Epidemiological Insights of Foot and Mouth Disease Virus Infection among Cattle and Buffaloes in Sharkia Governorate, Egypt

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Abstract
Foot-and-mouth disease (FMD) is endemic in Egypt and in most parts of Africa causing huge economic losses. Control of FMD using vaccination requires information on the occurrence of various FMDV serotypes. This study aimed to determine the prevalence of FMDV serotypes in Sharkia Governorate, Egypt. A total number of 643 different samples, within ten different localities, were collected from both cattle and buffaloes (n = 283) of different age, sex, immune status against FMD, and health status. Field samples (n = 360) have been screened for FMDV by RT-PCR using universal primers and were further subtyped using serotype-specific primers. Additionally, serum samples (n = 283) have been analyzed by applying FMDV serotype-specific antibody ELISA. The RT-PCR screening revealed that a total number of 39/283 (13.8%), 61/283 (21.6%) and 17/38 (44.7%) animals were positive for FMDV serotype O, A and SAT2, respectively. While, by ELISA, neutralizing antibodies directed against FMDV serotype O, A, and SAT2, were found in 177/283 (62.5%), 171/283 (60.4%) and 27/38 (71.1%) serum samples, respectively. These results indicated the endemic status of the FMDV serotypes O, A and SAT2 in Sharkia Governorate despite routine FMD vaccination programs. Although many variations of disease prevalence were recorded between animals of different age, sex and immune and health status but it was obvious that FMD was more prominent and prevalent in buffaloes (47.1%) than in cattle (34.1%). Therefore, control efforts should focus on reducing the circulation of FMDV among susceptible livestock with special attention towards water buffaloes. Continuous surveillance, at molecular and immunological levels, of FMDV serotypes is needed for the effectiveness of any adopted control strategy targeting FMD including vaccination.

Keywords: Prevalence, FMDV, Cattle, Buffaloes, Egypt.

Introduction
Foot-and-mouth disease (FMD) is a highly contagious viral disease affecting both domestic and wild cloven-hoofed animals [1]. The FMD virus (FMDV) belongs to the genus Aphthovirus, the family Picornaviridae and the order Picornavirales [2]. The virus is highly mutable because its genome is composed of a linear, positive single-stranded RNA molecule with a quasispecies nature allowing the continuous evolution of new variants [3,4]. There are seven immunological distinct FMDV serotypes with multiple subtypes within each serotype (O, A, C, Asia 1, South African Territories (SAT) 1, SAT 2, and SAT 3). With the exception of serotype C, FMDV serotypes are still circulating worldwide (Africa, Asia, west Eurasia, and South America) [5,6]. There is no antigenic relationship between the different FMDV serotypes, therefore, the cross-protection does not exist totally. Moreover, in many cases, the cross-protection between different subtypes of the same serotype fails to be induced [7]. Consequently, continuous updating of data regarding to the field circulating topotypes is necessary for appropriate vaccine manufacture and disease control [8,9].

In many developing countries including Egypt, FMD is endemic and considered as a major transboundary disease that causes great

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limitations on sales and exports of livestock and livestock products [10, 11]. Serotype O was considered the predominant serotype in Egypt because it induced all outbreaks between 1964 and 2005 excluding an outbreak in 1972 that was caused by serotype A [12,13]. In 2006, Sharkia and many Egyptian Governorates were struck by severe FMD outbreaks caused by serotype A [12,14]. Vaccination programs depending on locally produced bivalent vaccines, against both serotypes A and O, were applied however severe FMD outbreaks existed in February 2012. Sharkia and Gharbia were the first Egyptian Governorates in which these outbreaks were recognized. Large numbers of cattle and water buffaloes showed severe clinical signs of FMD and a high mortality rate (up to 50%) particularly in young animals as a result of FMDV-induced myocarditis. An exotic FMDV serotype (SAT2) was the primary cause of the 2012- FMD epidemic in Egypt [15,16]. During 2012-2014, the three FMDV serotypes, O, A, and SAT2 were detected in many outbreaks among cattle and water buffaloes in Egypt [6].

