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

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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. Viral protein 1 (VP1) for Asia 1 serotype represented the best result as a vaccine candidate. 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).Phylogenetic tree acts as harbinger to find out the ancestral relationship between different types of viruses. In this research Phylogenetic tree analysis depicts that four types of virus are closely related to each other. So it will act as quintessence to develop single type of vaccine to unfold the intricateness of these viruses.

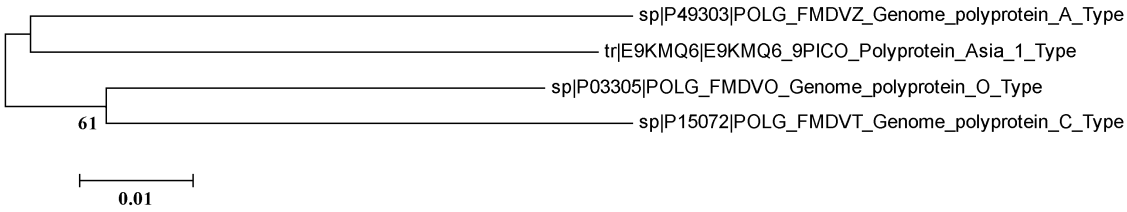

Fig. 1A. *Original phylogenetic tree for O, A, Asia 1 and C serotypes of FMDV.*

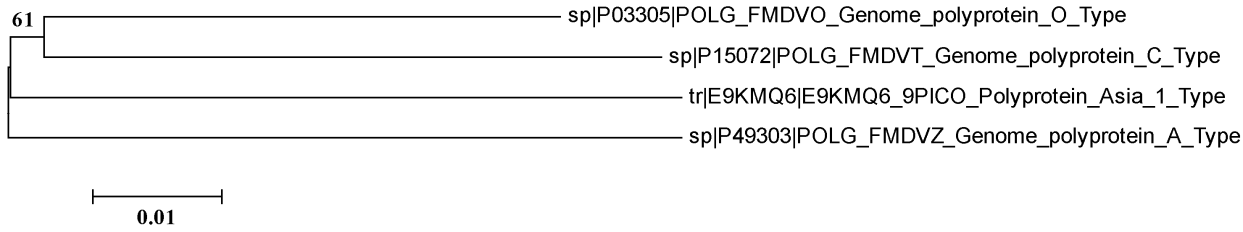

Fig. 1B. *Bootstrapped consensus phylogenetic tree.*

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*

FMDV serotype	Primer label	Sequence(5´-3´)	Location	PCR products (bp)
All Serotypes	P32	CAGATGCAGGAGGACATGTC	2B	131 bp
	P33	AGCTTGTACCAGGGTTTGGC	2B	
Asia 1	P74	GACACCACTCAGGACCGCCG	VP1(1D)	292 bp
	P75	GACACCACCCAGGACCGCCG	VP1(1D)	
	P76	GACACCACACAAGACCGCCG	VP1(1D)	
	P77	GACACGACTCAGAACCGCCG	VP1(1D)	

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)*

Protein	HMMTOP Analysis		Swiss model analysis		RANKPEP for MHC I			RANKPEP for MHC II			Vaxign analysis
	No. of TM helix	Entropy	QMEAN Score	Z Score	Optimal score	Score	% OPT	Optimal	Score	% OPT	Adhesin Probability
VP1	0	17.0120	0.61	-2.53	128	85.0	66.41	48.247	17.528	36.33	0.282
VP2	0	17.0135	0.75	-0.53	128	83.0	64.84	48.247	24.199	50.16	0.467
VP3	0	17.0136	0.67	-1.62	128	78.0	60.94	48.247	13.852	28.71	0.445
VP4	0	17.0079	0.08	-4.33	128	57.0	44.53	48.247	24.199	50.16	0.580

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)*

Protein	HMMTOP analysis		Swiss model analysis		RANKPEP for MHC I			RANKPEP for MHC II			Vaxign analysis
	No. of TM helix	Entropy	QMEAN Score	Z score	Optimal score	Score	% OPT	Optimal Score	Score	% OPT	Adhesin Probability
VP1	0	17.0119	0.63	-2.26	128.0	87.0	67.97	48.247	17.528	36.33	0.352
VP2	0	17.0133	0.66	-1.79	128.0	90.0	70.31	48.247	24.199	50.16	0.558
VP3	0	17.0125	0.69	-1.34	128.0	81.0	63.28	48.247	13.852	28.71	0.519
VP4	0	17.0080	0.08	-4.33	128.0	90.0	70.31	48.247	24.199	50.16	0.580

With the highest % OPT antigenecity, 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)*

Protein	HMMTOP Analysis		Swiss model analysis		RANKPEP for MHC I			RANKPEP for MHC II			Vaxign analysis
	No. of TM helix	Entropy	QMEAN Score	Z Score	Optimal score	Score	% OPT	Optimal Score	Score	% OPT	Adhesin Probability
VP1	0	17.0093	0.72	-1.04	128.0	88.0	68.75	65.642	19.542	29.77	0.273
VP2	0	17.0136	0.69	-1.42	128.0	97.0	75.78	65.642	13.432	20.46	0.588
VP3	0	17.0145	NA	NA	128.0	97.0	75.78	65.642	8.128	12.38	0.534
VP4	0	17.0086	0.08	-4.35	128.0	57.0	44.53	65.642	6.686	10.19	0.571

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)*

Protein	HMMTOP Analysis		Swiss model analysis		RANKPEP for MHCI			RANKPEP for MHC II			Vaxign analysis
	No of TM helix	Entropy	QMEAN Score	Z Score	Optimal score	Score	% OPT	Optimal score	Score	% Opt	Adhesin Probability
VP1	0	17.0094	0.63	2.12	128.0	85.0	66.41	65.642	11.9	18.13	0.435
VP2	0	17.0136	0.6	-2.6	128.0	80.0	62.50	65.642	13.432	20.46	0.613
VP3	0	17.0144	0.61	-2.51	128.0	82.0	64.06	65.642	6.056	9.23	0.493
VP4	0	17.0079	0.08	-4.33	128.0	57.0	44.53	65.642	6.726	10.25	NA

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 2-4). 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 thatVP4 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)

