Zag. Vet. J. (ISSN. 1110-1458) Vol. 41 No. 1 (2013) pp.69-80

Molecular Comparison Between FMDV Causing Recent Outbreaks In Egypt And The Used Vaccine Strains

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ABSTRACT

Foot and mouth disease virus (FMD) had taken an enzootic form in Egypt since 1950, since then continues outbreaks occurs, serotype A, O and SAT2 are the most common serotypes isolated in Egypt. In this study, The suspected isolates were diagnosed and typed using an RT - PCR test. The nucleotide sequences of the VP1-coding region was determined and phylogenetic analysis was performed. The results showed that FMDV serotype O were confirmed to be serotype O topotype ME-SA in all localities,while the isolated type A during 2009 was confirmed to be serotype A topotype Africa, while the isolated type A during 2010 and 2011 belong to the Asia topotype and FMDV serotype SAT was confirmed to be SAT2 topotype VII.

INTRODUCTION

Foot and mouth disease virus (FMDV) is the causative agent of an acute devastating, febrile, infectious and highly contagious viral disease of cattle, sheep, goat, swine and other wild cloven-footed animals*(1)*.It's characterized by vesicle formation on the dorsum of the tongue, nose, muzzle, and coronary bands. Infected animals develop salivation, lameness, drop in milk production, with the high morbidity rate in adult animals and mortality rate reach to 50% in young animals*(2)*.It may be transmitted primarily by contact and aerosol in addition to the ingestion of contaminated matter and the use of contaminated vaccines and/or semen *(3)*.FMDV is a member of Family Picornaviridae, Genus Aphthovirus. It has single stranded positive sense RNA molecule of about 8.2 kilo bases (kb). The virus contains four structural proteins (1A, 1B, 1C, and 1D) of the virus capsid and eight non structural (NS) proteins (2A, 2B, 2C, 3A, 3B, 3C, 3D and L protein) involved in the life cycle of the virus inside the infected cells *(4)*. Seven immunological serotypes of FMDV were recorded, which are O, A, C, SAT_1, SAT_2, SAT_3 and Asia1 *(5)*.There was no antigenic relation between the seven serotype and the infection with one serotype doesn't protect the animal against the other serotypes and they can only be differentiated in the laboratory *(6)*.The nucleotide sequence of the viral RNA has allowed unequivocal characterization of the genetic relationships between strains. Phylogenetic tree based on the VP1 (1D) region of FMDV is widely used for genetic characterization because of its significance for virus attachment and entry, protective immunity, and serotype specificity*(7)*.Control of FMDV has been based on large scalevaccinations with whole inactivated virus vaccines, limitationof animal movements and destruction of herds exposed to thevirus *(8)*. In Egypt, a local monovalent vaccine of strain O_1/3/93 FMDV routinely used to vaccinate dairy cattle, buffaloes and fattening bulls. By the occurring of the last outbreak of FMDV type A in 2006, there is a need to produce a good quality bivalent inactivated FMDV vaccine containing strains A/1/Egypt/2006 and O_1/3/93 to control both field types of FMDV.Identifying and quantifying the importance of sites that predict viral strain

cross-reactivity not just for single viruses but across entire serotypes can help in the design of vaccines with better targeting and broader coverage*(9)*.This approach quickly and cheaply increases both our understanding of antigenic relationships and our power to control disease. Thus, in the present study, we investigated the molecular relationship between FMDV causing recent outbreaks in Egypt and the used vaccinal strains.

MATERIAL AND METHODS

Samples

Epithelial tissue samples **(ET)**and Oesophageal pharyngeal fluid **(OP)** were collected during the course of the study between 2009 and 2012 (Table1).These samples were placed in a virus transport medium, composed of equal amounts of glycerol and phosphate buffer containing antibiotic mixture in a final concentration of 100IU /ml penicillin, 100ug /ml streptomycin and 40mg /ml gentamycin and pH in the range pH 7.2–7.6, and were stored at -70°C until used *(10)*.

Table 1. Number and types of samples collected from naturally infected animals in different Egyptian governorates during the study

province	Year of Sampling	Types of samples			
		T.E		O.P	
		No	Species	No	Species
El Sharquia	2009	5	Buffalo	10	F.C
	2010	8	Buffalo	15	F.C
	2011	18	Cattle	15	F.C
	2012	32	Cattle	--	--
El Menoufia	2009	5	Buffalo	15	F.C
	2010	8	Cattle	18	F.C
	2011	12	Cattle	11	F.C
	2012	28	Cattle	--	--
El Qaliubia	2009	11	Cattle	18	F.C
	2010	5	Buffalo	15	F.C
	2011	18	Cattle	10	F.C
	2012	28	Cattle	--	--
Fayoum	2012	11	Cattle	--	--
El Garbia	2012	30	Cattle	--	--
El Suiz	2012	5	Cattle	3	F.C
Alex	2012	10	Cattle	8	F.C
El Menia	2012	10	Buffalo	--	--
Kafr El Shaik	2012	8	Cattle	--	--
Total		252		138	

(ET) Epithelial tissue samples **(OP)**Oesophageal pharyngeal fluid

Genomic RNA Extraction

RNA was extracted from Epithelial tissue samples(ET) and Oesophageal pharyngeal fluid (OP) using GeneJET™ RNA Purification Kit (Fermentas) following the manufacturer's instructions.