The control of FMD is depending largely on the disease epidemiological data which in turn affected by many factors including the role of different susceptible hosts in disease transmissibility and persistency. In addition, the incursion of exotic viral strains in FMD endemic areas including Egypt has a great impact on the epidemiological map of the disease [10]. This study was carried out to generate data regarding the prevalence of FMDV serotypes in Sharkia Governorate, Egypt. For this reason, the different FMDV serotypes and their specific antibodies were tested in clinically sick and apparently healthy cattle and buffaloes in different localities across Sharkia Governorate, Egypt.

**Material and methods**

**Area and animals under investigation**

The study was conducted in Sharkia Governorate, Egypt during 2008-2015. Samples were collected randomly from both sick or apparently healthy cattle and buffaloes of different, ages (from 7 days to 6 years), sexes, and immune status (vaccinated and non-vaccinated animals). The selected animals (n = 283) were reared in villages/houses and farms that reported FMD outbreaks within ten cities/centers in Sharkia Governorate. A total number of 196 houses/farms (cattle = 56, buffalos = 99 and integrated rearing system of cattle and buffalos together = 41) were investigated (Figure 1 Upper panel). These localities had active FMD outbreaks 2 weeks to 8 months before sampling.

**Clinical specimens**

Clinical specimens were collected from animals with typical signs and lesions of FMD (Figure 1 Lower panel) and from apparently healthy animals during sampling. At sampling time, the owners of the farms/animals have been questioned in regard to their FMD vaccine practice.

A total number of 360 field samples were collected from cattle and buffaloes. These samples comprised of 154 samples (88 mouth epithelia, 19 vesicular fluids, and 47 oral swabs) from cattle and buffaloes suspected of being infected with FMDV and 206 samples (87 oropharyngeal (OP) swabs, 82 fecal and 37 milk samples) from apparently healthy animals. In addition, 283 blood samples were collected from cattle and buffaloes, of which, 126 were collected from 33 sick and 93 apparently healthy cattle. The remaining 157 blood samples were collected from 88 sick and 69 apparently healthy buffalos. The samples were used for preparation of sera to detect antibodies against FMDV serotypes (O, A and SAT2).

**Reverse transcription and Polymerase chain reaction**

Total RNA was extracted from the collected filed samples using the GeneJET RNA Purification Kit (Thermo scientific, EU) according to the manufacturer’s recommendations. The extracted RNA was examined firstly by RT-PCR using universal primers 1F/1R generating 328 bp product regardless of the serotype [17]. The RT-PCR was performed using Verso™ One Step RT-PCR Kit (Thermo scientific, EU). The thermal profile was started at 50°C for 30 min for reverse transcription; then PCR activation at
95°C for 15 min; followed by 35 cycles at 94°C for 30 sec, 55°C for 30 sec, and 72°C for 90 sec. Finally, the PCR reaction was completed at 72°C for 10 min and the PCR products were then analyzed by gel electrophoresis. For identifying the serotype in each of the FMDV PCR positive samples, another RT-PCR was performed using serotype-specific primers for serotypes O, A and SAT2 as previously described [17,18].

**Virus isolation on BHK-21 cells**

Positive serotype-specific RT-PCR samples for serotypes O, A and SAT2 were prepared for the isolation of FMDV according to the directions of OIE [19]. The prepared samples (150 µL) were added in a triplicate manner to pre-formed monolayers of baby hamster kidney-21 (BHK-21) cells grown in 24-well plates. The plates were incubated at 37°C for 1 h, followed by change of media and continued incubation at 37°C for 4 days with daily observation for the development of cytopathic effect (CPE). The harvest of positive isolates was further tested by the serotype-specific RT-PCR for the presence of FMDV. Aliquots of infected cell lysate of each sample were processed and used for coating ELISA plates [20] to be used for the detection of serotype specific antibodies.