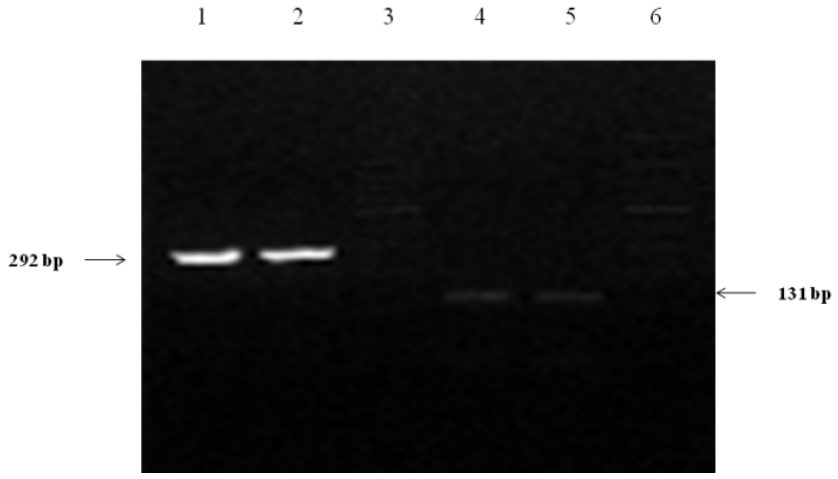

Fig. 2. *Confirmation of FMDV and VP1 in tissue samples using RT-PCR. Total RNA was extracted from FMDV-infected vascular fluid of tongue epithelium tissue and reverse-transcribed using two specific primers designated as 2B and VP1 (1D) regions of the viral genome for the detection of FMDV and FMDV serotypes. 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.

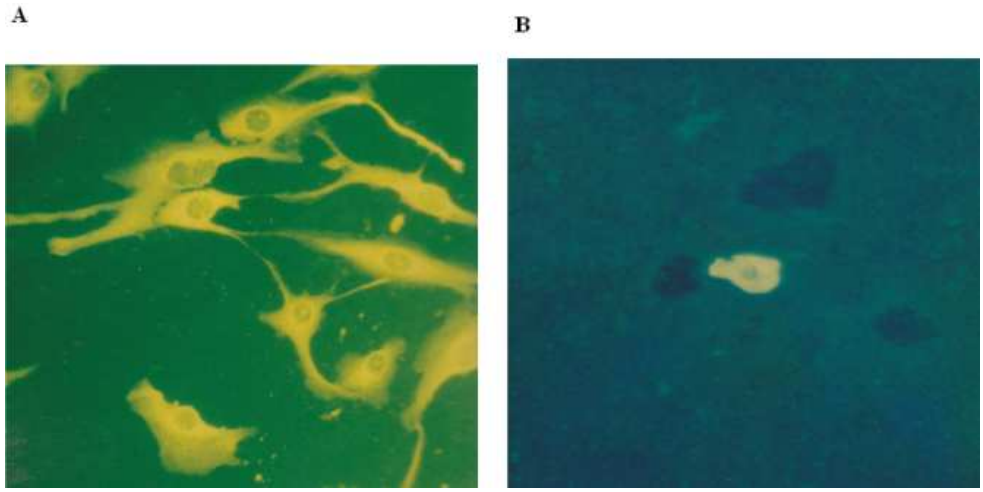

Fig. 3. *Cytopathic effects of FMDV in BHK-21 cells. About 1.6 × 10^5 BHK-21 cells were grown onto 60 mm cell culture plate and infected with FMDV at multiplicity of infection (MOI) of 1. After 72 hrs cells were rinsed with 1 ml of 1X PBS buffer and the cellular morphological appearance was observed 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.

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References

[1] Raju S, Uma Maheshwari Rao: Current development strategies for vaccines and the role of reverse vaccinology. *PHRC 2010,*2(4): 339-346.

[2] Grammatikos, Alexandros P, Mantadakis, Elpis, Falagas, Matthew E: Meta-analyses on pediatric infections and vaccines.*Infectious Disease Clinics of North America* 2009, 23 (2): 431–57.

[3] RinoRappuoli: Reverse vaccinology.*Current Opinion in Microbiology*2000, 3: 445–450.

[4] Martinez-Salas E, Saiz M, Sobrino F: "Foot-and-Mouth Disease Virus". *Animal Viruses: Molecular Biology* 2008,*Caister Academic Press.* pp. 1–38.

[5] Belsham GJ: Translation and replication of FMDV RNA in 'Foot and Mouth Disease Virus. *Curr Top MicrobiolImmunol.* 2005, 288: 43–70.

[6] Coetzer JAW, Thomsen GR, Tustin RC, Kriek NPJ: Infectious diseases of livestock with special reference to Southern Africa. *Cape Town: Oxford University Press;* 1994. Foot-and-mouth disease.

[7] Alexandersen S, Zhang Z, Donaldson AI and Garland AJM: The pathogenesis and diagnosis of Foot and Mouth Disease.*J. Comp. Pathol.* 2003c, 129:1–36.

[8] Carrillo C, Tulman ER, Delhon G, Lu Z, Carreno A, Vagnozzi A, Kutish GF, Rock DL: Comparative genomics of Foot and Mouth Disease. *J Virol.* 2005, 70: 6487–6504.

[9] Grubman MJ: Development of novel strategies to control Foot-and-Mouth Disease: Marker vaccines and antivirals.*Biologicals*2005, 33 (4): 227–234.

[10] Balinda SN *et al*: Phylogenetic analyses of the polyproteincoding sequences of serotype O Foot-and-Mouth Disease Viruses in East Africa: Evidence for interserotypic recombination.*Virol J.* 2010,7 (199): 3-9.

[11] Domingo E, Escarmısa C, Martinez MA, Martinez-Salas E, Mateu MG: Foot-and-Mouth Disease Virus populations are quasispecies. *Curr Top MicrobiolImmunol.* 1992, 176: 33–47.

[12] Domingo E, Pariente N, Airaksinen A, Gonzalez-Lopez C, S S, Herrera M, Grande-Perez A, Lowenstein PR, Manrubia SC, Lazaro E, Escarm'ısa C: Foot-and-Mouth Disease Virus: Exploring pathways towards virus extinction. *Curr Top MicrobiolImmunol.* 2005, 288:149–173.

[13] Jackson AL, O'Neill H, Maree F, Blignaut B, Carillo C, Rodriguez L, Haydon DT: Mosaic structure of Foot-and-Mouth Disease Virus genomes. *J Gen Virol.* 2007, 88: 487–492.