RT-PCR amplification

PCR for amplification VP1 (ID) of FMDV specific fragments were performed using Primers describedpreviously *(11)* (Table 2). It was carried out according to the manufacture's protocol to perform the reverse transcription and the subsequent PCR in a single reaction tube. The RT-PCR program consisted of 30 min at 45°C and 5 min at 94°C and a three-step cycling protocol was used as 94°C for 30 s, 68°C for 1min and 72°C for 1min for 35 cyclesand cycle of final extension at 72°C for10 min. Negative controls were included in each assay for detection of any contamination using Maxime™ RT-PCR PreMix (Fermentas,USA). Five microliters of amplified PCR products were separated by 1 % ethidium bromide strained agarose gel electrophoresis at 120 V for20 min. 1-kbp DNA Marker (Fermentas,USA) was used as standard and the amplified products were visualized using ultraviolet light transilluminator.

Table 2. Oligonucleotide primers used for RT-PCR reaction for detection of VP1 (ID) of FMDV serotypes

Primer Name	Sequence (5'- 3')	nmoles	Serotype specificity
G.FMDV-3R	AGCTTGTACCAGGGTTTGGC	53.11	For all types
O402-3F	GCTGCCTACCTCCTTCAA	12.80	O
A732-3F	GTCATTGACCTCATGCAGACCCAC	8.94	A
C.SAT257-3F	GGCGTTGAGAAACAACTGTG	9.98	C. SAT
C596-3F	GTTTCTGCACTTGACAACACA	10.09	C
Asia292-3F	GACACCACTCAGGACCGCCG	10.67	Asia

C-SAT, Common SAT primer

Purification and sequencing of PCR product

PCR products were purified using Gene JET PCR purificationkit (Fermentas) and resuspended in 50ul H_2O. Each purified amplicon was sequenced in both forward and reverse directions using the amplification primers.The sequencing reaction was performed in an automatedsequencer (Macrogen Inc., Korea ABI 3730XL DNA analyzer).The accession numbers of reference sequences obtained from the Genbank database were listed in (Tables 3&4).

Nucleotide sequencing and phylogeneticanalysis

Sequencing of PCR product was performed by Macrogen, Korea. Comparative analyses and phylogenetic trees were performed using MEGA5 program*(12)*

Table 3. Details of reference FMDV serotype O used for alignments and sequence analysis of FMDV serotype O VP1 gene of recent isolates

	Accession No	Description	Location	Species
1.	gi|413968623|JX666333.1	O/EGY/ALX/2011	Egypt	Cattle
2.	gi|391234182|JQ837833.1	O/EGY/MNF-2009	Egypt	Cattle
3.	gi|76564171|DQ164871.1	O1/Sharquia/EGY/72	Egypt	Cattle
4.	gi|183579037|EU553840.1	O/EGY/3/93	Egypt	Cattle
5.	gi|46810902|AY593823.1	O1manisa iso87, CG.	Turkey,1969	--
6.	gi|291294194|GU566055.1	O_SUD/30/2004	Sudan	Cattle
7.	gi255761952EU919246.1	O/UGA/6/76, P1	Uganda	--
8.	gi|183579051|EU553847.1	O/SAU/29/93	KSA	CCS
9.	gi|76564415|DQ164993.1	O/UAE/4/99	UAE	Antelope
10.	gi|220898645|FJ561317.1	O/JOR/6/2006	Jordan	Cattle
11.	gi|46810918|AY593831.1	O_UK2001-ED	UK	-

Table 4. Details of reference FMDV serotype A used for alignments and_sequence analysis of FMDV serotype AVP1 gene of recent isolates

