

Spatial and Temporal Distribution of Foot-and-Mouth Disease in Mozambique between 2010 and 2020

José P. Mendonça¹, Lourenço P. Mapaco¹, Sara J. Acha¹, Virgínia Nhabomba¹, Iolanda V. Anahory¹

¹Agrarian Research Institute of Mozambique, Animal Science Directorate, Central Veterinary Laboratory, Maputo, Mozambique; Av. de Moçambique, km1,5. CP nº1922.

Abel Chilundo², Jossefa A. Ndaremba²

²Faculty of Veterinary, Eduardo Mondlane University, Maputo, Mozambique. Av. de Moçambique, km 1,5 CP nº257.

Denise R. Brito³, Fernando C. Mulandane³

³Biotechnology Center, Eduardo Mondlane University, Maputo, Mozambique. Av. de Moçambique, km 1,5 CP nº257.

Venâncio M. Nhavoto⁴

⁴Ministry of the Sea Inland Waters and Fisheries

Carlos Quembo⁵

⁵Agrarian Research Institute of Mozambique, Central Region Office Regional Veterinary Laboratory, Chimoio, Mozambique. EN6. CP nº42

Correspondence Author: José P. Mendonça

Abstract:- Abstract: Foot-and-mouth disease (FMD) is a transboundary animal disease that has negative socio-economic consequences including impacts on trade and food security. A retrospective study on the outbreaks and suspected case of FMD in Mozambique, between the years 2010 and 2020, based on the data collected through passive surveillance, was undertaken. A total of 1,680 positives cases of FMD was reported as a result of outbreaks and suspected occurrence cases in 45 out of 50 districts analyzed in nine provinces of the country. The overall prevalence of FMD was 10.7% (1,680/15,661). A significant difference ($p < 0.01$) between the years was observed in the period analyzed. Spatial distribution showed that, there is a significant difference between districts ($p < 0.01$, $df=1$, $OR=0.120$). Analysis showed that districts in the southern part were of the country more prone to FMD (75.3%; 1,265/1,680) than those in the center (22%; 370/1,680) and north regions (2.6%; 45/1,680). The temporal pattern indicates a higher number of FMD cases in the dry seasons (72.7%; 95% IC: 68.9% – 76.5%) than in the rainy seasons (27.3% 95% IC: 23.2% – 31.4%). A significant difference on FMD seasonality was observed during the period (p -value=0.001, $df=1$, $OR=1.214$). The spatial distribution of the FMD cases suggested that serotype SAT 2 was the only widespread cause of the outbreaks in Mozambique, although SAT 3 serotype was detected in central part of the country.

Keywords:- Mozambique, FMD cases, Outbreak, Spatial, Temporal.

I. INTRODUCTION

Foot-and-mouth disease (FMD) is a severe, highly contagious viral disease of livestock that has significant economic impact. It is trans-boundary animal disease that affects cattle, swine, sheep, goats and other cloven-hoofed ruminants (OIE, 2019b). The disease is caused by infection with FMD virus (FMDV) which belongs to the genus *Aphthovirus* within the family *Picornaviridae* (Kitching et al., 2005). There are seven strains (A, O, C, Asia 1 and Southern African Territories – SAT 1, 2 and 3) endemic in different countries worldwide (Knowles et al., 2005).

The epidemiology of FMDV in Southern Africa differs from the disease in other parts of the world, such as South America, the Middle East, and Asia, as the SAT types uniquely involve wildlife (Blignaut, 2020). African buffalo (*Syncerus caffer*) are the natural maintenance hosts of FMDV and provide a potential source of infection for other wildlife and domestic livestock in endemic areas (Ayeabazibwe, 2010; Jori et al., 2016; Thomson, Vosloo, & Bastos, 2003; Vosloo, Bastos, Sangare, Hargreaves and Thomson, 2002).