[14] Parida S: Accination against Foot-and-Mouth Disease Virus: Strategies and effectiveness.*Expert Rev. Vaccines* 2009, 8(3): 347–365.

[15] Kahn S:Vaccination against Foot-and-Mouth Disease: The implications for Canada.*Can Vet J.* 2002, 43:349–354.

[16] Zhang L: Research in advance for FMD novel vaccines.*Virology Journal* 2011, 8: 268.

[17] Thompson JD, Higgins DG. and Gibson TJ: CLUSTAL W: Improving the sensitivity of progressive multiple sequence alignments through sequence weighting, position specific gap penalties and weight matrix choice.*Nucl. Acids Res.* 1994, 22: 4673-4680.

[18] The UniProt Consortium: Reorganizing the protein space at the universal protein resource (UniProt).*Nucleic Acids Research 40 (Database issue)* 2012: D71–D75.

[19] Tusnády GE and Simon I: Principles governing amino acid composition of integral membrane proteins: applications to topology prediction.J. Mol. Biol. 1998, 283:489-506.

[20] Tusnády GE and Simon I: The HMMTOP transmembrane topology prediction server. *Bioinformatics* 2001, 17: 849-850.

[21] Reche PA, Glutting JP, Reinherz EL: Prediction of MHC class I binding peptides using profile motifs. *Human Immunology* 2002,63: 701-709.

[22] Reche PA, Glutting JP, Zhang H and Reinherz EL: Enhancement to the RANKPEP resource for the prediction of peptide binding to MHC molecules using profiles. *Immunogenetics*2004, 56: 405-419.

[23] He Y, Xiang Z, and Mobley HLT Vaxign: The first web-based vaccine design program for reverse vaccinology and applications for vaccine development.*Journal of Biomedicine and Biotechnology* 2010, 2010: 1-15

[24] Schwede T, Kopp J, Guex N, Peitsch MC: SWISS-MODEL: An automated protein homology-modeling server. *Nucleic Acids Research* 2003, 31(13): 3381–3385.

[25] Arnold K, Bordoli L, Kopp J, and Schwede T: The SWISS-MODEL Workspace: A web-based environment for protein structure homology modelling. *Bioinformatics* 2006, 22: 195-201.

[26] Arnold K, Bordoli L, Kopp J, and Schwede T: The SWISS-MODEL Workspace: A web-based environment for protein structure homology modelling. *Bioinformatics* 2009, 22 (2): 195-201.

[27] Vangrysperre W and De Clercq K: Rapid and sensitive polymerase chain reaction based detection and typing of Foot and Mouth Disease Virus in clinical samples and cell culture isolates, combined with a simultaneous differentiation with other and/ or symptomatically related viruses.*Arch. Virol.* 1996,141: 331–344.

[28] Reche PA, Reinherz EL: Prediction of peptide-MHC binding using profiles. *Methods Mol Biol.* 2007, 409: 185-200.

[29] U.S.F Tambunan and A.A. Parikesit: In silico analysis of envelope Dengue Virus-2 and envelope Dengue Virus-3 protein as the backbone of Dengue Virus tetravalent vaccine by using homology modeling method.OnLine Journal of Biological Sciences 2009, 9 (1): 6-16.

[30] Benkert P, Biasini M, Schwede T: Toward the estimation of the absolute quality of individual protein structure models. *Bioinformatics* 2011, 27(3): 343-50.

[31] Xiang Z, He Y: Vaxign: A web-based vaccine target design program for reverse vaccinology. *ProcediainVaccinology* 2009, 1(1): 23-29.

[32] Knowles NJ, Samuel AR: Molecular epidemiology of Foot-and-Mouth Disease Virus. *Virus Res.* 2003, 91: 65–80.

[33] Pfaff E, Mussgay M, Bóhm HO, Schultz GE and Schaller H: Antibodies against a preselected peptide recognize and neutralize Foot and Mouth Disease Virus.*EMBO J.* 1982, 1: 869-874.

Genome Polyprotein Sequences of Different Serotypes of FMDV

O Type

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>sp|P03305|POLG_FMDVO Genome polyprotein
OS=Foot-and-mouth disease virus (isolate
Bovine/Germany/O1Kaufbeuren/1966 serotype
O) PE=1 SV=1
MNTTDCFIALVQAIREIKALFLSRTTGKMELTLYNGEKKTF
YSRPNNHDNCWLNAILQLF
RYVEEPFFDWVYSSPENLTLEAIKQLEDLTGLELHEGGPPA
LVIWNIKHLLHTGIGTASR
PSEVCMVDGTDMCLADFHAGIFLKGQEHAVFACVTSNGWYA
IDDEDFYPWTPDPSDVLVF
VPYDQEPLNGEWKAKVQRKLKGAGQSSPATGSQNQSGNTGS
IINNYYMQQYQNSMDTQLG
DNAISGGSNEGSTDTTSTHTTNTQNNDWFSKLASSAFSGLF
GALLADKKTEETTLLEDRI
LTTRNGHTTSTTQSSVGVTYGYATAEDFVSGPNTSGLETRV
VQAERFFKTHLFDWVTSDS
FGRCHLLELPTDHKGVYGSLTDSYAYMRNGWDVEVTAVGNQ
FNGGCLLVAMVPELYSIQK
RELYQLTLFPHQFINPRTNMTAHITVPFVGVNRYDQYKVHK
PWTLVVMVVAPLTVNTEGA
PQIKVYANIAPTNVHVAGEFPSKEGIFPVACSDGYGGLVTT
DPKTADPVYGKVFNPPRNQ
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A type

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OS=Foot-and-mouth disease virus (isolate
-/Azerbaijan/A22-550/1965 serotype A)
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Asia 1 Type

>tr|E9KMQ6|E9KMQ6_9PICO Polyprotein
OS=Foot-and-mouth disease virus - type
Asia 1
PE=3 SV=1
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VNAVCGDA

C Type

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

Capsid Protein Sequences of Different Serotypes of FMDV

O Type

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A Type

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Asia 1 Type

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vp2
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vp4