	Accession No	Description	Location	Species
1.	gi|122938368|EF159977.1	A/Egy/2006/iso_Ism	Egypt: Ismailia	Cattle
2.	gi|145573118|EF208757.1	A/EGY/1/2006	Egypt: Ismailia	Bovine
3.	gi|145573116|EF208756.1	A/EGY/1/72	Egypt: Alex	Bovine
4.	gi|258590106|FJ798150.1	A/ETH/4/2007	Ethiopia	Cattle
5.	gi|145573150|EF208773.1	A/KEN/29/2005	Kenya: Embu,	Bovine
6.	gi|291294218|GU566067.1	SUD/2/84	Sudan	Cattle
7.	gi|354551401|JN099696.1	A/IRQ/09 -4247	Iraq: Baghdad	
8.	gi|225032249|FJ755037.1	A/IRN/27/2005	Iran	Cattle
9.	gi|225032349|FJ755087.1	A/SAU/16/2005	Saudi Arabia	Cattle
10.	gi|225032419|FJ755122.1	A/TUR/10/2007	Turkey	Cattle
11.	gi|225032335|FJ755080.1	A/JOR/4/2006	Jordan	Cattle
12.	gi|225032195|FJ755010.1	A/BAR/6/2008	Bahrain	Cattle

Table 5. Details of reference FMDV serotypeAT2 used for alignments and sequence analysis of FMDV serotype SAT2 VP1 gene of recent isolates

	Accession No	Description	Location	Species
1.	gi|399221028|JX014256.1	PAT/1/2012, C.G	Palestinian, Rafa"	Cattle
2.	gi|399221026|JX014255.1	EGY/9/2012, C.G	El-Suiz	Cattle
3.	gi|408358898|JX570620.1	EGY/5/2012	Menia Governorate	Cattle
4.	gi|408358920|JX570631.1	LIB/1/2003	Sabratah, ZawiyaDistr	Cattle
5.	gi|408358928|JX570635.1	LIB/41/2012	Abu Attni, Benghazi,	Cattle
6.	gi|38046553|AY343967.1	UGA/9/95	Uganda	Bovine
7.	gi|291294228|GU566072.1	SUD/1/2008	Sudan	Cattle
8.	gi|301088148|HM623697.1	K77/96	Kenia- Nakuru	Cattle
9.	gI|258590128|FJ798161.1	ETH/2/2007	Ethiopia	Cattle
10.	gi|28625607|AF367135.1	SAU/6/2001	Saudi Arabia	Cattle
11.	gi|408358880|JX570611.1	BAR/12/2012	Bahrain	Cattle

RESULTS

Detection and typing of FMDV new isolates by RT-PCR using specific primers

Each sample was tested against five specific primers to serotype O, A, C, Common SAT and ASIA. Samples are loaded on agarose gel without adding a loading-dye buffer and perform electrophoresis. Positive samples were seen at the position specific for each serotype (Table 6 & photo1).

Table 6.Typing of FMDV new isolates by RT-PCR using specific primers

province	No of Sampling	Date of Sampling	Types of specific primers				
			O	A	C	C.SAT	ASIA
El Sharquia	15	2009	+	+	-	-	-
	23	2010	+	+	-	-	-
	33	2011	-	+	-	-	-
	32	2012	-	-	-	+	-
El Menoufia	20	2009	-	+	-	-	-
	26	2010	+	+	-	-	-
	23	2011	-	+	-	-	-
	28	2012	-	-	-	+	-
El Qaliubia	29	2009	+	+	-	-	-
	20	2010	+	+	-	-	-
	28	2011	-	+	-	-	-
	28	2012	-	-	-	+	-
El Fayoum	11	2012	-	-	-	+	-
El Garbia	30	2012	-	-	-	+	-
El Suiz	8	2012	-	-	-	+	-
Alex	18	2012	-	-	-	+	-
El Menia	10	2012	-	-	-	+	-
Kafr El Shaik	8	2012	-	-	-	+	-