**Serum antibody assay**

The collected serum samples were checked for specific antibodies against O, A, and SAT2 serotypes of FMDV in enzyme-linked immunosorbent assay (ELISA) microtiter plates by the Solid Phase Blocking (SPB) indirect ELISA [20]. Each serum sample was run in duplicates; the tests were carried out on a screening basis at a dilution of 1/16. As controls, antigen, known positive and negative sera were included in each ELISA plate. Optical density (OD) values were determined using ELISA reader (Behring EL311) at a wave length of 492 nm. The formula is as follows, where $OD = \text{optical density}$:

$$\text{Value} = \frac{OD\ \text{sample} - OD\ \text{negative}}{OD\ \text{positive} - OD\ \text{negative}}$$

**Statistical analysis**

Prevalence of FMDV determined as the proportion of the samples in which infection was detected by RT-PCR. The statistical analysis for RT-PCR results was done using Chi-Square test in SPSS 11.0 software (SPSS Inc., Chicago, IL, USA). The WinPepi software, Version 11.65 [21] was used for calculation of prevalence and 95% confidence interval (95% CI). The seropositivity rates were determined by dividing the total number of positive sera by the total number of tested samples and were expressed as a percentage.

**Results**

**Clinical signs**

The clinical signs during the FMD epidemic among buffaloes included fever, anorexia, vesicles and ulcers in lips (Figure 1 Lower panel A), tongue, gum with excessive salivation, and lameness. Same lesions were also observed in cattle in addition to ulcers in nostrils (Figure 1 Lower panel B). Some young animals exhibited diarrhea and sudden deaths without previous clinical signs, especially buffalo calves less than 1 month old. Others were clinically examined and showed a cardiac arrhythmia followed by respiratory distress and grunting just before death. At sampling time, mortality rates of 21% and 18% were recorded among sick cattle and buffalos, respectively.

**Molecular detection of FMDV serotypes by RT-PCR**

The RT-PCR targeting 5' UTR, using universal primers, revealed 117 FMDV infected animals (Table 1) with an overall prevalence of 41.3% (117/283, 95% CI 35.6%-47%). This percentage varied according to species, health status, locality, age, sex and immune status (Table 1). The FMDV detection rates in cattle and buffalos were 34.1% and 47.1%, respectively. FMDV was detected in 76% of sick and 15.4% of apparently healthy animals. There was a significant variation between the tested samples that were collected from diseased and apparently healthy animals. In sick animals, the FMDV was detected in 22/33 cattle and 70/88 buffaloes with the percentages of 66.7%
and 79.5%, respectively. However, the apparently healthy animals that tested positive for FMDV were 21/93 cattle and 4/69 buffaloes with the percentages of 22.6% and 5.8%, respectively.

According to the locality of sampling, the highest positivity rate of FMDV infection (83.3%) came from EL-Hosayneya, followed by Kafr Sakr (57.1%), Minet Elkamh (56.5%), Zagazig (48.1%) and Abu Kabier (45.5%). The lowest detection rate was observed in Mashtul assuq (4.8%). The virus detection rate was significantly higher in animals older than one year than in younger animals (48.5% versus 24.7%, respectively. Regarding to gender, the virus detection rate in females (43.8%) was insignificantly higher than in males (32.2%). The non-vaccinated animals showed a higher detection rate of FMD (46.1%) than that of vaccinated ones (39.2%), however, this difference was non-significant.