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C Type

vp0

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vp1

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vp2

>sp|P15072|287-504
DKKTEETTLLEDRILTTRNGQTTSTTQSSVGVTFGYATAED
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RNGWDVEVTAVGNQFNGGC
LQAALVPEMGDISDREKYQLTLYPHQFINPRTNMTAHITVP
YVGVNRYDQYKQHRPWTLV
VMVVAPLTTNTAGAQQIKVYANIAPTNVHVAGELPSKE

vp3

>sp|P15072|505-723
GIFPVACSDGYGNMVTTDPKTADPAYGKVYNPPRTALPGRF
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PYVSTRTDGQRLLAKFDVSLAAKHMSNTYLAGLAQYYTQYT
GTINLHFMFTGPTDAKARY
MVAYVPPGMDAPDNPEEAAHCIHAEWDTGLNSKFTFSIPYI
SAADYAYTASHEAETTCVQ
GWVCVYQITHGKADADALVVSASAGKDFELRLPVDARQQ

vp4

>sp|P15072|202-286
GAGQSSPATGSQNQSGNTGSIINNYYMQQYQNSMDTQLGDN
AISGGSNEGSTDTTSTHTT
NTQNNDWFSKLASSAFSGLFGALLA

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
MNTTDCFIALVQAIREIKALFLSRTTGKMELTLYNGEKKTF
YSRPNNHDNCWLNAILQLF
RYVEEPFFDWVYSSPENLTLEAIKQLEDLTGLELHEGGPPA
LVIWNIKHLLHTGIGTASR
PSEVCMVDGTDMCLADFHAGIFLKGQEHAVFACVTSNGWYA
IDDEDFYPWTPDPSDVLVF
VPYDQEPLNGEWKAKVQRKLKGAGQSSPATGSQNQSGNTGS
IINNYYMQQYQNSMDTQLG
DNAISGGSNEGSTDTTSTHTTNTQNNDWFSKLASSAFSGLF
GALLADKKTEETTLLEDRI
LTTRNGHTTSTTQSSVGVTYGYATAEDFVSGPNTSGLETRV
VQAERFFKTHLFDWVTSDS
FGRCHLLELPTDHKGVYGSLTDSYAYMRNGWDVEVTAVGNQ
FNGGCLLVAMVPELYSIQK
RELYQLTLFPHQFINPRTNMTAHITVPFVGVNRYDQYKVHK
PWTLVVMVVAPLTVNTEGA
PQIKVYANIAPTNVHVAGEFPSKEGIFPVACSDGYGGLVTT
DPKTADPVYGKVFNPPRNQ
LPGRFTNLLDVAEACPTFLRFEGGVPYVTTKTDSDRVLAQF
DMSLAAKQMSNTFLAGLAQ
YYTQYSGTINLHFMFTGPTDAKARYMVAYAPPGMEPPKTPE
AAAHCIHAEWDTGLNSKFT
FSIPYLSAADYAYTASGVAETTNVQGWVCLFQITHGKADGD
ALVVLASAGKDFELRLPVD
ARAETTSAGESADPVTTTVENYGGETQIQRRQHTDVSFIMD
RFVKVTPQNQINILDLMQI
PSHTLVGALLRASTYYFSDLEIAVKHEGDLTWVPNGAPEKA
LDNTTNPTAYHKAPLTRLA
LPYTAPHRVLATVYNGECRYNRNAVPNLRGDLQVLAQKVAR
TLPTSFNYGAIKATRVTEL
LYRMKRAETYCPRPLLAIHPTEARHKQKIVAPVKQTLNFDL
LKLAGDVESNPGPFFFSDV
RSNFSKLVETINQMQEDMSTKHGPDFNRLVSAFEELAIGVK
AIRTGLDEAKPWYKLIKLL
SRLSCMAAVAARSKDPVLVAIMLADTGLEILDSTFVVKKIS
DSLSSLFHVPAPVFSFGAP
VLLAGLVKVASSFFRSTPEDLERAEKQLKARDINDIFAILK
NGEWLVKLILAIRDWIKAW
IASEEKFVTMTDLVPGILEKQRDLNDPSKYKEAKEWLDNAR
QACLKSGNVHIANLCKVVA
PAPSKSRPEPVVVCLRGKSGQGKSFLANVLAQAISTHFTGR
IDSVWYCPPDPDHFDGYNQ
QTVVVMDDLGQNPDGKDFKYFAQMVSTTGFIPPMASLEDKG
KPFNSKVIIATTNLYSGFT
PRTMVCPDALNRRFHFDIDVSAKDGYKINSKLDIIKALEDT
HANPVAMFQYDCALLNGMA
VEMKRMQQDMFKPQPPLQNVYQLVQEVIDRVELHEKVSSHP
IFKQISIPSQKSVLYFLIE
KGQHEAAIEFFEGMVHDSIKEELRPLIQQTSFVKRAFKRLK
ENFEIVALCLTLLANIVIM
IRETRKRQKMVDDAVNEYIEKANITTDDKTLDEAEKSPLET

SGASTVGFRERTLPGQKAC
DDVNSEPAQPVEEQPQAEGPYAGPLERQKPLKVRAKLPQQE
GPYAGPMERQKPLKVKAKA
PVVKEGPYEGPVKKPVALKVKAKNLIVTESGAPPTDLQKMV
MGNTKPVELILDGKTVAIC
CATGVFGTAYLVPRHLFAEKYDKIMVDGRAMTDSDYRVFEF
EIKVKGQDMLSDAALMVLH
RGNRVRDITKHFRDTARMKKGTPVVGVINNADVGRLIFSGE
ALTYKDIVVCMDGDTMPGL
FAYRAATKAGYCGGAVLAKDGADTFIVGTHSAGGNGVGYCS
CVSRSMLLKMKAHIDPEPH
HEGLIVDTRDVEERVHVMRKTKLAPTVAHGVFNPEFGPAAL
SNKDPRLNEGVVLDEVIFS
KHKGDTKMSEEDKALFRRCAADYASRLHSVLGTANAPLSIY
EAIKGVDGLDAMEPDTAPG
LPWALQGKRRGALIDFENGTVGPEVEAALKLMEKREYKFVC
QTFLKDEIRPLEKVRAGKT
RIVDVLPVEHILYTRMMIGRFCAQMHSNNGPQIGSAVGCNP
DVDWQRFGTHFAQYRNVWD
VDYSAFDANHCSDAMNIMFEEVFRTEFGFHPNAEWILKTLV
NTEHAYENKRITVGGGMPS
GCSATSIINTILNNIYVLYALRRHYEGVELDTYTMISYGDD
IVVASDYDLDFEALKPHFK
SLGQTITPADKSDKGFVLGHSITDVTFLKRHFHMDYGTGFY
KPVMASKTLEAILSFARRG
TIQEKLISVAGLAVHSGPDEYRRLFEPFQGLFEIPSYRSLY
LRWVNAVCGDA