C-SAT, Common SAT primer

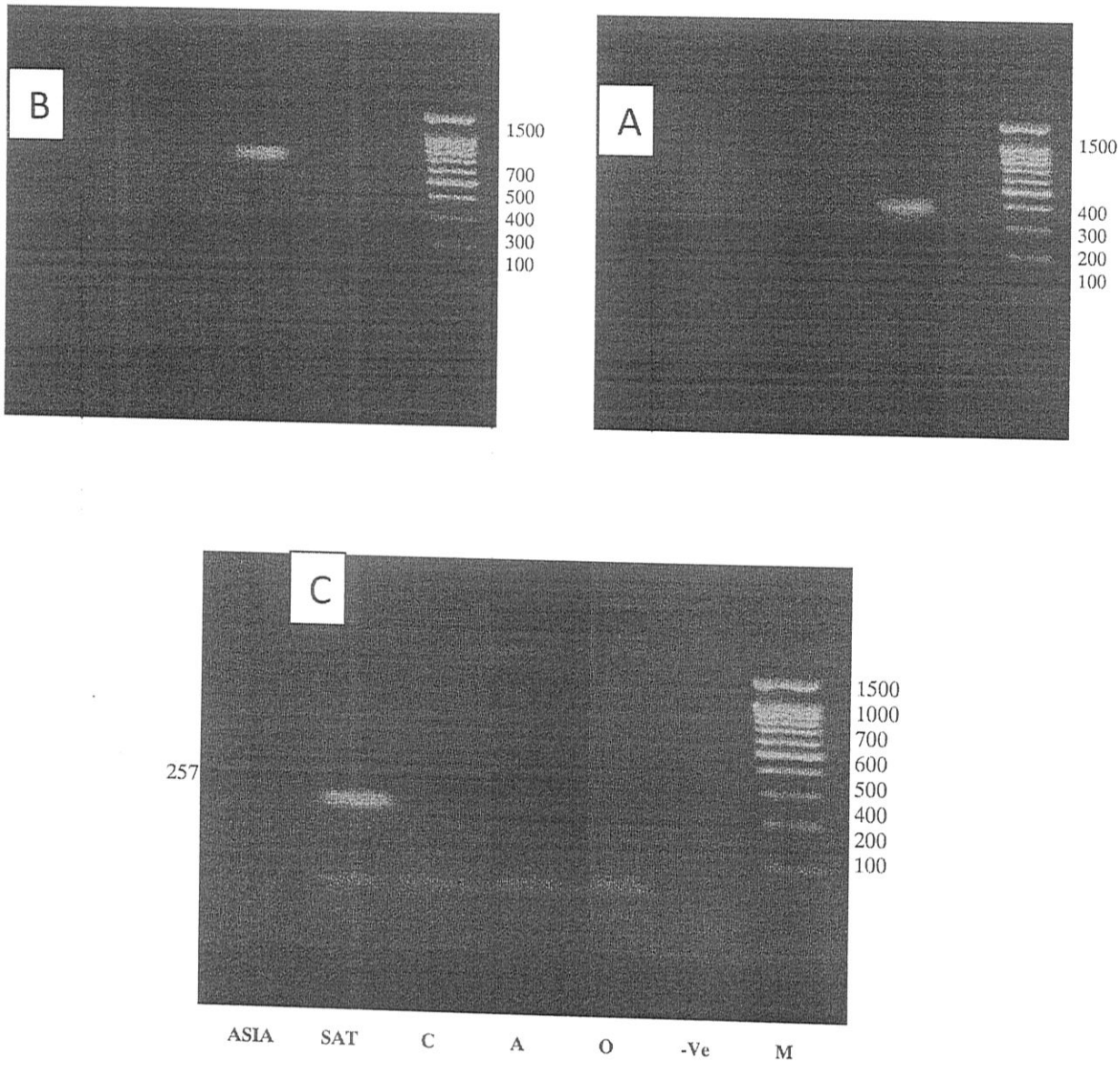

Photo 1. RT-PCR amplification for detection and typing of FMDV new isolates of the present study. (**A**)Serotype O detected at 402bp in lane O, (**B**)serotype A detected at 732 bp in lane A, and (**C**)serotype SAT detected at 257bp in lane SAT. Lane M, 1500bp DNA ladder, Lane -ve, negative control. Lane 1 O primer, Lane 2 A, Lane 3 C, Lane 4 C-SAT, AND Lane 5 ASIA primer.

Alignment and phylogenetic analysis of VP1 gene of FMDV serotype O.

The nucleotide sequence alignment analysis of VP1 gene was performed between the recently isolated Egyptian FMDV serotype O and 11 reference strains by the Clustal W method using MEGA5 program (Table 7& Figure1).

Table 7. Estimates of evolutionary divergence between sequences of FMDV serotype O VP1 gene of recent isolates and the reference FMDV serotype O strains

	Strains description	No of base difference				% of identity			
		1	2	3	4	1	2	3	4
1.	O/Egy/Sharquia/2009		3.0	72.0	72.0		99.24	81.73	81.73
2.	O/Egy/Qaliubia/2009	3.0		75.0	75.0	99.24		80.96	80.96
3.	O/Egy/Sharquia/2010	72.0	75.0		0.0	81.73	80.96		100
4.	O/Egy/Menoufia/2010	72.0	75.0	0.0		81.73	80.96	100	
5.	O/EGY/ALX/2011	35.0	38.0	68.0	68.0	91.12	90.36	82.74	82.74
6.	O/EGY/MNF-2009	66.0	69.0	3.0	3.0	83.25	82.49	99.24	99.24
7.	O1/Sharquia/EGY/72	17.0	20.0	56.0	56.0	95.69	94.92	85.79	85.79
8.	O/EGY/3/93	60.0	63.0	53.0	53.0	84.77	84.01	86.55	86.55
9.	O1manisa iso87 CG	45.0	48.0	54.0	54.0	88.58	87.82	86.29	86.29
10.	O_SUD/30/2004	59.0	62.0	69.0	69.0	85.03	84.26	82.49	82.49
11.	O/UGA/6/76	50.0	53.0	56.0	56.0	87.31	86.55	85.79	85.79
12.	O/SAU/29/93	56.0	59.0	52.0	52.0	85.79	85.03	86.8	86.8
13.	O/UAE/4/99	60.0	63.0	29.0	29.0	84.77	84.01	92.64	92.64
14.	O/JOR/6/2006	65.0	68.0	14.0	14.0	83.5	82.74	96.45	96.45
15.	O_UK2001-FB_CG.	63.0	66.0	32.0	32.0	84.01	83.25	91.88	91.88