Table 1: Epidemiological data for FMDV infection in cattle and buffalos in Sharkia Governorate, Egypt

<table>
<thead>
<tr>
<th>Variable</th>
<th>Sample collected, No. (%)</th>
<th>FMDV-positive samples, No. (%)</th>
<th>p value</th>
<th>95% CI</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Species</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Cattle</td>
<td>126 (44.5%)</td>
<td>43 (34.1%)</td>
<td>0.027</td>
<td>25.9-43.1</td>
</tr>
<tr>
<td>Buffalo</td>
<td>157 (55.5%)</td>
<td>74 (47.1%)</td>
<td></td>
<td>39.1-55.3</td>
</tr>
<tr>
<td><strong>Health status</strong></td>
<td></td>
<td></td>
<td>&lt;0.001</td>
<td></td>
</tr>
<tr>
<td>Healthy</td>
<td>162 (57.2%)</td>
<td>25 (15.4%)</td>
<td></td>
<td>10.2-21.9</td>
</tr>
<tr>
<td>Sick</td>
<td>121 (42.8%)</td>
<td>92 (76.0%)</td>
<td></td>
<td>67.4-83.3</td>
</tr>
<tr>
<td><strong>Sample type</strong></td>
<td></td>
<td></td>
<td>&lt;0.001</td>
<td></td>
</tr>
<tr>
<td>Oral samples (mouth epithelium, vesicular fluid, oral swab)</td>
<td>154 (42.8%)</td>
<td>116 (75.3%)</td>
<td></td>
<td>67.7-81.9</td>
</tr>
<tr>
<td>OP (oropharyngeal)</td>
<td>87 (24.2%)</td>
<td>25 (28.7%)</td>
<td></td>
<td>19.5-39.4</td>
</tr>
<tr>
<td>Feces</td>
<td>82 (22.8%)</td>
<td>0 (0)</td>
<td></td>
<td>0</td>
</tr>
<tr>
<td>Milk</td>
<td>37 (10.3%)</td>
<td>1 (2.7%)</td>
<td></td>
<td>0-14.2</td>
</tr>
<tr>
<td><strong>Locality</strong></td>
<td></td>
<td></td>
<td>&lt;0.001</td>
<td></td>
</tr>
<tr>
<td>Zagazig</td>
<td>81 (28.6%)</td>
<td>39 (48.1%)</td>
<td></td>
<td>36.9-59.5</td>
</tr>
<tr>
<td>Minet Elkamh</td>
<td>46 (16.3%)</td>
<td>26 (56.5%)</td>
<td></td>
<td>41.1-71.1</td>
</tr>
<tr>
<td>Abu-Hamad</td>
<td>35 (12.4%)</td>
<td>11 (31.4%)</td>
<td></td>
<td>16.9-49.3</td>
</tr>
<tr>
<td>Fakus</td>
<td>15 (5.3%)</td>
<td>2 (13.3%)</td>
<td></td>
<td>1.7-40.5</td>
</tr>
<tr>
<td>Belbis</td>
<td>23 (8.1%)</td>
<td>7 (30.4%)</td>
<td></td>
<td>13.2-52.9</td>
</tr>
<tr>
<td>Hihya</td>
<td>20 (7.1%)</td>
<td>8 (40%)</td>
<td></td>
<td>19.1-63.9</td>
</tr>
<tr>
<td>Abu Kabier</td>
<td>22 (7.8%)</td>
<td>10 (45.5%)</td>
<td></td>
<td>24.4-67.8</td>
</tr>
<tr>
<td>Kafr Sakr</td>
<td>14 (4.9%)</td>
<td>8 (57.1%)</td>
<td></td>
<td>28.9-82.3</td>
</tr>
<tr>
<td>El-Hosayneya</td>
<td>6 (2.1%)</td>
<td>5 (83.3%)</td>
<td></td>
<td>35.9-99.6</td>
</tr>
<tr>
<td>Mashtul assuq</td>
<td>21 (7.4%)</td>
<td>1 (4.8%)</td>
<td></td>
<td>0.1-23.8</td>
</tr>
<tr>
<td><strong>Age (year)</strong></td>
<td></td>
<td></td>
<td>&lt;0.001</td>
<td></td>
</tr>
<tr>
<td>≤ 1 year</td>
<td>85 (30.0%)</td>
<td>21 (24.7%)</td>
<td></td>
<td>15.9-35.3</td>
</tr>
<tr>
<td>&gt; 1 year</td>
<td>198 (70.0%)</td>
<td>96 (48.5%)</td>
<td></td>
<td>41.3-55.7</td>
</tr>
<tr>
<td><strong>Sex</strong></td>
<td></td>
<td></td>
<td>0.1089</td>
<td></td>
</tr>
<tr>
<td>Male</td>
<td>59 (20.8%)</td>
<td>19 (32.2%)</td>
<td></td>
<td>20.6-45.6</td>
</tr>
<tr>
<td>Female</td>
<td>224 (79.2%)</td>
<td>98 (43.8%)</td>
<td></td>
<td>37.2-50.5</td>
</tr>
<tr>
<td><strong>Immune status</strong></td>
<td></td>
<td></td>
<td>0.2733</td>
<td></td>
</tr>
<tr>
<td>Vaccinated</td>
<td>194 (68.6%)</td>
<td>76 (39.2%)</td>
<td></td>
<td>32.3-46.4</td>
</tr>
<tr>
<td>Non vaccinated</td>
<td>89 (31.4%)</td>
<td>41 (46.1%)</td>
<td></td>
<td>33.4-56.9</td>
</tr>
</tbody>
</table>
Table 2: Typing of FMDV in sick and apparently healthy cattle and buffalos