A type

>sp|P49303|POLG_FMDVZ Genome polyprotein
OS=Foot-and-mouth disease virus (isolate
-/Azerbaijan/A22-550/1965 serotype A)
PE=1 SV=1
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YSRPNNHDNCWLNTILQLF
RYVDEPFFDWVYDSPENLTCEAIRQLEEITGLELHEGGPPA
LVIWNIKHLLHTGIGTASR
PSEVCMVDGTDMCLADFHAGIFLKGQEHAVFACVTSDGWYA
IDDEDFYPWTPDPSDVLVF
VPYDQEPLNGEWKAKVQKRLKGAGQSSPATGSQNQSGNTGS
IINNYYMQQYQNSMDTQLG
DNAISGGSNEGSTDTTSTHTTNTQNNDWFSKLASSAFSGLF
GALLADKKTEETTLLEDRI
LTTRNGHTTSTTQSSVGVTYGYSTQEDHVSGPNTSGLETRV
VQAERFFKKYLFDWTPDKA
FGHLEKLELPTDHKGVYGHLVDSFAYMRNGWDVEVSAVGNQ
FNGGCLLVAMVPEWKELTP
REKYQLTLFPHQFISPRTNMTAHIVVPYLGVNRYDQYKKHK
PWTLVVMVVSPLTTNTVSA
GQIKVYANIAPTHVHVAGELPSKEGIVPVACSDGYGGLVTT
DPKTADPVYGMVYNPPRTN
YPGRFTNLLDVAEACPTFLCFDDGKPYVVTRTDEQRLLAKF
DLSLAAKHMSNTYLSGIAQ
YYAQYSGTINLHFMFTGSTDSKARYMVAYVPPGVETPPDTP
EKAAHCIHAEWDTGLNSKF
TFSIPYVSAADYAYTASDVAETTNVQGWVCIYQITHGKAEQ
DTLVVSVSAGKDFELRLPI
DPRSQTTSTGESADPVTTTVENYGGETQVQRRQHTDVTFIM
DRFVKIQNLNPIHVIDLMQ
THQHGLVGALLRAATYYFSDLEIVVRHDGNLTWVPNGAPEA
ALSNMGNPTAYPKAPFTRL
ALPYTAPHRVLATVYNGTGKYSAGGMGRRGDLEPLAARVAA
QLPTSFNFGAIQATTIHEL
LVRMKRAELYCPRPLLAVEVSSQDRHKQKIIAPAKQLLNFD
LLKLAGDVESNPGPFFFSD
VRSNFSKLVETINQMQEDMSTKHGPDFNRLVSAFEELATGV
KAIRTGLDEAKPWYKLIKL
LSRLSCMAAVAARSKDPVLVAIMLADTGLEILDSTFVVKKI
SDSLSSLFHVPAPVFSFGA
PILLAGLVKVASSFFRSTPEDLERAEKQLKARDINDIFAIL
KNGEWLVKLILAIRDWIKA
WIASEEKFVTMTDLVPGILEKQRDLNDPSKYKEAKEWLDSA
RQACLKNGNVHIANLCKVV
TPAPSKSRPEPVVVCLRGKSGQGKSFLANVLAQAISTHFTG
RIDSVWYCPPDPDHFDGYN
QQTVVVMDDLGQNPDGKDFKYFAQMVSTTGFIPPMASLEDK
GKPFNSKVIITTTNLYSGF
TPRTMVCPDALNRRFHFDIDVSAKDGYKVNNKLDITKALED
THTNPVAMFKYDCALLNGM
AVEMKRMQQDMFKPQPPLQNVYQLVQEVIERVELHEKVSSH
QIFKQISIPSQKSVLYFLI
EKGQHEAAIEFFEGLVHDSIKEELRPLIQQTSFVKRAFKRL
KENFEIVALCLTLLANIVI
MIRETRKRQQMVDDAVNEYIEKANITTDDKTLDEAEKNPLE
TSGVSIVGFRERTLPGHRA
SDDVNSEPARPVEEQPQAEGPYTGPLERQKPLKVKAKLPQQ
EGPYAGPMERQKPLKVKVK
APVVKEGPYEGPVKKPVALKVKAKNLIVTESGAPPTDLQKM
VMGNTKPVELILDGKTVAI
CCATGVFGTAYLVPRHLFAEKYDKIMLDGRAMTDSDYRVFE
FEIKVKGQDMLSDAALMVL
HRGNRVRDITKHFRDTARMKKGTPVVGVINNADVGRLIFSG
EALTYKDIVVCMDGDTMPG
LFAYKAATKAGYCGGAVLAKDGADTFIVGTHSAGGNGVGYC
SCVSRSMLLKMKAHIDPEP
HHEGLIVDTRDVEERVHVMRKTKLAPTVAHGVFNPEFGPAA
LSNKDPRLNEGVVLDEVIF
SKHKGDTKMTEEDKALFRRCAADYASRLHNVLGTANAPLSI
YEAIKGVDGLDAMEPDTAP
GLPWALQGKRRGTLIDFENGTVGPEVASALELMEKRQYKFT
CQTFLKDEVRPMEKVRAGK
TRIVDVLPVEHILYTRMMIGRFCAQMHSNNGPQIGSAVGCN
PDVDWQRFGTHFAQYKNVW
DVDYSAFDANHCSDAMNIMFEEVFRTEFGFHPNAEWILKTL
VNTEHAYENKRITVEGGMP
SGCSATSIINTILNNIYVLYALRRHYEGVELDTYTMISYGD
DIVVASDYDLDFEALKPHF
KSLGQTITPADKSDKGFVLGQSITDVTFLKRHFRMDYGTGF
YKPVMASKTLEAILSFARR
GTIQEKLISVAGLAVHSGPDEYRRLFEPFQGLFEIPSYRSL
YLRWVNAVCGDAQSL

Asia 1 Type

>tr|E9KMQ6|E9KMQ6_9PICO Polyprotein
OS=Foot-and-mouth disease virus - type
Asia 1
PE=3 SV=1
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YSRPNNHDNCWLNTILQLF
RYVDEPFFDWVYDSPENLTLEAIRQLEEVTGLELHEGGPPA