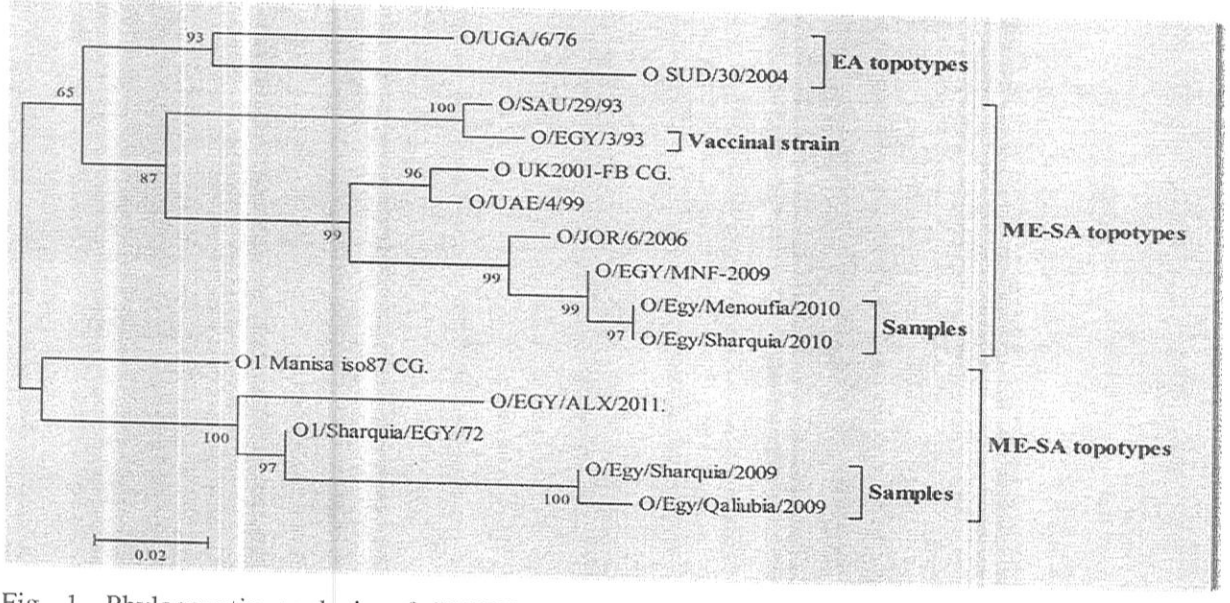

Fig. 1. Phylogenetic analysis of FMDV serotypes O based on VP1 gene nucleotide sequences. Phylogenetic tree was constructed via multiple alignments of 15 different nucleotide sequences. The tree was analyzed by neighbor-joining (N-J) analysis with bootstrapping (1000).

Alignment and phylogenetic analysis of VP1 gene of FMDV serotype A

The nucleotide sequence alignment analysis of VP1 gene were performed between the recently isolated Egyptian FMDV and 12 reference strains by Clustal W method using MEGA5 program (Table 8 & Figure2).

Table 8. Estimates of evolutionary divergence between sequences of FMDV serotype A VP1 gene of recent isolates and the reference FMDV serotype A strains

	Strains description	No of base difference			% of identity		
		1	2	3	1	2	3
1.	A/Egy/Sharquia/2009		151.0	151.0		77.76	77.76
2.	A/Egy/Menoufia/2010	151.0		1.0	77.76		99.85
3.	A/Egy/Qaliubia/2011	151.0	1.0		77.76	99.85	
4.	A/EGY/1/2006	7.0	145.0	145.0	98.97	78.77	78.77
5.	A/Egy/2006/iso_Ism	8.0	149.0	150.0	98.82	78.18	78.04
6.	A/EGY/1/72	108.0	138.0	138.0	84.09	79.8	79.8
7.	A_ETH/4/2007	33.0	140.0	140.0	95.14	79.5	79.5
8.	A/KEN/29/2005	22.0	144.0	144.0	96.76	78.92	78.92
9.	A/SUD/2/84	109.0	150.0	150.0	83.95	78.04	78.04
10.	A/IRQ/09-4247	147.0	16.0	17.0	78.35	97.66	97.51
11.	A/IRN/27/2005	145.0	40.0	40.0	78.65	94.14	94.14
12.	A/SAU/16/2005	147.0	40.0	40.0	78.35	94.14	94.14
13.	A/TUR/10/2007	145.0	43.0	43.0	78.65	93.7	93.7
14.	A/JOR/4/2006	143.0	44.0	44.0	78.94	93.56	93.56
15.	A/BAR/6/2008	140.0	21.0	21.0	79.38	96.93	96.93