In Mozambique FMD is considered endemic, particularly in the southern part of the country (FAO/OIE, 2011) due to the presence of infected buffaloes in Kruger National park and by Transfronteir Conservation Area related interventions. Several SAT (1, 2 and 3) serotypes and O prevail as responsible for the outbreaks recorded in the country between 1951 and 2020 (DNSV, 2011; Thomson, 1995; Vosloo et al., 2002; www.wrlfmd/mozambique). The source of infections for most of these outbreaks was associated with viral strains circulating at the wildlife/livestock interface of the Great Limpopo Transfrontier Conservation Area (Jori et al., 2016). FMD control in Mozambique is based on the annual vaccinations programs of cattle around protected areas and animal movement restrictions. The vaccinations programs

have however not been carried out regularly according to manufacturer's recommendations protocols (Massicame, 2012; Bastos, 2003), and this leads to inefficient vaccinations.

Currently, Mozambique has been identified as being in stage 2 of the Foot-and-Mouth Disease Progressive Control Pathway (PCP-FMD) and the country was expected to move from two to stage 3 in 2013 (FAO/OIE, 2017) with the implementation of the measures in the PCP-FMD programs. However, the recent deterioration of disease control programs, lack of funds to follow prescribed vaccination schedules and poor animal movement controlling resulted in an increased number of outbreaks in the FMD-free zone without vaccination (FAO/OIE, 2020).

Therefore, this study was carried out to describe the spatial and temporal distribution of reported outbreaks of

FMD during the period 2010 to 2020 and generate baseline epidemiological data of FMD in Mozambique.

II. MATERIAL AND METHODS

A. Study area

The study was performed in Mozambique located on the southeast coast of Africa and is bound by e-Swatini to the south, South Africa to the southwest, Zimbabwe to the west, Zambia and Malawi to the northwest, Tanzania to the north and the Indian Ocean to the east. A region with total area of 799,380 km², is located in between 10°27' and 26°52' South latitude and in between 30°12' and 40°51' East longitude. It is comprised of eleven provinces, subdivided into 161 districts (Fig.1) (INE, 2017). From these districts, only 50 were included in the study and had reported FMD outbreaks or suspected cases.