LVIWNIKHLLHTGVGTASR
PSEVCMVDGTDMCLADFHAGIFLKGQEHAVFACVTSNGWYA
IDDEDFYPWTPDPSDVLVF
VPYDQEPLNGEWKAKVQKRLKGAGQSSPATGSQNQSGNTGS
IINNYYMQQYQNSMDTQLG
DNAISGGSNEGSTDTTSTHTNNTQNNDWFSRLASSAFSGLF
GALLADKKTEETTLLEDRI
LTTRNGHTTSTTQSSVGVTYGYAVAEDAVSGPNTSGLETRV
TQAERFFKKHLFDWTPDLS
FGHCHYLELPSEHKGVFGSLMSSYAYMRNGWDVEVTAVGNQ
FNGGCLLVALVPELKELDT
RQKYQLTLFPHQFINPRTNMTAHINVPYVGVNRYDQYELHK
PWTLVVMVVAPLTVKTGGS
EQIKVYMNAAPTYVHVAGELPSKEGIVPVACVDGYGNMVTT
DPKTADPVYGKVSNPPRTS
FPGRFTNFLDVAEACPTFLRFGEVPFVKTVNSGDRLLAKFD
VSLAAGHMSNTYLAGLAQY
YTQYSGTMNIHFMFTGPTDAKARYMVAYIPPGMTPPTDPER
AAHCIHSEWDTGLNSKFTF
SIPYLSAADYAYTASDVAETTSVQGWVCIYQITHGKAEGDA
LVVSVSAGKDFEFRLPVDA
RQQTTTTGESADPVTTTVENYGGETQTARRLHTDVAFVLDR
FVKLTQPKSTQTLDLMQIP
SHTLVGALLRSATYYFSDLEVALVHTGPVTWVPNGAPKTAL
NNHTNPTAYQKQPITRLAL
PYTAPHRVLSTVYNGKTTYGEESSRRGDLAALARRVSNRLP
TSFNYGAVKADTITELLIR
MKRAETYCPRPLLALDTTQDRRKQEIIAPEKQTLNFDLLKL
AGDVESNPGPFFFSDVRSN
FTKLVDTINQMQEDMSTKHGPDFNRLVSAFEELATGVKAIR
TGLDEAKPWYKLIKLLSRL
SCMAAVAARSKDPVLVAIMLADTGLEILDSTFVVKKISDSL
SSLFHVPAPVFSFGAPVLL
AGLVKVASSFFRSTPEDLERAEKQLKARDINDIFAILKNGE
WLVKLILAIRDWIKAWIAS
EEKFVTMTDLVPGILEKQRDLNDPSKYEEAKEWLDNARQAC
LKSGNVHIANLCKVVAPAP
SKSRPEPVVVCLRGKSGQGKSFLANVLAQAISTHFTGRTDS
VWYCPPDPDHFDGYNQQTV
VVMDDLGQNPDGKDFKYFAQMVSTTGFIPPMASLEDKGKPF
NSKVIIATTNLYSGFTPRT
MVCPDALNRRFHFDIDVSAKDGYKINNKLDIIKALEDTHTN
PVAMFQYDCALLNGMAVEM
KRMQQDMFKPQPPLQNVYQLVQEVIDRVELHEKVSSHPIFK
QISIPSQKSVLYFLIEKGQ
HEAAIEFFEGMVHDSIKEELRPLIQQTSFVKRAFKRLKENF
EIVALCLTLLANIVIMIRE
TRKRQQMVNDAVNEYIDKANITTDDKTLDEAEKNPLETSGA
STVGFRERTLPGRKTSDDV
YSEPVKPVEEQPQAEGPYAGPLERQKPLEVRAKLPQQEGPY
AGPMERQKPLKVKAKAPVV
KEGPYEGPVKKPVALKVKAKNLIVTESGAPPTDLQKMVMGN
TKPVELILDGKTVAICCAT
GVFGTAYLVPRHLFAEKYDKIMLDGRAMTDSDYRVFEFEIK
VKGQDMLSDAALMVLHRGN
RVRDITKHFRDVAKMKKGTPVVGVINNADVGRLIFSGEALT
YKDIVVCMDGDTMPGLFAY
KAVTRAGYCGGAVLAKDGAETFIVGTHSAGGNGVGYCSCVS
RSMLLKMKAHIDPEPHHEG
LVVDTRDVEERVHVMRKTKLAPTVAHGVFNPEFGPAALSNK
DPRLNEGVVLDEVIFSKHK
GDTKMSEEDKALFRRCAADYASRLHSVLGTANAPLSIYEAI
KGVDGLDAMEPDTAPGLPW
ALQGKRRGALIDFENGTVGPEVEAALKLMEKREYKFACQTF
LKDEIRPMEKVRAGKTRIV
DVLPVEHILYTRMMIGRFCAQMHSNNGPQIGSAVGCNPDID
WQRFGTHFAQYRNVWDVDY
SAFDANHCSDAMNIMFEEVFRTEFGFHPNAEWILKTLVNTE
HAYENKRIVVEGGMPSGCS
ATSIINTILNNIYVLYALRRHYEGVELDTYTMISYGDDIVV
ASDYDLDFEALKPHFKSLG
QTITPADKSDKGFVLGHSITDVTFLKRHFHMDYGTGFYKPV
MASKTLEAILSFARRGTIQ
EKLTSVAGLAVHSGPDEYRRLFEPFQGLFEIPSYRSLYLRW
VNAVCGDA

