DOI: 10.29326/2304-196X-2021-2-37-113-120
UDC 619:616.98:578.835.2:616-036.22(6)

Analysis of SAT-1, -2, -3 FMD outbreaks in Africa in 2017–2019

M. V. Sidorovskaya[1], S. N. Fomina[2], S. R. Kremenchugskaya[3]
FGBI "Federal Centre for Animal Health" (FGBI "ARRIAH"), Vladimir, Russia
[1] *ORCID 0000-0001-6218-5846, e-mail: sidorovskaya@arriah.ru*
[2] *ORCID 0000-0002-2122-9096, e-mail: fomina@arriah.ru*
[3] *ORCID 0000-0002-8634-8205, e-mail: kremenchugskaya@arriah.ru*

SUMMARY

Data on FMD spread in Africa in 2017–2019 provided by the World Animal Health Organization (OIE) and World Reference Laboratory for Foot-and-Mouth Disease (WRLFMD) were analyzed with the emphasis on the current epidemic situation in Northern Africa, and the analysis results are demonstrated as well. Brief historical information on SAT-1, -2, -3 FMDV recovery in Africa is presented. Diagnostic test results demonstrate that the abovementioned virus serotypes are circulating in the Southern, East and West African countries. However, there are reports on detection of SAT-1 FMDV in the Near East (1961–1965 and 1970) and SAT-2 FMDV in Saudi Arabia (2000), Lebanon (2003), Bahrain, Egypt and Lebanon (2012). Infection of cattle with SAT-1, -2, -3 FMDV in Southern and East Africa is associated with the contacts between the domestic livestock and wild cloven-hoofed ungulates, specifically with African buffaloes (*Syncerus caffer*). FMDV persists in buffaloes for up to 4–5 years and in buffalo herds living within the limited area of the national reserves – for up to 24 years. Buffaloes are considered to be natural reservoir of the virus. The basic disease control measure in Africa is prevention of any contacts between FMD susceptible livestock and buffaloes in the national reserves and game sanctuaries. Moreover, crucial component of FMD prevention is vaccination of bovines kept in buffer zones around the wild cloven-hoofed ungulates' habitats against the virus serotypes spread by the latter. Foot-and-mouth disease remains one of the most economically significant infections in the world and it involves losses due to the decrease of the agricultural production as well as due to the international trade restrictions.

Keywords: Foot-and-mouth disease, serotypes, topotypes, Africa, natural reservoir.

Acknowledgements: The study was funded by the FGBI "ARRIAH" within the framework of "Veterinary Welfare" research work.

For citation: Sidorovskaya M. V., Fomina S. N., Kremenchugskaya S. R. Analysis of SAT-1, -2, -3 FMD outbreaks in Africa in 2017–2019. *Veterinary Science Today.* 2021; 2 (37): 113–120. DOI: 10.29326/2304-196X-2021-2-37-113-120.

Conflict of interest: The authors declare no conflict of interest.

For correspondence: Miroslava V. Sidorovskaya, Post-Graduate Student, Researcher, Reference Laboratory for FMD Diagnosis, FGBI "ARRIAH", 600901, Russia, Vladimir, Yur'evets, *e-mail: sidorovskaya@arriah.ru.*

УДК 619:616.98:578.835.2:616-036.22(6)

Анализ вспышек ящура серотипов SAT-1, -2, -3 на территории Африканского континента за 2017–2019 гг.

М. В. Сидоровская[1], С. Н. Фомина[2], С. Р. Кременчугская[3]
ФГБУ «Федеральный центр охраны здоровья животных» (ФГБУ «ВНИИЗЖ»), г. Владимир, Россия
[1] *ORCID 0000-0001-6218-5846, e-mail: sidorovskaya@arriah.ru*
[2] *ORCID 0000-0002-2122-9096, e-mail: fomina@arriah.ru*
[3] *ORCID 0000-0002-8634-8205, e-mail: kremenchugskaya@arriah.ru*

РЕЗЮМЕ

Представлены результаты анализа данных Всемирной организации здравоохранения животных (МЭБ) и Всемирной референтной лаборатории по ящуру (WRLFMD) о распространении ящура на территории Африканского континента в 2017–2019 гг. с акцентом на современную эпизоотическую ситуацию в Северной Африке. Дана краткая историческая справка об открытии серотипов SAT-1, -2, -3 вируса ящура в Африке. Как показывают результаты диагностических исследований, указанные серотипы циркулируют в странах Южной, Восточной и Западной Африки. Однако имеются сообщения об обнаружении серотипа SAT-1 на Ближнем Востоке (1961–1965 и 1970 гг.) и SAT-2 в Саудовской Аравии (2000 г.), Ливии (2003 г.), Бахрейне, Египте и Ливии (2012 г.). Заболеваемость крупного рогатого скота ящуром серотипов SAT-1, -2, -3 в Южной и Восточной Африке обусловлена контактом домашнего скота с дикими парнокопытными, в частности с африканским буйволом (*Syncerus caffer*). Вирус ящура персистирует в организме буйволов до 4–5 лет, а в стадах буйволов, обитающих на ограниченных территориях национальных парков, – до 24 лет. Буйволы считаются естественным резервуаром вируса. Основной мерой борьбы с заболеванием на Африканском континенте является пресечение контактов восприимчивого поголовья скота с буйволами в национальных парках и охотничьих заповедниках. Кроме того, важным аспектом профилактики ящура является вакцинация крупного рогатого скота, находящегося в буферных зонах вокруг ареалов обитания диких парнокопытных, против тех серотипов, которые переносятся ими. Ящур остается одной из наиболее экономически значимых инфекций животных в мире, при которой убытки складываются за счет снижения уровня производства сельскохозяйственной продукции и ограничения международной торговли.

Ключевые слова: Ящур, серотипы, топотипы, Африка, естественный резервуар.

Благодарность: Работа выполнена за счет средств ФГБУ «ВНИИЗЖ» в рамках научно-исследовательских работ по теме «Ветеринарное благополучие».