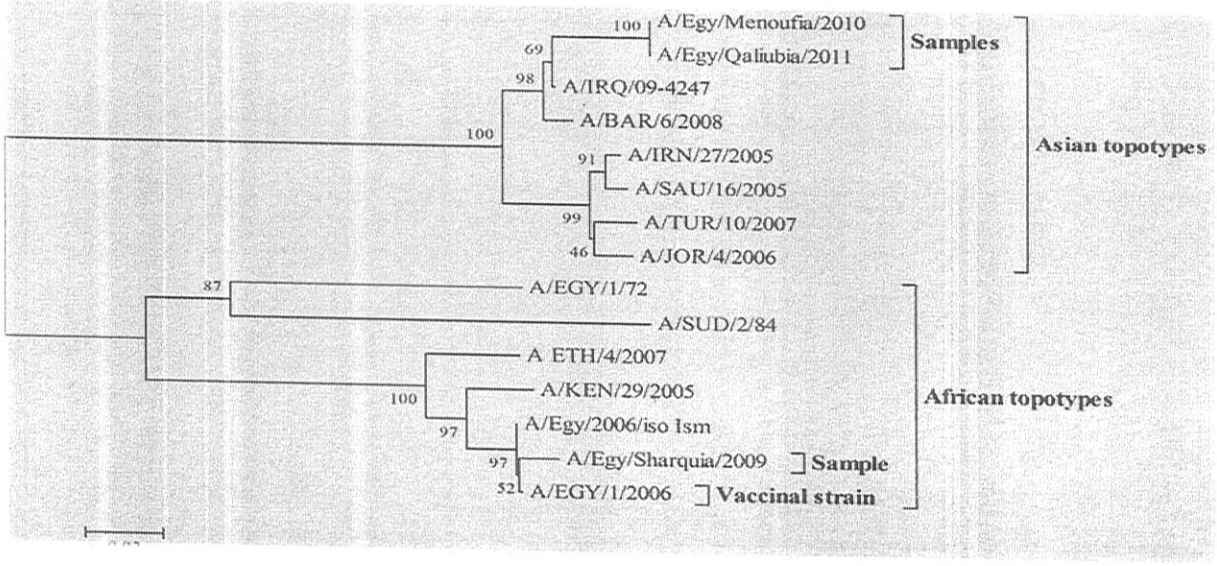

Fig. 2. Phylogenetic analysis of FMDV serotypes A based on VP1 gene nucleotide sequences. Phylogenetic tree was constructed via multiple alignments of 15 different nucleotide sequences. The tree was analyzed by neighbor-joining (N-J) analysis with bootstrapping (1000).

Alignment and phylogenetic analysis of VP1 gene of FMDV serotype SAT2

The nucleotide sequence alignment analysis of VP1 gene were performed between the recently isolated Egyptian FMDV and 11 reference strains by Clustal W method using MEGA5 program (Table 9& Figure3).

Table 9. Estimates of evolutionary divergence between sequences of FMDV serotype SAT2 VP1 gene of recent isolates and the reference FMDV serotype SAT2 strains

Strains description	No of base difference				% of identity			
	1	2	3	4	1	2	3	4
1. SAT2/Egy/Sharquia/2012		2.0	4.0	4.0		99.0	98.1	98.1
2. SAT2/Egy/Garbia/2012	2.0		2.0	2.0	99.05		99.05	99.05
3. SAT2/Egy/Alex/2012	4.0	2.0		4.0	98.1	99.05		98.1
4. SAT2/Egy/Menia/2012	4.0	2.0	4.0		98.1	99.05	98.1	
5. EGY/9/2012._C.G	11.0	9.0	11.0	11.0	94.76	95.71	94.76	94.76
6. EGY/5/2012	10.0	8.0	10.0	10.0	95.24	96.19	95.24	95.24
7. PAT/1/2012._C.G	10.0	8.0	10.0	10.0	95.24	96.19	95.24	95.24
8. LIB/1/2003	32.0	30.0	32.0	32.0	84.76	85.71	84.76	84.76
9. LIB/41/2012	39.0	37.0	38.0	39.0	81.43	82.38	81.9	81.43
10. UGA/9/95	68.0	66.0	68.0	66.0	67.62	68.57	67.62	68.57
11. K77/96	68.0	66.0	68.0	66.0	67.62	68.57	67.62	68.57
12. SUD/1/2008	69.0	67.0	69.0	69.0	67.14	68.1	67.14	67.14
13. ETH/2/2007	69.0	67.0	69.0	69.0	67.14	68.1	67.14	67.14
14. SAU/6/2001	36.0	34.0	36.0	36.0	82.86	83.81	82.86	82.86
15. BAR/12/2012	75.0	73.0	74.0	72.0	64.29	65.24	64.76	65.71

