNGQGNTSGIINNYMQQYQSMTDQLGDN
AISGSNGESESTTTTSTHT
NTQNNDDWFKLSASSAFSLFGALLA

C Type

vp0
>sp|P15072|202-504
GAGQSSPAGSNGQGNTSGIINNYMQQYQSMTDQLGDN
AISGSNGESESTTTTTSTHT
NTQNNDDWFKLSASSAFSLFGALLA

vp1
>tr|P15072|724-930
TSSNGESADPVTTVTENYGETQQRRHHDTDAFVLFVRKF
VTVSPQNYTDTLMDQAHKD
IVAGALLRAATYYFSDLEIAVTHTGKLWNPAGPVALDNT
TNPTAAYKPLTRLAFAYTP
APHRVLATGTYGRTTTYTASTRGDHAHTATAGHLPTSFN
GAVKAETITELLEMVKRA
LYCPRFLPLIQPTGDRHKQPLVAPKQ

vp2
>sp|P15072|287-504
DQKTEETTLEDRLRTLTRHHTTSTTTQSSVGVTYGAYAED
AVSGNPCSTLGRVTQAOER
FFKHEFDTWPDSLGFHCYELPESEHKVGFGSLMSYAM
RNGWDETVAVNOQIPNGGC
LHVAVELKEDLRKQYLTLHFQINFRTNMTAHINVP
YVGVRNYQYELKHPWTLV
VMVAPLTVKTGSSQIKYVMNAAPTYNVHVAGELPSKE

vp3
>sp|P15072|505-723
GIPVACDGYGMVTDIDTPKATAPDYGVKNPFRTPSFQGRF
TNNLDVAAECPTLPFGEV
FYYKVTNSGDRLLAFKFDVSLAAHMSNTLYALAGYQYTS
GMTNIFHPMTGFDKARY
MVAYIPPMGTPTDPERAACHISDNTGLNKSTEFISIPY
SAADYATASDVAETTSVQ
GWCVYIQTHKGAEKDVALVSAGKDIFEFRLPVDAQRQQ

vp4
>sp|P15072|202-286
GAGQSSPAGSNGQGNTSGIINNYMQQYQSMTDQLGDN
AISGSNGESESTTTTSTHT
NTQNNDDWFKLSASSAFSLFGALLA