Для цитирования: Сидоровская М. В., Фомина С. Н., Кременчугская С. Р. Анализ вспышек ящура серотипов SAT-1, -2, -3 на территории Африканского континента за 2017–2019 гг. *Ветеринария сегодня*. 2021; 2 (37): 113–120. DOI: 10.29326/2304-196X-2021-2-37-113-120.

Конфликт интересов: Авторы заявляют об отсутствии конфликта интересов.

Для корреспонденции: Сидоровская Мирослава Владимировна, аспирант, сотрудник референтной лаборатории диагностики ящура ФГБУ «ВНИИЗЖ», 600901, Россия, г. Владимир, мкр. Юрьевец, *e-mail: sidorovskaya@arriah.ru.*

INTRODUCTION

Foot-and-mouth disease (*Aphtae epizooticae*) was first reported in the XVI century and until now it remains one of the predominant vesicular diseases of the cloven-hoofed ungulates that causes losses to national economies and requires substantial investment in the prevention and management of disease outbreak consequences. In spite of the Progressive Control Pathway for Foot-and-Mouth Disease developed by the Food and Agriculture Organization (FAO) and European Commission for the Control of Foot-and-Mouth Disease (EuFMD), the disease is still reported in many countries of the world. The above mentioned document is the basis of the FAO/OIE Global Foot-and-Mouth Disease Control Strategy, and it allows FAO/OIE to approve national FMD control program developed by a country, which should include a number of progressive steps, *inter alia* a schedule of the susceptible animal vaccination. Continent of Africa is of particular significance as the majority of the disease outbreaks are being reported there. According to the World Animal Health Organization (OIE), from 2017 to 2019, FMD was reported in 41 African countries. The map in Figure 1 demonstrates global FMD epidemic situation as of late 2019, and it clearly illustrates that African continent leads in the number of affected countries. During the above mentioned period, there were 55 FMD affected countries in the world, of these 33 countries were African ones, 23 countries were Asian countries and only two countries were the European ones (Russian Federation, Turkey).

Sporadic cases of the infection have been reported in Africa for many decades. Figure 2 shows FMD epidemic situation in Africa in 2017–2019. Studies of the virus that caused the disease in the susceptible animal population demonstrated that serotype O virus prevailed over other FMDV serotypes (Fig. 3). The proportion of the registered SAT-1, -2, -3 viruses amounted, however, to 29% of the total number of FMD cases detected in the region. Therefore, this fact should deserve specific attention during the examination of the FMD outbreaks in Africa. Moreover, during the study period, the virus remained untyped in 15% of cases of FMD detections in cattle.

Due to the increased risk of exotic isolate introduction into the Russian Federation associated with the intensification of the trade relations with North African countries as well as due to the threat of the SAT FMD virus introduction from FMD affected African regions to the Near Eastern and West Asian countries and their further spread into the neighboring countries, the works were aimed at the detailed study of SAT FMD epidemic situation in Africa.

History of SAT-1, -2, -3 FMDV detection in Africa

The disease was continuously reported in Southern African countries back to the colonial era but only in the first half of the XX century, while studying FMDV, through the successive cross-protection tests in guinea pigs and cattle the researchers managed to determine its type difference. Development and implementation of such method as compliment fixation test allowed for further studies aimed at the FMD agent typing. As soon as such diagnostic tool as polymerase chain reaction appeared, molecular examination of the virus was made possible [1, 2].

SAT-1, -2 and -3 foot-and-mouth disease viruses were first isolated by the World Reference Laboratory for Foot-and-Mouth Disease (WRLFMD; Pirbright, Great Britain) from the samples collected from the livestock animals in Bechuanaland (Botswana) and Northern Rhodesia (Zambia) in 1948. Retrospective studies of the viruses isolated earlier in 1931 and 1937 in Southern Rhodesia demonstrated close relatedness to the isolates recovered in 1948. One more virus isolate from Southern Rhodesia appeared to be the third new serotype. The discovered serotypes were hereafter named as South Africa Territories 1, 2 and 3 (abbreviated as SAT-1, SAT-2 and SAT-3). The data on the above mentioned serotypes were published by J. B. Brooksby [1].

According to the results obtained by F. Duchatel et al. [3] during sequencing-based phylogenetic studies, SAT-1 and SAT-2 FMDV serotypes have been circulating in African wildlife for over 400 years. The scientists reconstructed the evolution of various FMDV serotypes including SAT-1 and -2 starting from the XVI century and until 2016, and they also evaluated potential influence of ecological and anthropological factors on their spread. Results of the studies were demonstrated as phylogenetic trees [3, 4].

Current FMD epidemic situation in Africa (SAT-1, -2, -3)

Spread of SAT-1 FMDV

SAT-1 virus serotype is widely spread in the countries in Sub-Saharan Africa (SSA). Singular disease outbreaks caused by the serotype were however reported on the