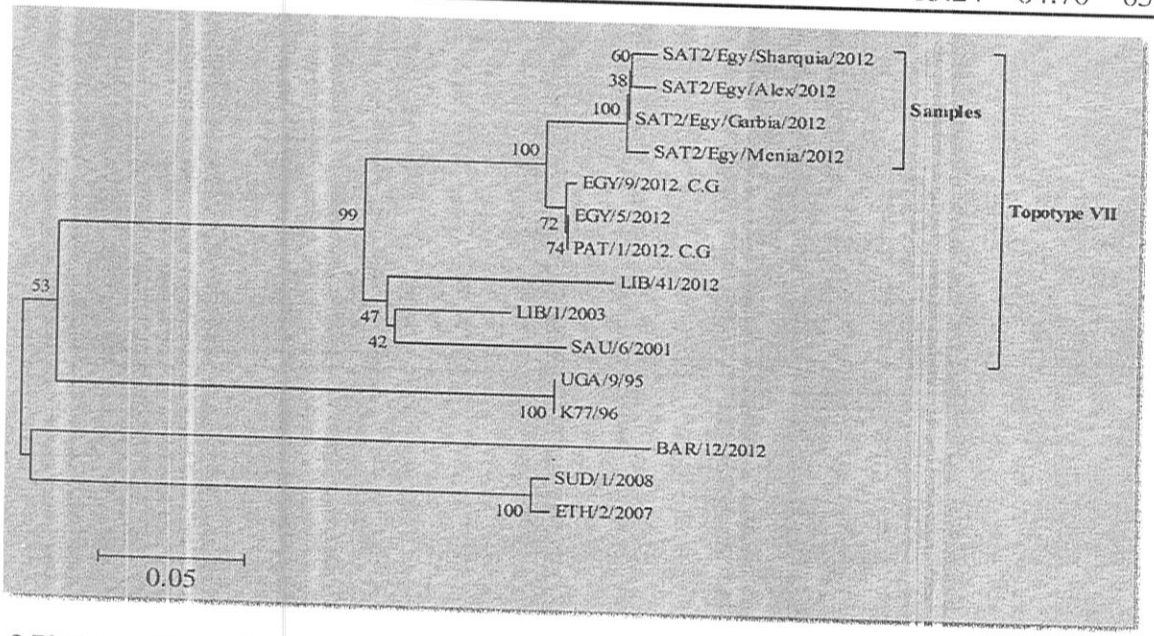

Fig. 3.Phylogenetic analysis of FMDV serotypes SAT2 based on VP1 gene nucleotide sequences. Phylogenetic tree was constructed via multiple alignments of 15 different nucleotide sequences. The tree was analyzed by neighbor-joining (N-J) analysis with bootstrapping (1000).