C Type

>sp|P15072|POLG_FMDVT Genome polyprotein OS=Foot-and-mouth disease virus (isolate -/Germany/C1Oberbayen/1960 serotype C) PE=1 SV=2
MNTTDCFIAVVNAIREIRALFLPRTTGKMEFTLHDGEKKVF
YSRPNNHDNCWLNTILQLF
RYVDEPFFDWVYNSPENLTLEAIKQLEELTGLELREGGPPA
LVIWNIKHLLHTGIGTASR
PSEVCMVDGTDMCLADFHAGIFMKGQEHAVFACVTSNGWYA
IDDEDFYPWTPDPSDVLVF
VPYDQEPLNEGWKANVQRKLKGAGQSSPATGSQNQSGNTGS
IINNYYMQQYQNSMDTQLG
DNAISGGSNEGSTDTTSTHTTNTQNNDWFSKLASSAFSGLF
GALLADKKTEETTLLEDRI
LTTRNGHTTSTTQSSVGVTFGYATAEDSTSGPNTSGLETRV
HQAERFFKMALFDWVPSQN
FGHMHKVVLPHEPKGVYGGLVKSYAYMRNGWDVEVTAVGNQ
FNGGCLLVALVPEMGDISD
REKYQLTLYPHQFINPRTNMTAHITVPYVGVNRYDQYKQHR
PWTLVVMVVAPLTTNTAGA
QQIKVYANIAPTNVHVAGELPSKEGIFPVACSDGYGNMVTT
DPKTADPAYGKVYNPPRTA
LPGRFTNYLDVAEACPTFLMFENVPYVSTRTDGQRLLAKFD
VSLAAKHMSNTYLAGLAQY
YTQYTGTINLHFMFTGPTDAKARYMVAYVPPGMDAPDNPEE
AAHCIHAEWDTGLNSKFTF
SIPYISAADYAYTASHEAETTCVQGWVCVYQITHGKADADA
LVVSASAGKDFELRLPVDA
RQQTTATGESADPVTTTVENYGGETQVQRRHHTDVAFVLDR
FVKVTVSGNQHTLDVMQAH
KDNIVGALLRAATYYFSDLEIAVTHTGKLTWVPNGAPVSAL
DNTTNPTAYHKGPLTRLAL
PYTAPHRVLATAYTGTTTYTASTRGDSAHLTATRARHLPTS
FNFGAVKAETITELLVRMK
RAELYCPRPILPIQPTGDRHKQPLVAPAKQLLNFDLLKLAG
DVESNPGPFFFSDVRSNFS
KLVETINQMQEDMSTKHGPDFNRLVSAFEELASGVKAIRTG
LDEAKPWYKLIKLLSRLSC
MAAVAARSKDPVLVAIMLADTGLEILDSTFVVKKISDSLSS
LFHVPAPAFSFGAPILLAG
LVKVASSFFRSTPEDLERAEKQLKARDINDIFAILKNGEWL
VKLILAIRDWIKAWIASEE
KFVTMTDLVPGILEKQRDLNDPSKYKDAKEWLDNTRQACLK

SGNVHIANLCKVVAPAPSK
SRPEPVVVCLRGKSGQGKSFLANVLAQAISTHLTGRTDSVW
YCPPDPDHFDGYNQQTVVV
MDDLGQNPDGKDFKYFAQMVSTTGFIPPMASLEDKGKPFSS
KVIIATTNLYSGFTPKTMV
CPDALNRRFHFDIDVSAKDGYKINNKLDIIKALEDTHTNPV
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LQQDMFKPQPPLQNVYQLVQEVIERVELHEKVSSHPIFKQI
SIPSQKSVLYFLIEKGQHE
AAIEFFEGMVHDSIKEELRPLIQQTSFVKRAFKRLKENFEI
VALCLTLLANIVIMIRETH
KRQKMVDDAVNEYIEKANITTDDKTLDEAEKNPLETSGAST
VGFRERTLPGQKARDDVNS
EPAQPTEEQPQAEGPYAGPLERQRPLKVRAKLPQQEGPYAG
PMERQKPLKVKARAPVVKE
GPYEGPVKKPVALKVKAKNLIVTESGAPPTDLQKMVMGNTK
PVELILDGKTVAICCATGV
FGTAYLVPRHLFAEKYDKIMLDGRALTDSDYRVFEFEIKVK
GQDMLSDAALMVLHRGNRV
RDITKHFRDVARMKKGTPVVGVINNADVGRLIFSGEALTYK
DIVVCMDGDTMPGLFAYKA
ATKAGYCGGAVLAKDGADTFIVGTHSAGGNGVGYCSCVSRS
MLLKMKAHIDPEPHHEGLI
VDTRDVEERVHVMRKTKLAPTVAHGVFNPEFGPAALSNKDP
RLNEGVVLDEVIFSKHKGD
TKMSEEDKALFRRCAADYASRLHSVLGTANAPLSIYEAIKG
VDGLDAMEPDTAPGLPWAL
QGKRRGALIDFENGTVGPEVEAALKLMEKREYKFACQTFLK
DEIRPMEKVRAGKTRIVDV
LPVEHILYTRMMIGRFCAQMHSNNGPQIGSAVGCNPDVDWQ
RFGTHFAQYRNVWDVDYSA
FDANHCSDAMNIMFEEVFRTEFGFHPNAEWILKTLVNTEHA
YENKRITVEGGMPSGCSAT
SIINTILNNIYVLYALRRHYEGVELDTYTMISYGDDIVVAS
DYDLDFEALKPHFKSLGQT
ITPADKSDKGFVLGHSITDVTFLKRHFHMDYGTGFYKPVMA
SKTLEAILSFARRGTIQEK
LISVAGLAVHSGPDEYRRLFEPFQGLFEIPSYRSLYLRWVN
AVCGDA

Capsid Protein Sequences of Different Serotypes of FMDV

O Type

vp0
>sp|P03305|202-504
GAGQSSPATGSQNQSGNTGSIINNYYMQQYQNSMDTQLGDN
AISGGSNEGSTDTTSTHTT
NTQNNDWFSKLASSAFSGLFGALLADKKTEETTLLEDRILT
TRNGHTTSTTQSSVGVTYG
YATAEDFVSGPNTSGLETRVVQAERFFKTHLFDWVTSDSFG
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IKVYANIAPTNVHVAGEFPSKE
vp1
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TNPTAYHKAPLTRLALPYT
APHRVLATVYNGECRYNRNAVPNLRGDLQVLAQKVARTLPT
SFNYGAIKATRVTELLYRM
KRAETYCPRPLLAIHPTEARHKQKIVAPVKQ
vp2
>sp|P03305|287-504
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FVSGPNTSGLETRVVQAER
FFKTHLFDWVTSDSFGRCHLLELPTDHKGVYGSLTDSYAYM
RNGWDVEVTAVGNQFNGGC
LLVAMVPELYSIQKRELYQLTLFPHQFINPRTNMTAHITVP
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vp3
>sp|P03305|505-724
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VPYVTTKTDSDRVLAQFDMSLAAKQMSNTFLAGLAQYYTQY
SGTINLHFMFTGPTDAKAR
YMVAYAPPGMEPPKTPEAAAHCIHAEWDTGLNSKFTFSIPY
LSAADYAYTASGVAETTNV
QGWVCLFQITHGKADGDALVVLASAGKDFELRLPVDARAE
vp4
>sp|P03305|202-286
GAGQSSPATGSQNQSGNTGSIINNYYMQQYQNSMDTQLGDN
AISGGSNEGSTDTTSTHTT
NTQNNDWFSKLASSAFSGLFGALLA