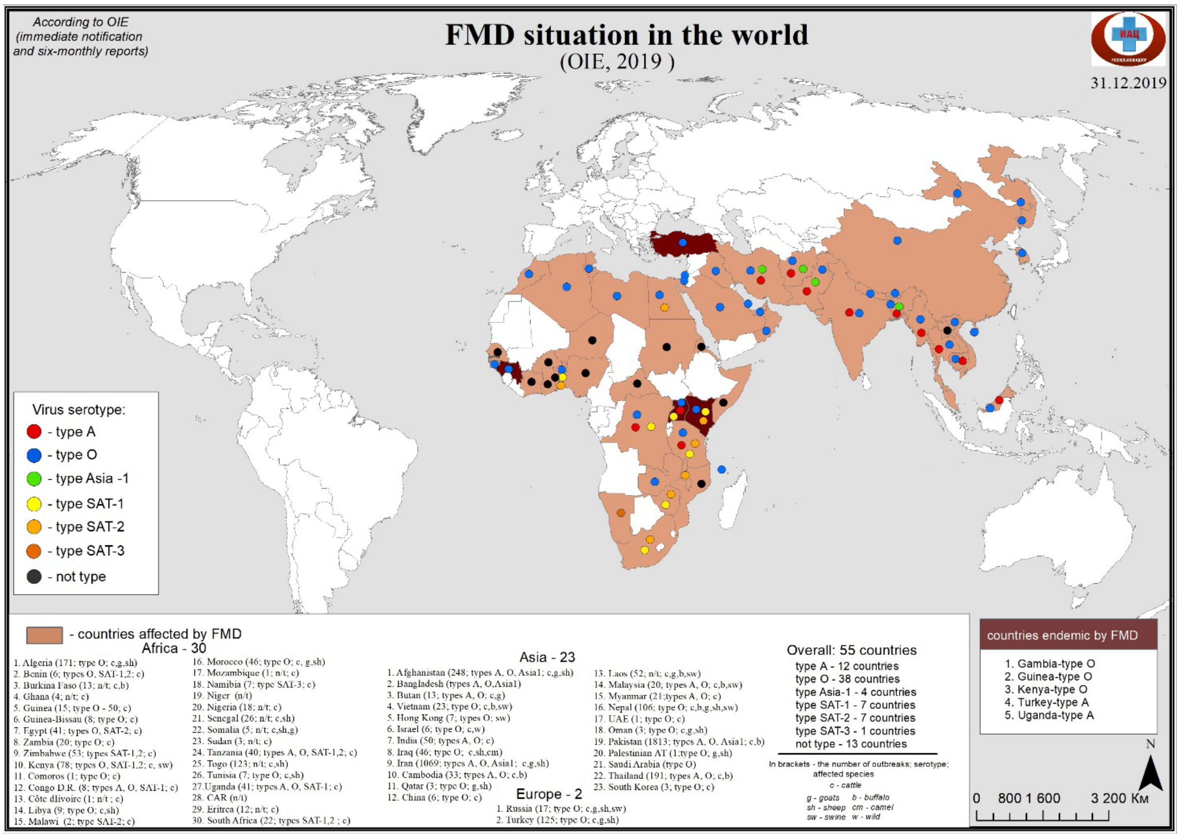

Fig. 1. Global FMD epidemic situation in 2019 (the map is made by the experts of the Information Analysis Center, FGBI "ARRIAH")

Рис. 1. Эпизоотическая ситуация в мире по ящуру в 2019 г. (карта подготовлена сотрудниками информационно-аналитического центра ФГБУ «ВНИИЗЖ»)

Near East in 1962–1965 and 1969–1970, and then in Greece in 1962 [5]. The serotype includes 13 topotypes currently numbered with Roman numerals I–XIII. Topotype I is also known as Northwest Zimbabwe (NWZ), topotype II – Southeast Zimbabwe (SEZ), topotype III – Western Zimbabwe (WZ), topotype IV – East Africa 1 (EA-1), topotype VII – East Africa 2 (EA-2) and topotype VIII – East Africa 3 (EA-3) [6].

SAT-1 FMDV genome was detected in samples collected from cattle in Kenia in 2017. Sequencing of VP1 structural protein demonstrated that this serotype belonged to topotype I that had never occurred in the region before. FMD virus of SAT-1 serotype and topotype I was also reported in Malawi. In August and October, 2017, six SAT-1 FMD outbreaks were reported in cattle in Greater Giyani municipality, Limpopo province (RSA) [7, 8].

In early 2018, sixty-two disease outbreaks were reported in eastern and western provinces of Zimbabwe; by July the outbreaks occurred in north-east part of the country – close to the border with Mozambique. It should be noted the FMD outbreaks are rare in this region. By September 2018, there were over 100 outbreaks caused by SAT-1 FMDV. The new outbreaks were reported in Midlands and Masvingo Provinces [9, 10].

In January 2019, two FMD outbreaks (SAT-1) were again reported in cattle in Masvingo and Matabeleland Provinces, Zimbabwe [11]. During 2019, over twenty SAT-1 FMD outbreaks were reported in Masvingo Province [12]. In the third quarter, same year, SAT-1 FMD virus was isolated in Cameroon, the disease caused by this virus serotype was most recently reported in the North and Adamawa Regions of the country in August – September, 2016. The phylogenetic analysis of the recovered isolates demonstrated that they belonged to topotype X, and they were phylogenetically related to the virus isolated in Nigeria, 2015–2016 [13].

Spread of SAT-2 FMDV

This serotype includes 14 topotypes numbered with Roman numerals I–XIV [6]. Out of the three SAT serotypes SAT-2 foot-and-mouth disease virus also prevails in Sub-Saharan Africa and thus it is sufficiently researched. The outbreaks associated with this FMDV serotype were however reported in north-eastern Africa and Near East: in Yemen in 1990, in Kuwait and Saudi Arabia in 2000. In 2012, SAT-2 FMDV were reported in Egypt, Libya and Palestine. The virus of this serotype was also isolated in Bahrain [5]. Forty-three outbreaks caused by this virus serotype were reported in fourteen Egyptian provinces from February to March, 2012. Studies of VP1 gene nucleotide sequence by the WRLFMD demonstrated that the recovered isolates belonged to topotype VII and two genetic lineages Ghb-12 and Alx-12, which had been previously widely spread. SAT-2 FMDV-associated epidemic in Egypt was its first occurrence in the country from 1950. The phylogenetic analysis of the isolates that caused FMD outbreaks in Palestine (Gaza Strip) in April 2012 indicated that the virus belonged to topotype VII of Ghb-12 genetic lineage and was related to the Egyptian isolates. Again in February 2012, SAT-2 FMDV isolates belonging to topotype VII of Lib-12 genetic lineage were recovered in Libya. In March – April that year SAT-2 FMD virus of topotype IV and genetic lineage Ken-09