DISCUSSION

In the present study,252Epithelial tissue samples(ET) and 138Oesophageal pharyngeal fluid (OP) samples were collected from 9 different Egyptian governorates during the period of 2009 to 2012. During 2009, FMDV serotype O was isolated in samples collected from El Sharquia, El Qaliubia and it was not isolated from El Menoufia while, FMDV serotype A was isolated in samples collected from El Sharquia, El Menoufia and El Qaliubia. The isolated serotypes were sequenced and the identified sequences fromEl Sharquia and El Qaliubia were named O/Egy/ Sharquia/2009, A/Egy/Sharquia/2009 and O/Egy/Qaliubia/ 2009 respectively. Comparative alignment and phylogenetic analysis reveal that, the isolated FMDV serotype O were confirmed to be serotype O topotype ME-SA PanAsia and they were highly related to FMDV strain (O1/Sharquia/EGY/72) isolated from Egypt, (O/EGY/ALX/2011) isolated from Egypt in 2011 and the isolated O strains has 84.5% nucleotide identity to the vaccinal strains (O/EGY/3/93) isolated in Egypt 1993 and the isolated FMDV serotype A was confirmed to be serotype A topotype Africa and it was highly related to strain (A/EGY/4/2006) isolated from Egypt in 2006, (A/KEN/29/2005) isolated from Kenya in 2005 and the isolated A strain has 98.97% nucleotide identity to the vaccinal strains (A/EGY/1/2006) isolated in Egypt 2006. These findings were agreed with previous study ***(13)*** which reported that, FMD type O was detected in samples collected in 2009, it belongs to the ME-SA topotype, PanAsia-2 sublineage. FMD type A was detected in samples collected in 2009, it belongs to the Africa topotype, G-VII^{KEN-05} sublineage. During 2010, FMDV serotype O was isolated in samples collected from El Sharquia, El Menoufia and El Qaliubia and FMDV serotype A was isolated in samples collected from El Sharquia, El Menoufia and El Qaliubia. the identified sequences from El Sharquia and El Menoufia was named O/Egy/Sharquia/2010, O/Egy/ Menoufia/2010 and A/Egy/ Menoufia/2010 respectively. Comparative alignment and phylogenetic analysis reveal that, the isolated FMDV serotype O are confirmed to be serotype O topotype ME-SA PanAsia and it was highly related to FMDV strains (O/EGY/15BH-2009) isolated from Egypt in 2009, (O/EGY/ FYM/ 2011) isolated from Egypt in 2011 and (O/JOR/6/2006) isolated from Jordon in 2006 and the isolated O strains has 86.5% nucleotide identity to the vaccinal strains (O/EGY/3/93) isolated in Egypt 1993, and the isolated FMDV serotype A are confirmed to be serotype A topotype Asia and it was highly related to FMDV strains (A/IRQ/09-4247) isolated from Iraq in 2009 and (A/IRN/5/2006) isolated from Iran in 2006 and the isolated A strains has 78.7% nucleotide identity to the vaccinal strains (A/EGY/1/2006) isolated in Egypt 2006. FMD type A was detected in samples collected in 2010 it belongs to Asia topotype, Iran-$^{05BAR-08}$ sublineage***(14)***. During 2011, FMDV serotype A was isolated in 100% of samples collected from 3 governorates and no other serotype were detected.the identified sequences from El Qaliubia was named A/Egy/Qaliubia/2011. Comparative alignment and phylogenetic analysis revile that, the isolated FMDV are confirmed to be serotype A topotype Asia and it was highly related to FMDV strains (A/IRQ/09-4247) isolated from Iraq in 2009 and (A/IRN/5/2006) isolated from Iran in 2006 and the isolated A strains has 78.7% nucleotide identity to the vaccinal strains (A/EGY/1/2006) isolated in Egypt 2006. FMD type A was detected in samples collected in 2010 and 2011 belong to the Asia topotype, Iran-$^{05BAR-08}$ sublineage ***(14)***.. And disagree with it in reporting that, FMD type O viruses were isolated from three samples collected in 2011 and were genotyped as O/ME-the identified sequences from El Sharquia, El Garbia, Alex and El Menia was named SAT2/Egy/ Sharquia/2012, SAT2/Egy/Garbia/2012, SAT2/ Egy /Alex/2012 and SAT2/Egy/Menia/2012 respectively. Comparative alignment and phylogenetic analysis reveal that, the isolated FMDV are confirmed to be serotype SAT2 topotype - 1 - and they were highly related to each other's with 98.8% nucleotide identity and they were highly related to all reference FMDV

strains isolated from Egypt during 2012, (PAT/1/2012) isolated from Palestine in 2012 and (LIB/41/2012) isolated from Libya in 2012.This findings are agree with *(14)*which reported that, between 18/02/2012 and 26/03/2012, 43 outbreaks of FMD type SAT 2 were reported in Egypt. The Egyptian viruses belonged to SAT2 topotype VII with the Libyan virus.

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الملخص العربى

المقارنة الجزينيه بين عترات الحمى القلاعية المعزولة حديثا و العترات المستخدمة في إنتاج اللقاح في مصر

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يعتبر مرض الحمى القلاعية من الامراض المتوطنة فى مصر من عام ١٩٥٠. منذ هذا التاريخ تتابع حدوث الاوبئة فى مصر من هذا المرض وكان اكثر الاوبة حدوثا كانت نتيجة العترات Aو O.فى هذة الدراسة تم تشخيص و تصنيف عترات الفيروس المسببة للمرض باستخدام اختبار انزيم البلمرة المتسلسل العكسى وتم معرفة التتابع النوكليوتيدى للجين VP1 للعترات المعزولة وتم عمل الشجرة الجينية لها واوضحت النتائج أن عترة الفيروس O المعزولة تتبع(O topotype ME-SA) فى جميع المناطق المعزول منها. في حين أن عترة الفيروس A المعزولة خلال عام ٢٠٠٩ترجع إلى النمط المصلي A topotype فى أفريقيا، في حين أن عترة الفيروس A المعزولة خلال عامي ٢٠١٠ و ٢٠١١ تنتمي إلى topotype آسيا بينما عترة الفيروسSAT2 ترجع الى topotype SAT2 السابع.