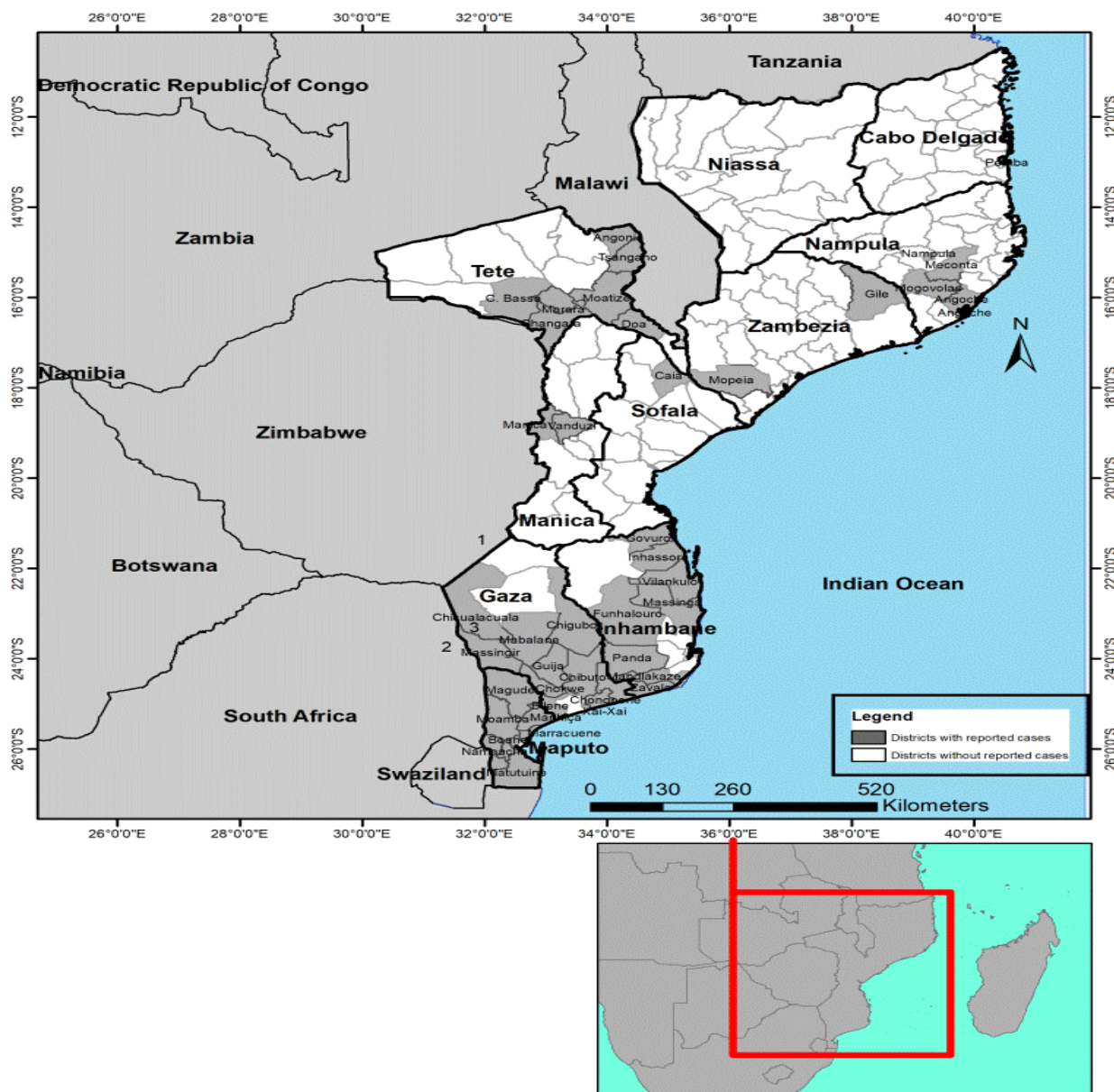


Fig.1: Map showing Mozambique location and reported FMD cases (Dark grey) at the district level (2010-2020)

B. Study design and data collection

This retrospective study was performed at a national level, in nine out of 11 provinces of Mozambique where the disease occurred (based on outbreaks reports and the passive surveillance) as shown in the Figure 1. The official FMD outbreaks database was obtained at the Central Veterinary Laboratory-Maputo (CVL) and Directorate of Livestock and Veterinary Service (DLVS) of the Ministry of Agriculture and Rural Development. The disease was diagnosed through the country's passive surveillance system operated by the network of the veterinary service and the veterinary laboratory technicians located across the country. When a FMD case is suspected, the livestock and extension officers located at the district level notifies the nearest veterinarian technician at the provincial and central levels which then conducts an epidemiological investigation to confirm the presence or absence of the disease. Diagnosis is usually done based on the clinical signs and other epidemiological features.

In Mozambique, the FMD reporting system works in such a way that FMD is considerable as one of the notifiable diseases of public concern and has to be reported within 24 hours to the DLVS. The FMD case data reported includes elements such as geographic positioning systems (GPS) locations, number of cases registered during the outbreaks and number of animals at risk. Maps reflecting the districts where FMD outbreaks had occurred over the last 10-years were prepared using the ArcGIS 10.5.1 software (ESRI, Redlands, USA).

C. Temporal and seasonal variation analysis

Seasonal determine environmental variables (e.g. rainfall, temperature) that can influence FMD epidemiology. The seasons were categorized based on the occurrence of rainfall and crop cultivation and related to the seasonal FMD prevalence during the period under analysis. The main seasons are rainy (November to April) and dry seasons (May to October) (INE, 2017).