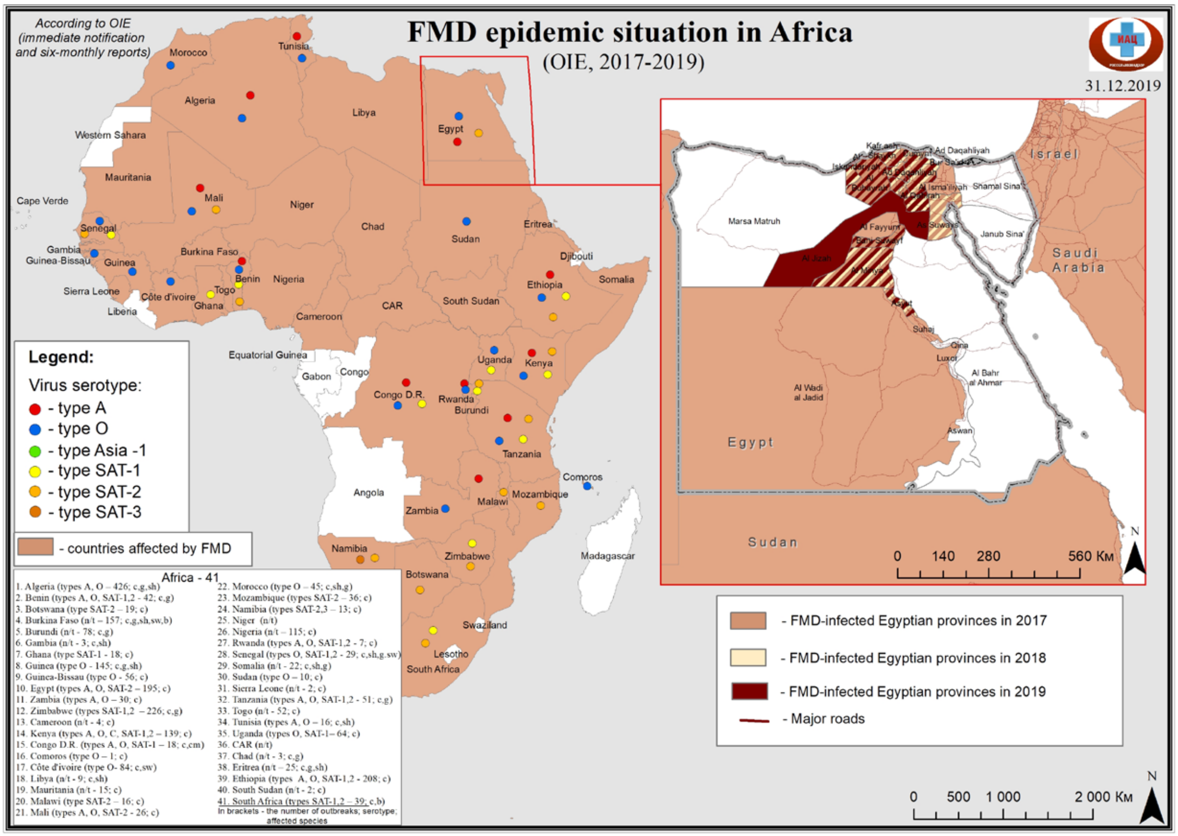

Fig. 2. FMD epidemic situation in Africa in 2017–2019 (the map is made by the experts of the Information Analysis Center, FGBI "ARRIAH")

Рис. 2. Эпизоотическая ситуация в Африке по ящуру в 2017–2019 гг. (карта подготовлена сотрудниками информационно-аналитического центра ФГБУ «ВНИИЗЖ»)

was isolated during the disease outbreak in imported livestock in the northern part of the Kingdom of Bahrain. This was the first emergence of this serotype in the country [14].

In January 2017, SAT-2 FMDV was reported in Matabeleland North and Midlands Provinces, Zimbabwe. The epidemic lasted until March 2017, and five outbreaks were reported in cattle. FMD outbreaks were registered in the same provinces in May. No data of the virus genotyping were reported. Again in March, singular SAT-2 FMD outbreak was reported in cattle in Bushbuckridge municipality, Mpumalanga Province, RSA. It should be noted that the above mentioned outbreaks were detected near Kruger National Park [15, 16].

In February – July 2017, an FMD outbreak was reported in Namanyane settlement, Ngamiland District, Botswana. The OIE Sub-Saharan Africa Regional Reference Laboratory (SSARRL, Botswana) identified SAT-2 virus and determined genetic sequence of capsid VP1 protein of the virus. The analysis of the isolate performed by the WRLFMD demonstrated that it belonged to topotype III and was closely related to the viruses isolated from cattle in Botswana in 2015 [7].

Five outbreaks caused by SAT-2 FMDV were reported in cattle in Namibia from July to September, 2017. The outbreaks were located near Katima Mulilo Urban, Zambezi Region. Topotype VII SAT-2 FMDV was also registered in Uganda [7].

In October – December 2017, topotype III SAT-2 virus was detected in Botswana, Mozambique, Namibia, and topotype II SAT-2 virus was isolated in Zimbabwe [17].

Serotyping and genotyping results in case of FMDV isolated in Ethiopia in March 2018 demonstrated that the virus belonged to serotype SAT-2, topotype VII of the genetic lineage Ghb-12 [9].

In May 2018, singular SAT-2 FMD outbreak was reported in Thulamela settlement, Limpopo Province (RSA). No genotyping was performed [9].

From June to August 2018, topotype III SAT-2 FMDV continued its spread in cattle in Botswana. In total, seventeen outbreaks were detected in North-West District of the country [10].

In August 2018, the French Agency for Food, Environmental and Occupational Health & Safety (ANSES) published the results of the phylogenetic examination of the virus isolated from the bovine sample in Koundjourou sub-prefecture, Republic of Chad in December 2016. The published data demonstrated that the isolate belonged to serotype SAT-2, topotype VII, genetic lineage Lib-12 [10].

From May to August 2018, fourteen SAT-2 FMD outbreaks were reported in cattle in Southern (Neno) and Central (Ntcheu, Dedza and Lilongwe) [9, 10] provinces of Malawi.