<table>
<thead>
<tr>
<th>Species</th>
<th>Status</th>
<th>Total No of samples</th>
<th>5'UTR No of positive (%)</th>
<th>O No of positive (%)</th>
<th>A No of positive (%)</th>
<th>SAT2 No of positive (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cattle</td>
<td>Sick</td>
<td>33</td>
<td>22 (66.7)</td>
<td>5 (15.2)</td>
<td>14 (42.4)</td>
<td>3 (9.1)</td>
</tr>
<tr>
<td></td>
<td>Apparently healthy</td>
<td>93</td>
<td>21 (22.6)</td>
<td>18 (19.4)</td>
<td>2 (2.2)</td>
<td>1 (1.1)</td>
</tr>
<tr>
<td>Buffalo</td>
<td>Sick</td>
<td>88</td>
<td>70 (79.5)</td>
<td>14 (15.9)</td>
<td>44 (50.0)</td>
<td>12 (13.6)</td>
</tr>
<tr>
<td></td>
<td>Apparently healthy</td>
<td>69</td>
<td>4 (5.8)</td>
<td>2 (2.9)</td>
<td>1 (1.4)</td>
<td>1 (1.4)</td>
</tr>
<tr>
<td>Total</td>
<td>283</td>
<td></td>
<td>117 (41.3)</td>
<td>39 (13.8)</td>
<td>61 (21.6)</td>
<td>17 (6.0)</td>
</tr>
</tbody>
</table>

* Total number of samples collected after incursion of SAT2 in Egypt was 38. Number of positive SAT2 in those samples was 17/38 with a percentage of 44.7%.

Typing of FMDV-positive samples using serotype-specific primers revealed FMDV serotypes O, A and SAT2 in 39 (13.8%), 61 (21.6%) and 17 (6%) animals, respectively (Table 2). Moreover, the results indicated that all FMDV-positive samples were of the SAT2 serotype (14/17) during outbreaks of 2012 and 2013 with the percentage of 83.2%. The amplification products were identified at the expected positions of 328 bp for FMDV and 1,301, 863–866 or 880 bp for O, A or SAT2, respectively (data not shown).

Sero-prevalence

Using SPB indirect ELISA method, specific antibodies against FMDV serotypes O, A and SAT2 were detected. Specific FMDV serotype O antibodies were detected in 88 (69.8%) cattle and 89 (56.7%) buffalo serum samples, respectively. Whereas, FMDV serotype A neutralizing antibodies were detected in 77 (61.1%) and 94 (59.9%) sera collected from cattle and buffalos, respectively. The specific antibodies against FMDV serotype SAT2 were detected in 20 (83.3%) cattle and 7 (50%) buffalo serum samples. The sero-positivity of the FMDV serotypes O, A and SAT2 appeared also variable according to other four factors; health status, age, sex, and immune status (Figure 2).