D. Serology assays

Serum samples collected across the districts level during the period (2010 to 2020) were tested for antibodies against non-structural protein (NSP). Sera from cattle, goats, sheep as well as pigs and buffalos were screened for the presence of NSP using liquid-phase blocking 3ABC-ELISA (LPBE) (OIE, 2019a). Antibodies against FMDV NSP detected in sera sample was performed using (PrioCHECK® FMDV NSP ELISA) indicating evidence of the previous contact to FMD field virus and infection. Selected positive sera were sent to Botswana Vaccine Institute (BVI) and Onderstepoort Veterinary Institute (OVI) as International Organization of Epizootics (OIE) Reference Laboratories

for FMD (RLFMD) diagnostic confirmation and serotyping.

E. RT-PCR and Sequencing

The epithelial tissues from lesions of mouth and feet, oropharyngeal fluids (probang) obtained in this outbreak or during active surveillance were sent to BVI and OVI for diagnosis confirmation and virus typing. The serotyping report data received from RLFMD for the outbreaks and suspected cases from 2010 till 2020 was also included in this analysis.

F. Data analysis

Descriptive analysis, graphics design and collected data were summarized by using a Microsoft Excel® (2016) data spreadsheet. Statistical analysis was performed by using Statistical Package for the Social Sciences (SPSS™) version 18.0 (IBM® Corp., Armonk, NY, USA). Data were used for the analysis the prevalence and calculate the crude odd ratio with 95% confidence intervals and variables significant at $p < 0.05$.

III. RESULTS

A total of 1,680 (10.7%) out of 15,661 tested serum samples collected at the district level in Mozambique between 2010 and 2020 were seropositive for FMD (average of 168 outbreaks/suspects cases per year). A total of 14,471 cattle, 982 goats, 131 sheep and 26 pigs were recorded to have been affected with the disease, and 51 buffalo samples were tested to monitor virus circulation in protected areas, during this 10-year period.

A. Spatial distribution

Between 2010 and 2020, the disease was reported in 45 out of 50 districts analyzed in nine provinces (Fig.2) The overall prevalence of FMD was 10.7% (95% IC: 10.22% – 11.18%). No occurrences of disease were reported in the surveyed districts of Magoé