In July 2018, diagnostic testing of 39 samples collected from bovines and submitted to the WRLFMD from Sudan demonstrated SAT-2 FMDV in five of them. Genotyping revealed that the virus belonged to topotype VII, genetic lineage Alx-12, while genome of topotype IV SAT-2 FMDV was isolated from the samples submitted from Kenia and collected during the period from January 2017 to June 2018 [10].

In late 2018, three new SAT-2 FMDV outbreaks were reported in cattle in the RSA (Limpopo Province). No genotyping results were published. Sub-clinical infection was detected in buffalo population in Maruleng Local Municipality, Limpopo Province [18].

Throughout 2019, SAT-2 FMDV outbreaks were still reported in Malawi, Zambia, Zimbabwe and Nigeria [11–13, 19].

In 2019, the WRLFMD tested samples collected in the Arab Republic of Egypt from January 2017 to November 2018. FMD agent of SAT-2 subtype was detected in the samples and its subsequent genotyping demonstrated that the virus belonged to topotype VII of genetic lineages Ghb-12 and Lib-12 [11].

In January 2019, five more SAT-2 FMD outbreaks occurred in cattle population in the Limpopo Province, RSA [11].

In February that year, an FMD outbreak of the mentioned serotype was reported in cattle in the Northern Region of Malawi. Phylogenetic tests demonstrated that the virus belonged to topotype I and was related to the virus previously reported in Zambia [19].

In March – April, 2019, eight SAT-2 FMD outbreaks were reported in Mashonaland East Province and fourteen outbreaks were registered in Mashonaland Central Province, Zimbabwe [11, 19].

Twelve samples collected from cattle during the period from January to April 2019 were tested by the WRLFMD, and FMD viruses of SAT-2 serotype, topotype I were identified in four of them [19]. Another SAT-2 FMD outbreak was also reported in cattle in Zambia-bordering region in Malawi in 2019 [13].

Three more FMD outbreaks were reported in the Eastern Province of Zambia in the second quarter of 2019. Testing of the recovered isolates demonstrated circulation of FMDV of serotype SAT-2, topotype I in this locality [13].

In December 2019, the Canadian Food Inspection Agency (CFIA/ACIA) in cooperation with the National Veterinary Research Institute of Nigeria (NVRI) obtained the genome sequence of the foot-and-mouth disease virus isolated from the samples collected from cattle in Plateau and Bauchi States of Nigeria in 2017–2018. SAT-2 FMDV was detected in eight samples. Sequencing of VP1 structural protein demonstrated that the virus belonged to topotype VII of genetic lineage Lib-12 [12].

In September 2019, singular SAT-2 FMD outbreak was again reported in Mashonaland Central Province, Zimbabwe. A series of fifteen SAT-2 FMD outbreaks was reported in cattle in the Limpopo Province (RSA) from November to December that year. One should emphasize that the epidemics occurred in the national buffer zone [12].

Spread of SAT-3 FMDV

Out of three SAT serotypes of the FMDV, SAT-3 has relatively small number of topotypes and the most limited prevalence. To date, five different topotypes were identified and numbered with Roman numerals I–V. The tested viruses were received from seven countries: RSA, Zimbabwe, Zambia, Namibia, Botswana, Malawi and Uganda [6, 20].

SAT-3 is one of the less studied virus serotypes. In 16 years after the last outbreak of this serotype FMDV that occurred in Kruger National Park in Limpopo Province (RSA) in 2006, the SAT-3 FMDV was isolated from clinically healthy Ankole Longhorn calf that had contact with wild buffaloes on the grasslands located in the Queen Elizabeth National Park in Uganda. According to VP1-coding nucleotide sequence, the emerged virus strain was approximately 20% different from the related isolates previously recovered from the buffaloes in Uganda in 1997. African buffaloes are considered to play an important role in the FMDV circulation maintenance in the National parks in Uganda, but no large-scale monitoring in wild animal population is carried out [21–23].

Over the study period (2017–2019), SAT-3 FMD outbreaks were reported in Zambia, Mozambique and Namibia.

Testing of a sample collected from cattle in Lukulu District (Western Province, Zambia) in May 2017 revealed topotype II SAT-3 virus and demonstrated its close phylogenetic relatedness to the isolates recovered in this area in 2015 [17].

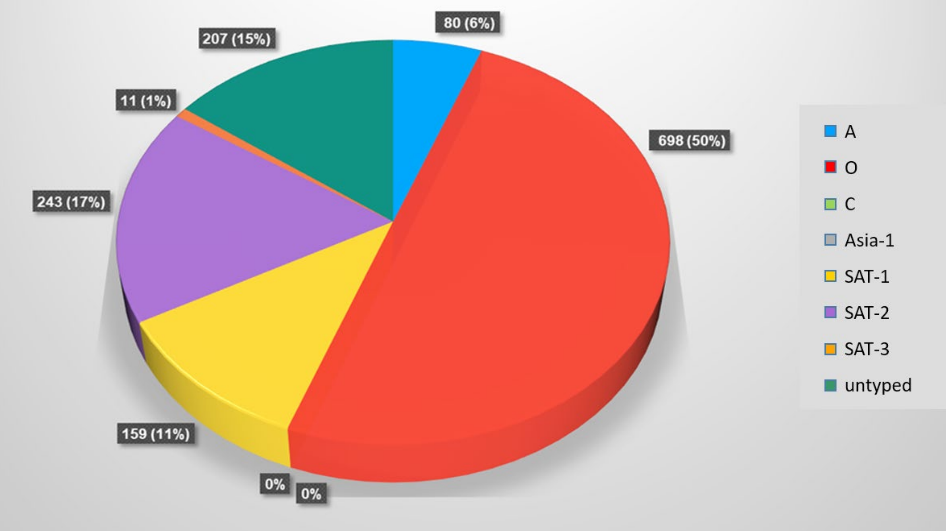

Fig. 3. Proportion of different FMDV serotypes detected in Africa in 2017–2019 (according to the OIE/FAO WRLFMD quarterly reports)

Рис. 3. Соотношение случаев обнаружения ящура разных серотипов на Африканском континенте в 2017–2019 гг. (по данным квартальных отчетов WRLFMD МЭБ/ФАО)

In December 2017, an FMD outbreak was reported in cattle in Chicualacuala District (Gaza Province, Mozambique). As the SSARRL stated (Botswana), the outbreak was caused by SAT-3 FMDV. Genotyping demonstrated that the virus belonged to topotype I and it was phylogenetically different from other viruses within this topotype [8].