There were great variations in the sero-positivity of the FMDV serotypes O, A and SAT2 in the different localities. For serotype A specific antibodies, the percentages of sero-positivity ranged from 25% in Fakus and Kafr Sakr to 100% in El-Hosayneya. The highest seropositive results (83.3%) against FMDV serotype O were detected in cattle sera collected from Abu Kabier, while the lowest results were 18.8% in Abu-Hamad. In buffalo sera, the highest antibody prevalence (100%) for both FMDV serotype A and O was recorded in Belbis. No antibodies against serotype A were detected in sera collected from Fakus. The SAT2 specific antibodies was detected in, one (33.3%) serum sample from cattle and buffaloes in El-Hosayneya, and in 19 (90.5%) serum samples from cattle and 6 (54.5%) serum samples from buffaloes in Mashtul assuq and Minet Elkamh, respectively (Fig. 3).

Discussion

Since its first detection in 1964 among Egyptian livestock [22], FMD is being the most frequent endemic viral disease affecting the Egyptian animal industry causing drastic economic losses. Both FMDV serotypes O and A were the only serotypes incriminated in the disease endemicity in Egypt until 2011 [12,15,23]. In February 2012, a different serotype, SAT2, was introduced causing an extensive FMD outbreak among Egyptian animals [16,24]. Up to date, several FMD outbreaks are still stroking the livestock in Egypt in spite of routine massive vaccination. This raises the question whether these outbreaks are caused by the same serotypes or by new one/s. Thereby, identification of circulating serotypes is essential and will aid in the proper vaccine choice and consequently reduce disease losses. Thus, at the immunological and molecular levels among clinically infected and apparently healthy Egyptian cattle and buffaloes in Sharkia Governorate were examined for the presence of FMDV infection.

It has been reported that the infection in African buffalo with FMDV is almost subclinical [25]. In this study, with the exception of one lesion (erosions or ulcers on the
nostrils, Figure 2B) which was observed only in many infected cattle, all clinically infected animals including buffaloes showed typical signs of FMD [26]. This assumes that water buffaloes are more susceptible to FMDV infection than African ones. Moreover, it was shown that water buffaloes are more resistant to FMDV infection and showed less signs and lesions than cattle [27]. However, in this study a total number of 70 (79.5%) buffaloes that tested positive for FMD showed moderate to severe typical clinical signs of the disease. In addition, the overall mortality rate among infected buffaloes (18%) was close to that of cattle (21%). This could be attributed to the adaptation of circulating FMDV serotypes to both animal species (cattle and buffalo) producing severe clinical signs [28,29].