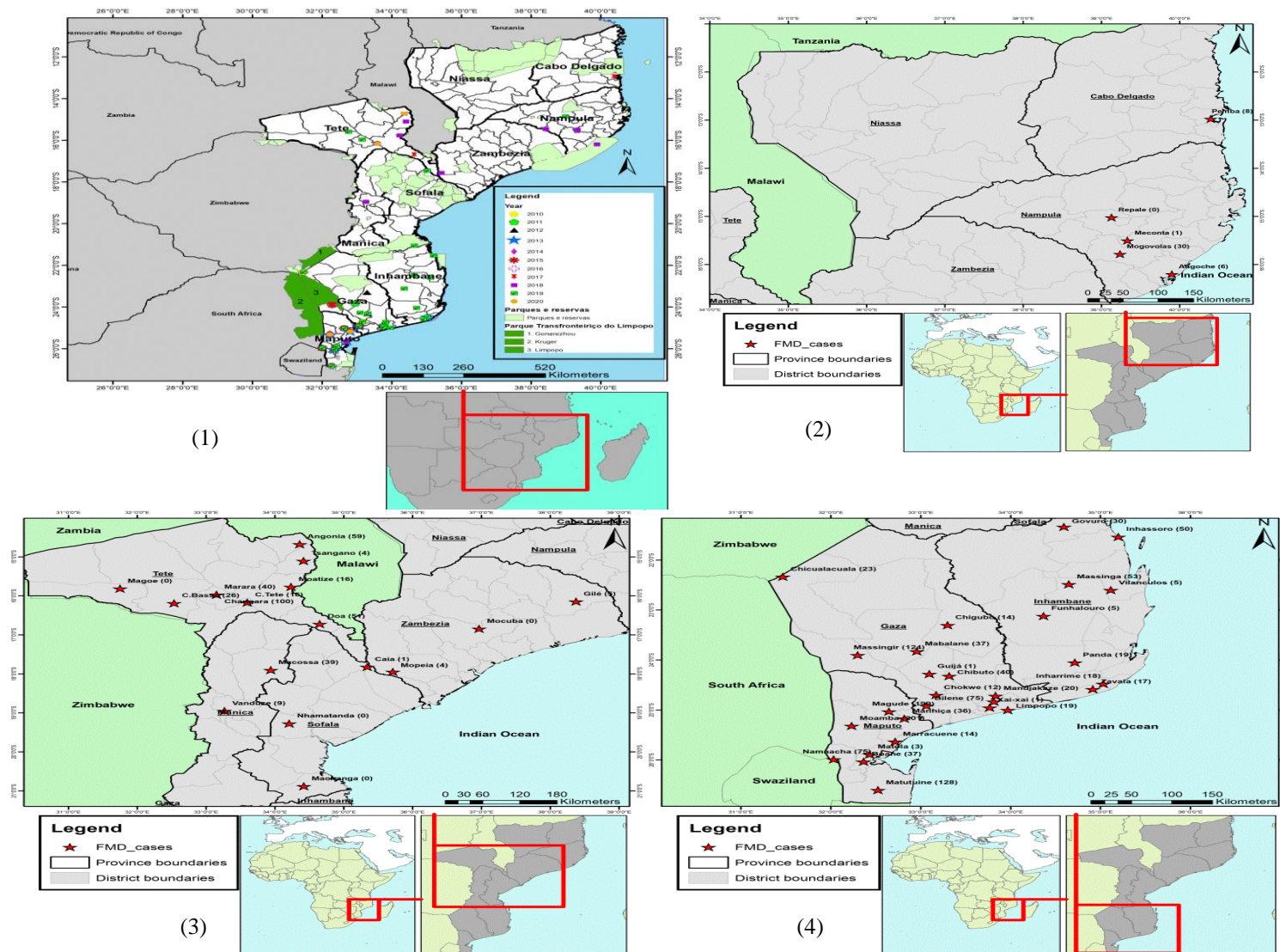


Fig. 2: Map showing the pattern distributions of FMD outbreaks from 2010 to 2020 in Mozambique (1) and the districts affected in the North (2) Central (3) and South (4) of the country.

Machanga, Mocuba Nhamatanda, and Repale. The estimate prevalence of FMD at different districts was highest in Angoche ($n=6$; 75%) and Moatize ($n=16$; 66.7%) and it was lowest in Caia ($n=1$; 2.2%). In this period, FMD outbreak were reported at least once every year in 31% of the districts (50/161) of the country and the map zone showed that the southern part of the region was more affected by FMD outbreak than the central and northern part (Fig. 2). A significant variance was detected between the prevalence of FMD in the districts analyzed during this period ($p<0.01$, $df=1$, $OR=0.120$). And spatial analysis demonstrated that FMD cases were persistently present in Moamba and Magude districts.

B. Temporal distribution of FMD

In the period of January 2010 to December 2020, high number of FMD cases were reported in 2019 ($n=425$ cases), 2018 ($n=384$) and 2016 ($n=279$) while the lowest number of cases were reported in 2011 ($n=6$). During this period, the distribution pattern of FMD cases showed a dramatic trend increase in 2015 and its maximum peak was recorded in 2019 (Fig.3). There were significant difference between the years under analysis ($p\text{-value}=0$). Seasonal variation in the number of FMD cases was found to be highest in the dry season (72.7% 95% IC: 68.9% – 76.5%) and the lowest in the rainy season (27.3% 95% IC: 23.2% – 31.4%). There was a significant difference in the disease between seasons ($p\text{-value}=0.001$, $df=1$, $OR=1.214$).