In July 2019, two SAT-3 FMDV outbreaks were reported in cattle in Katima Mulilo Urban (Zambezi Region, Namibia). Data on VP1 nucleotide sequencing were received in August 2019. Further genetic tests demonstrated that the virus belonged to topotype II [13]. During the period from October to December that year, five more outbreaks of topotype II SAT-3 FMD were reported in cattle in this region [12].

WRLFMD quarterly reports show that SAT-1, -2, -3 FMD viruses of different topotypes circulate in the African countries.

The following FMDV serotypes prevail in the Eastern Africa (Ethiopia, Kenia, Sudan and Uganda): SAT-1 of topotype I, SAT-2 of topotype IV and SAT-2 of topotype VII, genetic lineages Alx-12 and Ghb-12.

The following FMDV serotypes are relevant for Western African countries (Cameroon, Republic of Chad, Nigeria): SAT-1 of topotype X, SAT-2 of topotype VII; genetic lineage Lib-12.

In the Southern African countries (RSA, Zimbabwe, Botswana, Malawi, Namibia, Mozambique, Zambia) the following FMDV serotypes are being reported: SAT-1 of topotype I; SAT-2 of topotypes I, II, III; SAT-3 of topotypes I and II.

Since 2012, topotype VII SAT-2 FMDV of genetic lineages Lib-12 and Ghb-12 have been reported in Northern Africa, specifically in Egypt and Libya.

All three serotypes of SAT FMDV circulate only in Southern Africa and infect ruminant cloven-hoofed animals. FMD outbreaks in the countries of the Southern, Eastern and Western Africa are associated with the close contacts between the domestic livestock and wild cloven-hoofed animals during grazing, in particular with African buffalo and impala (*Aepyceros melampus*) [3]. The unique trait of FMD epidemiology in Africa involves continuous maintenance of all three SAT-serotypes in African buffalo population. When crowded these animals serve as potential source of sporadic infection for livestock and other FMDV susceptible animal species. The precise mechanism of FMD transmission from buffalo to cattle is understudied, and according to F. Maree et al., it is facilitated by direct contact between these two species [23]. Natural FMD outbreak has been formed on the African continent, and buffaloes serve as a natural reservoir of the disease agent for the domestic and wild animals. This is due to the virus persistence in wild cloven-hoofed animals as in some animals the virus is maintained for up to 4–5 years and for up to 24 years in small isolated herds (30–100 animals) [24].

A. N. Burdov et al. [24] defined four factors of FMD spread in Africa associated with the animal movements:

1. Livestock animals are moved from Niger, Chad, Northern Region of Nigeria and Mali to be sold in municipal centers along the Atlantic coast and from North-Eastern Africa to be sold in the Near East.

2. Livestock movements associated with the use of community pastures, barter relations and normadism.

3. In the Western Africa, humans and livestock animals migrate in large numbers to the south during the annual drought seasons (January – February) and back to the north as soon as monsoon season starts.

4. Natural migration of wild animals in the East-African and South-African plateaus.

In spite of FMD control measures taken by a number of African countries the situation on the continent is still unstable [25].

The majority of the disease outbreaks are reported in Eastern and Western Africa, but the serotypes prevailing in the Southern Africa tend to spread deep into the continent. Data of the WRLFMD reports suggest SAT-2 FMD spread to Northern Africa. Detailed information on FMDV outbreaks in the Northern Africa in 2017–2019 are shown in Figure 4. However noteworthy is the fact that not all outbreaks are typed. This fact significantly aggravate FMD control on the continent.

According to the data published by I. McLachlan et al., many livestock owners in the African countries face annual FMD outbreaks. Grave economic losses are due to the declined production of agricultural products and loss of draft cattle. Basic activities of the private and backyard farms involve keeping and breeding of livestock for livelihood and food security purposes. In the developing countries with low and medium income the loss of profit in agriculture results in decline of health, education and meal expenses. Livestock is also an integral part of social status and cultural identity of the population in the majority of the African countries. Therefore, further measures should be taken in order to intensify FMD control in enzootic regions of Africa [26].

CONCLUSION

Current SAT-1, -2, -3 FMD epidemic situation in the African continent indicates that SAT-2 FMD continues its spread towards Northern Africa and poses real threat of introduction to the Near East and Western Asia. The disease spread is accompanied with the steadily intensified trade relations between Northern African countries, in particular, Egypt, Tunisia, Algeria, and Northern Asia as well as Russian Federation. This fact encourages the interest in thorough study of the specific features of epidemic FMDV isolates in Africa, as they are genetically different from the strains previously detected in our and neighboring countries.

SAT-1, -2, -3 FMDV demonstrate significant infectivity and they can infect different animal species in mixed populations not only in the African countries but generally outside the continent.

The fact that African buffaloes and impalas serve as natural reservoirs of all three SAT serotypes of the foot-and-mouth disease virus should be also considered. The virus can persist in wild cloven-hoofed animals for many years. This explains the existence and maintenance of the persisting FMD natural outbreak in Africa and, therefore, the threat of new outbreak occurrence is still high.

REFERENCES

1. Brooksby J. B. The virus of foot-and-mouth disease. *Adv. Virus Res.* 1958; 5: 1–37. DOI: 10.1016/s0065-3527(08)60670-3.