Figure 1: Sites and animals investigated for FMDV infection in Sharkia Governorate, Egypt. Map of Egypt showing Sharkia Governorate (grey). The samples were collected from ten cities/centers within Sharkia Governorate, Egypt. Figure shows the number of investigated cattle- and buffalo- houses/farms per center (Upper panel). Clinical manifestation of animal suspected to be affected by FMDV, Sharkia Governorate. A) Blanching of epithelium after vesicle rupture on the upper lip of a buffalo. B) Erosion in the nostril of a cow (Lower panel).
The molecular detection of FMDV among cattle and buffaloes using specific RT-PCR revealed a relatively high rate (41.3%) of active virus infection. The quasispecies nature of FMDV [3] along with inefficient routine vaccination may be implicated in such high infection rate. It was also reported that FMDV may circulate undetectable among vaccinated herds [30]. Further studies showed that experimental infection in non-vaccinated buffalos and cattle with FMDV induced more prominent clinical signs in buffaloes compared to cattle [28]. In our study, contrary to the apparently healthy buffaloes which showed lower percent (5.8%) of FMDV positive animals than apparently healthy cattle (22.6%), a higher proportion (79.5%) of FMDV positive animals were detected among symptomatic buffaloes compared to symptomatic cattle (66.7%) (Table 2). These results confirm that a higher percent of Egyptian water buffaloes rather than cattle escaped from vaccination or improperly vaccinated and became highly adapted to the circulating FMDV strains [29]. Most samples that tested positive for FMDV using RT-PCR were the oral samples (75.3%) and then the oropharyngeal (OP) swabs (28.7%) (Table 1). This indicates that most studied FMD infected animals were in the acute state of the disease whereas other animals were sub-clinically or persistently infected [13]. Only one milk sample (2.7%) tested positive for the presence of FMDV (Table 1). A possible explanation is that all the examined milk samples were collected from apparently healthy animals and there was no evidence for the persistence of FMDV in mammary tissue at 28 dpi [31]. In addition, all fecal samples were collected from apparently healthy animals and tested negative for FMDV, although some OP swabs from the same animals were positive. This assumes that the fecal sample is not ideal for the detection and consequently the surveillance of FMDV especially among sub-clinically or persistently infected cattle or buffaloes. The percent of FMD infected animals above 1 year age (48.5%) was nearly the double of those less than 1 year age (24.7%) (Table 1). This may be attributed to colostral antibodies which
protect animals up to 6 months of age which in turn decrease the rate of FMDV infection among calves of less than 1 year old [13]. However, most deaths were among animals less than 1 year age (data not shown). This could be attributed to that naïve calves develop more prominent clinical FMD signs and lesions than older animals including cardiac affections which are considered the main cause of high mortalities among younger animals [32]. This also highlights the importance of proper vaccination of the dams to protect their young calves.

The three FMDV serotypes, O, A, and SAT2 were identified in the examined samples using RT-PCR and indirect SPB ELISA (for antibody detection). By RT-PCR, our results revealed variable detection rates, ranged from 4.8% to 83.3% among investigated localities (Table 1). In the same accordance, ELISA results showed antibodies against the three FMDV serotypes, O, A and SAT2, ranged from 18.8-100% and 0-100% in sera collected from cattle and buffaloes, respectively. These variations may be attributed to sample size and site, sampling time, age and sex and immune and health status of investigated animals particularly considering the intensive movement of animals and the lack of good hygiene and quarantine precautions especially during outbreaks [29]. By ELISA, the results demonstrated that the overall sero-prevalence of antibodies against FMDV serotype O and A was 69.8% and 56.7% in the examined cattle and buffalo populations, respectively. Specific FMDV serotype A neutralizing antibodies of 61.1% and 59.9% were detected in cattle and buffalo sera, respectively. On the contrary, lower prevalence against the both serotypes was reported by detecting specific antibodies against FMDV serotypes A and O in 17.5% and 4.17% of apparently healthy bovine sera [33]. Those variations may be attributed to the difference in the method of ELISA used. The specific antibodies against FMDV serotype SAT2 were detected in 83.3% cattle and 50% buffalo serum samples. Similarly, Wekesa and his colleagues recorded the presence of SAT2 neutralizing antibodies in 51.96% of African buffaloes [34]. In this study, 68.6% of all questioned owners vaccinated their animals. Of those, 11% were vaccinated their animals.
on regular manner twice per year, whereas the majority of the owners vaccinated only the newly introduced animals. They administered the vaccine only once without any additional booster vaccination. Besides, the overall sero-prevalence against FMDV serotype O, A, and SAT 2, was 62.5% (177/283), 60.4% (171/283) and 71.1% (27/38). Therefore, this does not essentially mean that the animals have acquired the immunity by becoming infected with each serotype. It may be suggested that those animals have been vaccinated with bi-or multi-valent vaccines, either after they have had an infection or the vaccine strain has not matched with the circulating one [35].