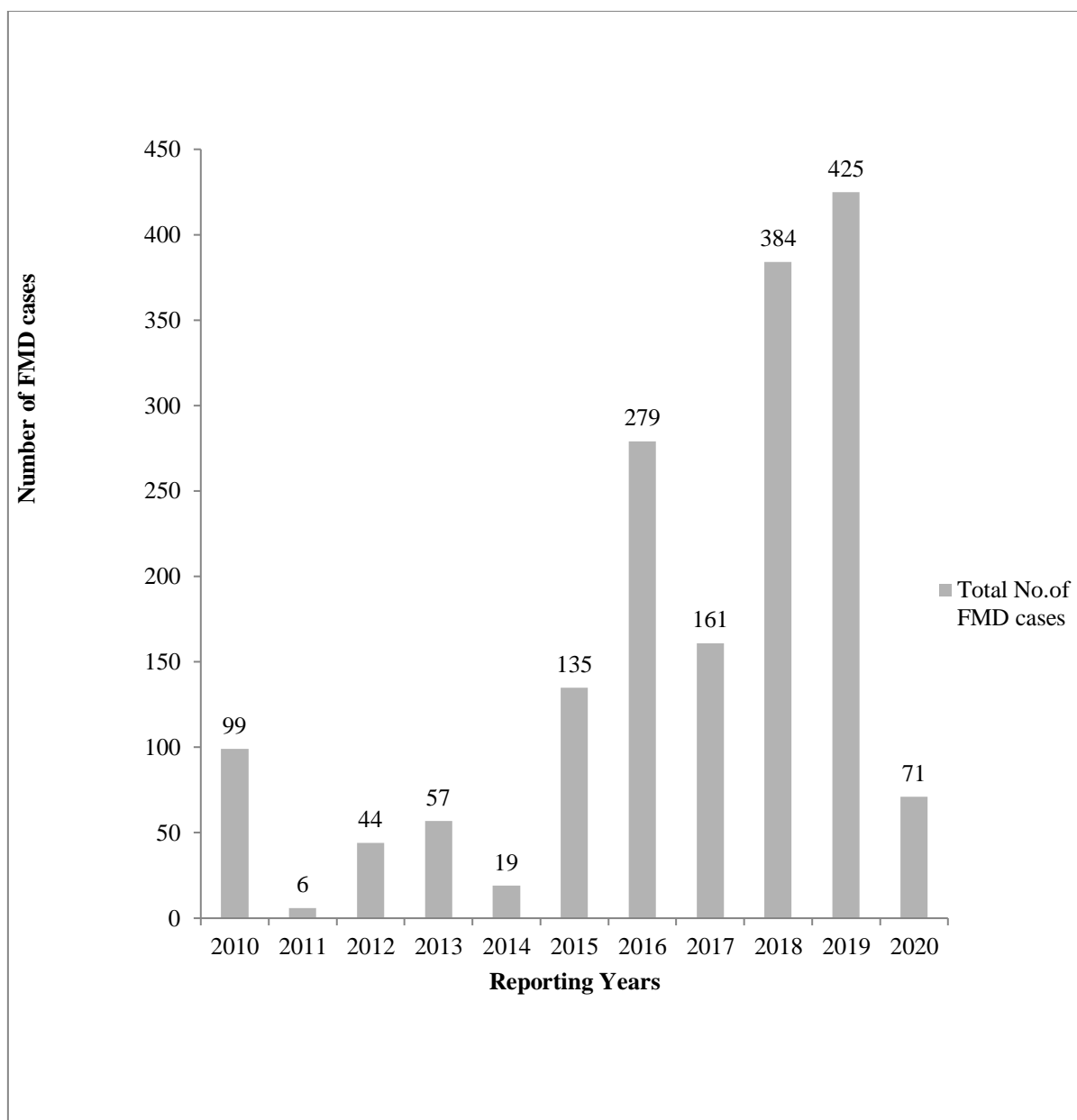


Fig. 3: Annual FMD cases from 2010 to 2020, showing an increase in the number of cases in the last six years period

C. Species affected

Cattle were the most predominant species affected with FMD, being involved in all of the cases reported (94.8%; 95% IC: 93.7% – 95.4%). Goats were the second commonly affected domestic species (1.6%; 95% IC: 1.1% – 2.3%) followed by sheep (0.7%; 95% IC: 0.2 7% – 1.03%) and buffaloes (2.8%; 95% IC: 2.6% – 3.1%) and no cases reported in pigs.