A Type

vp0
>sp|P49303|202-504
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NTQNNDWFSKLASSAFSGLFGALLADKKTEETTLLEDRILT
TRNGHTTSTTQSSVGVTYG
YSTQEDHVSGPNTSGLETRVVQAERFFKKYLFDWTPDKAFG
HLEKLELPTDHKGVYGHLV
DSFAYMRNGWDVEVSAVGNQFNGGCLLVAMVPEWKELTPRE
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IKVYANIAPTHVHVAGELP
SKE
vp1
>sp|P49303|726-936
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LVGALLRAATYYFSDLEIVVRHDGNLTWVPNGAPEAALSNM
GNPTAYPKAPFTRLALPYT
APHRVLATVYNGTGKYSAGGMGRRGDLEPLAARVAAQLPTS
FNFGAIQATTIHELLVRMK
RAELYCPRPLLAVEVSSQDRHKQKIIAPAKQ
vp2
>sp|P49303|287-504
DKKTEETTLLEDRILTTRNGHTTSTTQSSVGVTYGYSTQED
HVSGPNTSGLETRVVQAER
FFKKYLFDWTPDKAFGHLEKLELPTDHKGVYGHLVDSFAYM
RNGWDVEVSAVGNQFNGGC
LLVAMVPEWKELTPREKYQLTLFPHQFISPRTNMTAHIVVP

YLGVNRYDQYKKHKPWTLV
VMVVSPLTTNTVSAGQIKVYANIAPTHVHVAGELPSKE

vp3

>sp|P49303|505-725
GIVPVACSDGYGGLVTTDPKTADPVYGMVYNPPRTNYPGRF
TNLLDVAEACPTFLCFDDG
KPYVVTRTDEQRLLAKFDLSLAAKHMSNTYLSGIAQYYAQY
SGTINLHFMFTGSTDSKAR
YMVAYVPPGVETPPDTPEKAAHCIHAEWDTGLNSKFTFSIP
YVSAADYAYTASDVAETTN
VQGWVCIYQITHGKAEQDTLVVSVSAGKDFELRLPIDPRSQ

vp4

>sp|P49303|202-286
GAGQSSPATGSQNQSGNTGSIINNYYMQQYQNSMDTQLGDN
AISGGSNEGSTDTTSTHTT
NTQNNDWFSKLASSAFSGLFGALLA

Asia 1 Type

vp1

>tr|E9KMQ6|724-932
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LVGALLRSATYYFSDLEVALVHTGPVTWVPNGAPKTALNNH
TNPTAYQKQPITRLALPYT
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NYGAVKADTITELLIRMKR
AETYCPRPLLALDTTQDRRKQEIIAPEKQ

vp2

>tr|E9KMQ6|287-504
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RNGWDVEVTAVGNQFNGGC
LLVALVPELKELDTRQKYQLTLFPHQFINPRTNMTAHINVP
YVGVNRYDQYELHKPWTLV
VMVVAPLTVKTGGSEQIKVYMNAAPTYVHVAGELPSKE

vp3

>tr|E9KMQ6|505-723
GIVPVACVDGYGNMVTTDPKTADPVYGKVSNPPRTSFPGRF
TNFLDVAEACPTFLRFGEV
PFVKTVNSGDRLLAKFDVSLAAGHMSNTYLAGLAQYYTQYS
GTMNIHFMFTGPTDAKARY
MVAYIPPGMTPPTDPERAAHCIHSEWDTGLNSKFTFSIPYL
SAADYAYTASDVAETTSVQ
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vp4

>tr|E9KMQ6|202-286
GAGQSSPATGSQNQSGNTGSIINNYYMQQYQNSMDTQLGDN
AISGGSNEGSTDTTSTHTN
NTQNNDWFSRLASSAFSGLFGALLA

C Type

vp0

>sp|P15072|202-504
GAGQSSPATGSQNQSGNTGSIINNYYMQQYQNSMDTQLGDN
AISGGSNEGSTDTTSTHTT
NTQNNDWFSKLASSAFSGLFGALLADKKTEETTLLEDRILT
TRNGQTTSTTQSSVGVTFG
YATAEDSTSGPNTSGLETRVHQAERFFKMALFDWVPSQNFG
HMHKVVLPHEPKGVYGGLV
KSYAYMRNGWDVEVTAVGNQFNGGCLQAALVPEMGDISDRE
KYQLTLYPHQFINPRTNMT
AHITVPYVGVNRYDQYKQHRPWTLVVMVVAPLTTNTAGAQQ
IKVYANIAPTNVHVAGELP
SKE

vp1

>sp|P15072|724-930
TTTTGESADPVTTTVENYGGETQVQRRHHTDVAFVLDRFVK
VTVSGNQHTLDVMQAHKDN
IVGALLRAATYYFSDLEIAVTHTGKLTWVPNGAPVSALDNT
TNPTAYHKGPLTRLALPYT
APHRVLATGYTGTTTYTASTRGDLAHLTATRAGHLPTSFNF
GAVKAETITELLVRMKRAE
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vp2

>sp|P15072|287-504
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FFKMALFDWVPSQNFGHMHKVVLPHEPKGVYGGLVKSYAYM
RNGWDVEVTAVGNQFNGGC
LQAALVPEMGDISDREKYQLTLYPHQFINPRTNMTAHITVP
YVGVNRYDQYKQHRPWTLV
VMVVAPLTTNTAGAQQIKVYANIAPTNVHVAGELPSKE

vp3

>sp|P15072|505-723
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TNYLDVAEACPTFLMFENV
PYVSTRTDGQRLLAKFDVSLAAKHMSNTYLAGLAQYYTQYT
GTINLHFMFTGPTDAKARY
MVAYVPPGMDAPDNPEEAAHCIHAEWDTGLNSKFTFSIPYI
SAADYAYTASHEAETTCVQ
GWVCVYQITHGKADADALVVSASAGKDFELRLPVDARQQ

vp4

>sp|P15072|202-286
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