Conclusion

In conclusion, the three serotypes of FMDV; O, A, and SAT 2 are constantly circulating among cattle and buffaloes in different localities within Sharkia Governorate, Egypt. For an effective and realizable FMD control program in Sharkia Governorate, Egypt, we suggest ensuring that mass vaccination covers all cattle and buffaloes twice annually at least, with special and district attention to animals in villages (house rearing). Those vaccinations should be administered along with the already individual performed vaccinations to provide a continuous high level of herd immunity.

Conflict of interest

The authors declare no conflicts of interest.

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References


الملخص العربى

روي ويبانية لعبدو فيروس مرض الحمى القلاعية بين الأبقار والجاموس في محافظة الشرقية بمصر

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يعد مرض الحمي القلاعية من الأمراض المتوطنة في جمهورية مصر العربية وكذلك في معظم أجزاء قارة أفريقيا

مسحب خسائر اقتصادية ضخمة للسيطرة على مرض الحمي القلاعية باستخدام اللقاحات، من الضروري الحصول على

معلومات عن وبائيات الأنواع المصلية المختلفة للفيروس المسبب للمرض. وبناء عليه تهدف هذه الدراسة إلى تحديد مدى

انتشار الأنواع المصلية المختلفة لفيروس مرض الحمي القلاعية في محافظة الشرقية - مصر. تم تجميع 643 عينة (من عشرة

أماكن مختلفة) من أبقار وجاموس (283 حيوان) مختلفة في مزارها وجنسها وحالتها المناعية ضد مرض الحمي القلاعية و

ذلك حالتها الصحية. تم عمل مسح لفيروس مرض الحمي القلاعية لـ360 عينة بحثية باستخدام اختبار انتريم البلمرة المتسلسل

ذو انزيم النسخ العكسي وذلك باستخدام بوادئ محددة عالميا. وكذلك تم تصنيف الأنواع المصلية للفيروس باستخدام بوادئ

مخصصة للأنواع المصلية المختلفة. بالإضافة إلى ذلك، تم تحليل عدد 283 عينة مصلية باستخدام اختبار الاليزا المحدد

للإصابة المضادة الخاصة بكل نوع مصلي من فيروس مرض الحمي القلاعية. واستخدام اختبار انتريم البلمرة المتسلسل ذو

انزيم النسخ العكسي، وجد مجموع 283/238 (13.8%) و38/283 (13.7%) و24/283 (8.5%) حيوانات كل نوع مصلي. بينما، تم

تعتبر سلالة الجاموس A و SAT2 وO في 283/38 (71.1%) و 171/283 (60.4%) و 27/38 (71.1%) حيوانات كل نوع مصلي. وقد خلصت نتائج هذه الدراسة إلى

توطن الثلاثة أنواع المصلية لمرض الحمي القلاعية في محافظة الشرقية رغم برامج التحصينات الدورية ضد المرض. 

بالرغم من وجود تباينات عدة في مدى انتشار المرض بين الحيوانات المختلفة في ظلها وجنسيتها وحالتها المناعية والصحية

الا أنه كان من الواضح أن مرض الحمي القلاعية أكثر ضرراً وانتشار بين الحيوانات الجاموس (71.1%) عبر قطعان الجاموس

الإقبال (34.1%). لذلك فإن المهجرات المبكرة للسيطرة على المرض يجب أن توجه للحد من انتشار فيروس مرض الحمي القلاعية

القلاعية بين قطعان الماشية القابلة للإصابة بالإقبال. بالإضافة إلى أن البحوث المبكرة لlesai برتبط بالمباشرات

المستمرة على المستوي الجزيئي والمناعي للأنواع المصلية المختلفة لفيروس مرض الحمي القلاعية والذي يعتبر من المتطلبات

الضرورة لتفعيل أي استراتيجيات توجه للسيطرة على المرض بما في ذلك استخدام اللقاحات.