D. Serotype distribution

Overall, from the data available on serotypes, two serotypes (SAT 2 and SAT 3) were found to be circulating in the districts of the southern and center region of Mozambique, more frequently in those districts that share borders with conservation areas in neighboring countries as shown in table 1. Serotype SAT 2 were found to be the most common in Mozambique, implicated in FMD outbreaks from 2010 to 2016, although new incursion of SAT 3 occurred in 2017 in the district of Doa, central part of the country.

Table 1: Summary of foot-and-mouth disease serotypes responsible for outbreaks between 2010 and 2020 in the districts analyzed in Mozambique.

| Year | No. of FMD positive Cases | Serotypes | WRLFMD Validated | Districts |
|------|---------------------------|-----------|------------------|---|
| 2010 | 99 | SAT 2* | Yes | Bilene*, Chockwe*, Chicualcuala*, Massingir and Mabalane |
| 2011 | 6 | SAT 2* | Yes | Mabalane and Limpopo* |
| 2012 | 44 | N/A | N/A | Moamba, Namaacha, Chibuto and Chigubo |
| 2013 | 57 | N/A | N/A | Bilene, Moamba, Manhiça, Inharrime, Boane and Marracuene |
| 2014 | 19 | SAT 2* | Yes | Magude, Moamba* and Marracuene |
| 2015 | 135 | SAT 2* | Yes | Magude*, Boane, Namaacha and Massingir |
| 2016 | 279 | SAT 2* | Yes | Bilene*, Boane, Chicualcuala, Mabalane, Magude, Massingir, Matutuine, Moamba, Namaacha, Macossa* |
| 2017 | 161 | SAT 3** | Yes | Doa**, Boane, Bilene, Massingir, Magude, Manhiça, Matutuine, Moamba, Namaacha, Pemba |
| 2018 | 384 | N/D | N/D | Angoche, Angonia, Bilene, Boane, C.Bassa, Changara, Chibuto, Chongone, C. Tete, Gilé, Inharrime, Limpopo, Magude, Manhiça, Mandjacaze, Marara, Marracuene, Matutuine, Meconta, Moamba, Moatize, Mogovolas, Mopeia, Namaacha, Panda, Tsangano, Vanduzi and Zavala. |
| 2019 | 425 | N/D | N/D | Bilene, Boane, C.Bassa, Caia, Chibuto, Chicualcuala, Chokwe, Chongoene, Funhalouro, Guvuro, Guijá, Inharrime, Inhassoro, Limpopo, Magude, Manhiça, Manjacaze, Marrara, Massinga, Matola, Matutuine, Moamba, Mogovolas, Namaacha, Panda, Vilanculos, Xai-xai and Zavala. |
| 2020 | 71 | N/D | N/D | Angónia, C. Tete, Manhiça and Moamba. |

WRLFMD -World Reference Laboratory for Foot-and-mouth disease

Districts sampled tested with (*) SAT 2 and (**) SAT 3

N/D - Positive FMD, but serotype test Not Done.

N/A - Not available,

IV. DISCUSSION

The results showed that FMD outbreaks occurred in all 45 districts analyzed over the period (2010-2020) and mostly in the southern districts on the border line between Mozambique and the neighboring countries of the Republic of South Africa and Zimbabwe, reflecting the endemic nature of FMD in this border region, this is consistent with the previous study (Jori et al., 2016).

The spatial distribution showed that FMD cases was persistently present in the districts of Moamba and Magude located in southern part of Mozambique at the border zone with Mpumalanga Province of South Africa. These two districts together accounted for 24% (400/1,680) of the total FMD cases in the period of analysis. In addition, these districts share long and porous borders with Kruger National Park (KNP) in South Africa. This specific region is therefore prone to abundant wildlife/livestock interfaces where direct and indirect contacts between wild and domestic ruminants occur for common grazing and water source areas (Jori et al, 2016; Pereira et al., 2006).