2. Guerrini L., Pfukenyi D. M., Etter E., Bouyer J., Njagu C., Ndhlovu F., et al. Spatial and seasonal patterns of FMD primary outbreaks in cattle in Zimbabwe between 1931 and 2016. *Vet. Res.* 2019; 50 (1):73. DOI: 10.1186/s13567-019-0690-7.

3. Duchatel F., Bronsvoort B. M. de C., Lycett S. Phylogeographic analysis and identification of factors impacting the

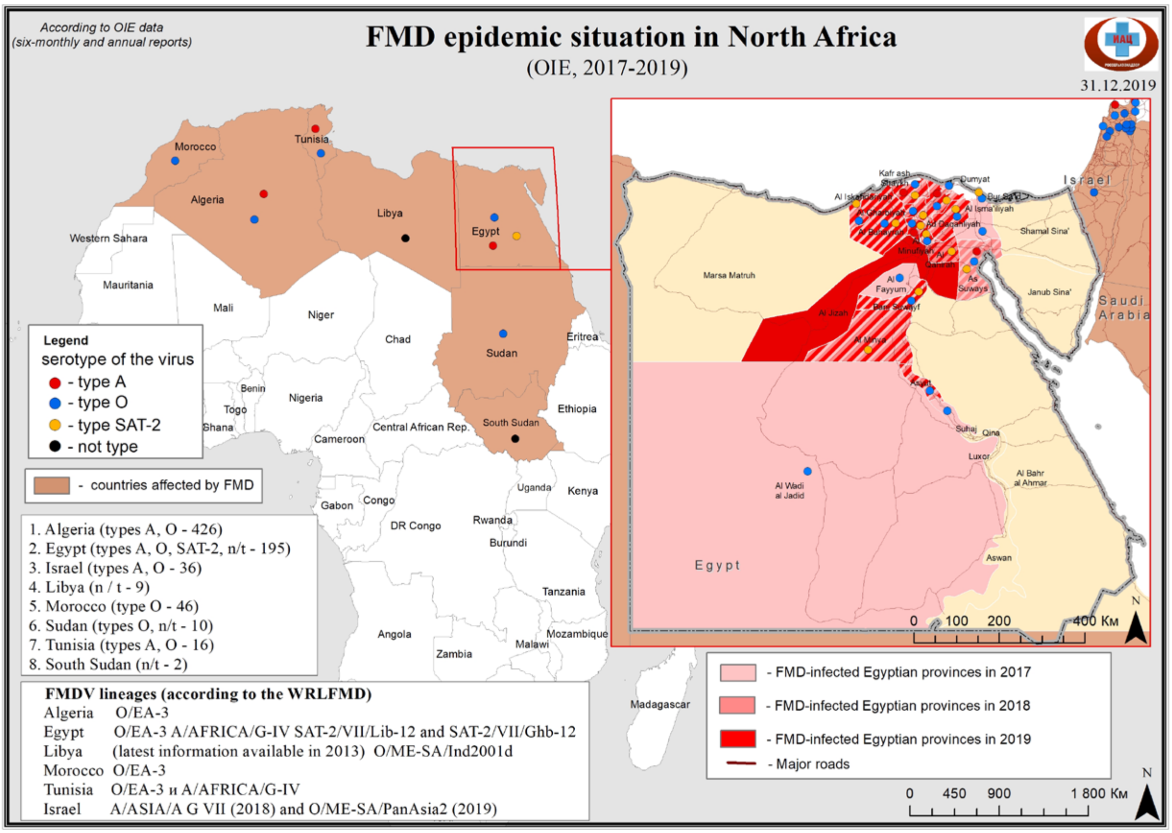

Fig. 4. FMD epidemic situation in North Africa in 2017–2019 (the map is made by the experts of the Information Analysis Center, FGBI "ARRIAH")

Рис. 4. Эпизоотическая ситуация в Северной Африке по ящуру в 2017–2019 гг. (карта подготовлена сотрудниками информационно-аналитического центра ФГБУ «ВНИИЗЖ»)

diffusion of foot-and-mouth disease virus in Africa. *Front. Ecol. Evol*. 2019; 7:371. DOI: 10.3389/fevo.2019.00371.

4. Lycett S., Tanya V. N., Hall M., King D. P., Mazeri S., Mioulet V., et al. The evolution and phylodynamics of serotype A and SAT2 foot-and-mouth disease viruses in endemic regions of Africa. *Sci. Rep*. 2019; 9 (1):5614. DOI: 10.1038/s41598-019-41995-4.

5. Jamal S. M., Belsham G. J. Foot-and-mouth disease: past, present and future. *Vet. Res*. 2013; 44 (1):116. DOI: 10.1186/1297-9716-44-116.

6. OIE/FAO Reference Laboratory Network for Foot-and-Mouth Disease. Foot-and-Mouth Disease Virus Serotypes, Topotypes and Lineages. Available at: https://www.foot-and-mouth.org/FMDV-nomenclature-working-group/nomenclature#topotypes.

7. WRLFMD Quartely Report. Foot-and-Mouth Disease: July to September 2017. Available at: https://www.wrlfmd.org/sites/world/files/quick_media/OIEFAO%20FMD%20Ref%20Lab%20Report%20Jul-Sep%202017.pdf.

8. WRLFMD Quartely Report. Foot-and-Mouth Disease: January to March 2018. Available at: https://www.wrlfmd.org/sites/world/files/quick_media/OIEFAO%20FMD%20Ref%20Lab%20Report%20Jan-Mar%202018.pdf.

9. WRLFMD Quartely Report. Foot-and-Mouth Disease: April to June 2018. Available at: https://www.wrlfmd.org/sites/world/files/quick_media/OIEFAO%20FMD%20Ref%20Lab%20Report%20Apr-Jun%202018.pdf.

10. WRLFMD Quartely Report. Foot-and-Mouth Disease: July to September 2018. Available at: URL:https://www.wrlfmd.org/sites/world/files/quick_media/OIEFAO%20FMD%20Ref%20Lab%20Report%20Jul-Sep%202018.pdf.

11. WRLFMD Quartely Report. Foot-and-Mouth Disease: January to March 2019. Available at: https://www.wrlfmd.org/sites/world/files/quick_media/OIEFAO%20FMD%20Ref%20Lab%20Report%20Jan%20-%20Mar%202019.pdf.

12. WRLFMD Quartely Report. Foot-and-Mouth Disease: October to December 2019. Available at: https://www.wrlfmd.org/sites/world/files/quick_media/OIE-FAO%20FMD%20Ref%20Lab%20Report%20Oct%20-%20Dec%202019%20v2.pdf.

13. WRLFMD Quartely Report. Foot-and-Mouth Disease: July to September 2019. Available at: https://www.wrlfmd.org/sites/world/files/quick_media/OIE-FAO%20FMD%20Ref%20Lab%20Report%20Jul%20-%20Sep%202019.pdf.

14. OIE/FAO FMD Reference Laboratory Network Annual Report 2012. Available at: http://www.fao.org/fileadmin/user_upload/eufmd/docs/Pirbright_reports/OIE-FAO_FMD_Reference_Laboratory_Network_report_2012__.pdf.

15. WRLFMD Quartely Report. Foot-and-Mouth Disease: January to March 2017. Available at: https://www.wrlfmd.org/sites/world/files/quick_media/OIEFAO%20FMD%20Ref%20Lab%20Report%20Jan-Mar%202017.pdf.

16. WRLFMD Quartely Report. Foot-and-Mouth Disease: April to June 2017. Available at: https://www.wrlfmd.org/sites/world/files/quick_media/OIEFAO%20FMD%20Ref%20Lab%20Report%20Apr-Jun%202017.pdf.

17. WRLFMD Quartely Report. Foot-and-Mouth Disease: October to December 2017. Available at: https://www.wrlfmd.org/sites/world/files/quick_media/OIEFAO%20FMD%20Ref%20Lab%20Report%20Oct-Dec%202017.pdf.

18. WRLFMD Quartely Report. Foot-and-Mouth Disease: October to December 2018. Available at: https://www.wrlfmd.org/sites/world/files/quick_media/OIEFAO%20FMD%20Ref%20Lab%20Report%20Oct-%20Dec%202018.pdf.

19. WRLFMD Quartely Report. Foot-and-Mouth Disease: April to June 2019. Available at: https://www.wrlfmd.org/sites/world/files/quick_media/OIEFAO%20FMD%20Ref%20Lab%20Report%20Apr%20-%20Jun%202019.pdf.

20. Vosloo W., Bastos A. D., Sangare O., Hargreaves S. K., Thomson G. R. Review of the status and control of foot and mouth disease in sub-Saharan Africa. *Rev. Sci. Tech*. 2002; 21 (3): 437–449. DOI: 10.20506/rst.21.3.1349.

21. Dhikusooka M. T., Tjørnehøj K., Ayebazibwe C., Namatovu A., Ruhweza S., Siegismund H. R., et al. Foot-and-mouth disease virus serotype SAT 3 in long-horned Ankole calf, Uganda. *Emerg. Infect. Dis*. 2015; 21 (1): 111–114. DOI: 10.3201/eid2101.140995.

22. Bastos A. D., Anderson E. C., Bengis R. G., Keet D. F., Winterbach H. K., Thomson G. R. Molecular epidemiology of SAT3-type foot-and-mouth disease. *Virus Genes*. 2003; 27 (3): 283–290. DOI: 10.1023/a:1026352000959.

23. Maree F. F., Kasanga C. J., Scott K. A., Opperman P. A., Melanie C., Sangula A. K., et al. Challenges and prospects for the control of foot-and-mouth disease: An African perspective. *Veterinary Medicine: Research and Reports*. 2014; 5: 119–138. DOI: 10.2147/VMRR.S62607.

24. Burdov A. N., Dudnikov A. I., Malyarets P. V. Foot-and-mouth disease [Yashchur]. Ed. by A. N. Burdov. M.: Agropromizdat; 1990. 320 p. (in Russian)

25. Timitei A., Parshin P. A., Sukharev O. I., Makarov V. V. Special aspects of FMD epidemiology in West Africa [Osobennosti epizootologii yashchura v Zapadnoj Afrike]. *Veterinarnaya patologiya*. 2009; 4 (31): 107–114. eLIBRARY ID: 16769804. (in Russian)

26. McLachlan I., Marion G., McKendrick I. J., Porphyre T., Handel I. G., Bronsvoort B. M. D. Endemic foot and mouth disease: pastoral in-herd disease dynamics in sub-Saharan Africa. *Sci. Rep*. 2019; 9 (1):17349. DOI: 10.1038/s41598-019-53658-5.

Received on 11.03.2021
Approved for publication on 20.04.2021

INFORMATION ABOUT THE AUTHORS / ИНФОРМАЦИЯ ОБ АВТОРАХ

Miroslava V. Sidorovskaya, Post-Graduate Student, Researcher, Reference Laboratory for FMD Diagnosis, FGBI "ARRIAH", Vladimir, Russia.

Svetlana N. Fomina, Candidate of Science (Veterinary Medicine), Head of Reference Laboratory for FMD Diagnosis, FGBI "ARRIAH", Vladimir, Russia.

Svetlana R. Kremenchugskaya, Doctor of Science (Veterinary Medicine), Leading Researcher, Reference Laboratory for FMD Diagnosis, FGBI "ARRIAH", Vladimir, Russia.

Сидоровская Мирослава Владимировна, аспирант, сотрудник референтной лаборатории диагностики ящура ФГБУ «ВНИИЗЖ», г. Владимир, Россия.

Фомина Светлана Николаевна, кандидат ветеринарных наук, заведующий референтной лабораторией диагностики ящура ФГБУ «ВНИИЗЖ», г. Владимир, Россия.

Кременчугская Светлана Ревдитовна, доктор ветеринарных наук, ведущий научный сотрудник референтной лаборатории диагностики ящура ФГБУ «ВНИИЗЖ», г. Владимир, Россия.