The study also showed that, the high occurrences of the FMD in the districts adjacent to the border zone in Mozambique is consistent with the findings in previous study (Fana, 2021, Jori et al, 2016; and Vosloo, 2002) as part of southern African countries, where the disease in livestock has progressively increased over the last decade.

During our 10-year study period, to primary the FMD cases were limited to the southern part of the country (225 reported cases) from 2010 to 2014. Then a sharp increase (1,455 cases) of FMD cases was observed from 2015 to 2020, resulting in the spillover of the disease covering areas FMD-free zone without vaccination on the central and northern part of the country, this strongly suggests to a deterioration of control measures and surveillance, this findings is consistent with the previous reported by FAO/OIE (2012).

Focused most of FMD outbreaks occurred in the dry season (72.7%) than in the rainy season (27.3%), this is consistent with previous findings (Sirdar, 2021; Guerrini et al., 2019) in southern African countries, where the majority (70%) of outbreaks occurred in dry season. In addition, during the dry season the water sources and pastures are scarce and livestock/wildlife interface frequently pose risk infections of FMD (Pereira et al., 2006).

This study also highlighter that, cattle were found to be the main species affected by the FMD in Mozambique. Goats, sheep and pigs were rarely affected and do not appear to play a significant role in the epidemiology of FMD outbreaks in Mozambique, although the presence of small ruminants could be a risk factor for occurrence or propagation of the disease (Lazarus et al., 2017), while they are herded together with cattle in many communal areas of southern African countries (Bester et al., 2009).

Our study typically showed that, during this period (2010 to 2020), SAT 2 was the most prevalent and dominant serotype in Mozambique, this is consistently with previous findings (Jori et al., 2016; Vosloo et al., 2002). SAT 2 serotype were involved in five FMD outbreaks (from 2010 to 2016) and sequence analysis showed a close relationship with the virus isolates in buffalo and impala circulating in South Africa and Zimbabwe (Knowles, 2016; Dwarka, 2010) adjoining the Great Limpopo Transfrontier Conservation Area (GLTFCA).

The detection of serotype SAT 3 in samples collected in Doa district in 2017 (FAO/OIE, 2020), central part of Mozambique border region with Malawi, which was last detected in 1959s (www.wrlfmd/mozambique), provides a great challenge to the routine disease surveillance. This was reported after long drought period, and it was believed to be caused by the introduction of FMDV from neighboring country, this is consistent with the findings by Rweyemamu, (2008).

Our results suggest that; the current endemic situation of FMD in Mozambique (FAO/OIE, 2011), which affects the southern and center regions of the country, might have contributed to an adaptation of some FMDV strains to cattle. In addition, the role of the wildlife livestock interface as well as the animal movement and transactions such as buying and selling could also be potential risk factors for the spread of disease (Wieland, 2015).

The result of this study might possibly be biased by the outbreak reporting rate of the districts. Fana et al., (2021), have already documented serious underreported and outdated information about FMD outbreaks in southern African countries. The impact of underreporting will have more bias, if the underreporting is different across districts and time. Even though our study might have the above mentioned limitations, it generally attempted to generate quite important epidemiological information about the spatial and temporal distribution of FMD in the study area, which could be valuable inputs to support the regional and national decision making regarding FMD control.

V. CONCLUSION

FMD is wide spread and well established all over the regions of Mozambique. It occurred in all zones and more than 75% of cases were reported from districts located in the southern part of the country in the time between 2010 and 2020. Outbreaks are seasonal and more often occurred in the dry season (72.7%). Identification of spatial distribution and temporal patterns can indicate particular areas and time when and where attention should be given to prevent and control the disease in cost-effective ways. The incursion of strains into a FMD-free zone without vaccination should be of concern to the veterinary authority and some critical strategies need to be adapted at regional and national level. Since the current study was based on data collected in the laboratory subsequent study needs to be undertaken on the field to have a good insight in the spatial and temporal distribution of FMD in Mozambique.

CONFLICT OF INTEREST

The authors declare that there are no conflicts of interest.

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