# SCIENTIFIC OPINION

# Rift Valley Fever: risk of persistence, spread and impact in Mayotte (France)

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## Abstract

Rift Valley fever (RVF) is a vector-borne disease transmitted by different mosquito species, especially Aedes and Culex genus, to animals and humans. In November 2018, RVF re-emerged in Mayotte (France) after 11 years. Up to the end of October 2019, 126 outbreaks in animals and 143 human cases were reported. RVF mortality was 0.01%, and the number of abortions reported in polymerase chain reaction (PCR)-positive ruminants was fivefold greater than the previous 7 years. Milk loss production in 2019 compared to 2015–2018 was estimated to be 18%, corresponding to an economic loss of around €191,000 in all of Mayotte. The tropical climate in Mayotte provides conditions for the presence of mosquitoes during the whole year, and illegal introductions of animals represent a continuous risk of (re) introduction of RVF. The probability of RVF virus (RVFV) persisting in Mayotte for 5 or more years was estimated to be < 10% but could be much lower if vertical transmission in vectors does not occur. Persistence of RVF by vertical transmission in Mayotte and Réunion appears to be of minor relevance compared to other pathways of re-introduction (i.e. animal movement). However, there is a high uncertainty since there is limited information about the vertical transmission of some of the major species of vectors of RVFV in Mayotte and Réunion. The only identified pathways for the risk of spread of RVF from Mayotte to other countries were by infected vectors transported in airplanes or by wind currents. For the former, the risk of introduction of RVF to continental France was estimated to $4 \times 10^{-6}$ epidemic per year (median value; 95% CI: $2 \times 10^{-8}$; 0.0007), and 0.001 epidemic per year to Réunion (95% CI: $4 \times 10^{-6}$; 0.16). For the latter pathway, mosquitoes dispersing on the wind from Mayotte between January and April 2019 could have reached the Comoros Islands, Madagascar, Mozambique and, possibly, Tanzania. However, these countries are already endemic for RVF, and an incursion of RVFV-infected mosquitoes would have negligible impact.

**Amendment:** An editorial amendment was carried out that does not materially affect the contents or outcome of this scientific output. In the abstract, a sentence was amended to: 'For the former, the risk of introduction of RVF to continental France was estimated to $4 \times 10^{-6}$ epidemic per year (median value; 95% CI: $2 \times 10^{-8}$; 0.0007), and 0.001 epidemic per year to Réunion (95% CI: $4 \times 10^{-6}$; 0.16).' To avoid confusion, the original version of the statement has been removed from the EFSA Journal, but is available on request, as is a version showing all the changes made.

## Summary

Rift Valley fever (RVF) is a vector-borne disease transmitted by a broad spectrum of mosquito species, especially the Aedes and Culex genera, to animals (domestic and wild ruminants and camels) and humans. RVF is endemic in sub-Saharan Africa and in the Arabian Peninsula, with periodic epidemics characterised by 5–15 years of inter-epizootic periods.

The European Commission requested EFSA to assess the probability of overwintering of RVF virus (RVFV), the risk of RVF spreading from Mayotte (located in the Indian Ocean between Madagascar and Southeast coast of Africa (Mozambique) and close to Comoros) to other areas including other French departments in the Indian Ocean or to continental France as well as the impact of the disease on animal health and farm production in Mayotte.

The assessment of the impact of RVF on animal health and farm production from the time of its initial occurrence to date in Mayotte is based on the data and information obtained from different sources: (i) the official websites of the related ministries, authorities and services, (ii) the available databases, (iii) the farmer association in Mayotte, COOPADEM, iii) the French Veterinary Authorities, (iv) the laboratory of CIRAD[1] in Réunion, (v) experts and (vi) from the scientific publications.

Mayotte is a small French Department with a high density of population and can be considered as a unique epidemiological unit in relation to RVF epidemiology. The climate in Mayotte is tropical with a temperature remaining high (25.4°C average) all year round and small variations in daily and annual temperatures ranging from 15°C in the night to 31°C in the day. Rainfall is present all year round with high peaks from late November to March. This climate provides favourable conditions for the presence of RVF competent vectors almost all year round. The last agricultural census in 2010 reported that 12,000 small ruminants are present in Mayotte while for the bovines, the most recent update of the population in 2017 shows that around 20,000 bovines are present in Mayotte. The size of the herds is small, with 4.8 and 5.8 animals per farm on average for bovines and small ruminants, respectively. The farming system in both bovines and small ruminants is traditional, mainly based on tethered grazing, with low levels of biosecurity. Most of the herds are mixed herds with cattle and small ruminants. There is evidence of illegal introductions of animals seropositive for RVF from the Union of Comoros into Mayotte.

RVF had not been officially reported in EU and neighbouring countries until November 2018, when it (re) emerged in Mayotte, a region that had remained disease free since 2007. This recent epidemic lasted 10 months (November 2018 to August 2019) counting 126 outbreaks in animals and 145 cases in humans. The recorded RVF mortality was 0.01%, and the number of abortions reported in PCR-positive ruminants was fivefold greater than years before. Milk loss in 2019 compared to 2015–2018 or production was estimated to be 18%, corresponding to an economic loss of around 191,000 EUR in all of Mayotte. Since the limited data available do not allow for a solid estimation of the impact of the RFV infections on animal health and production in Mayotte, it is recommended to implement a more structured system for the recording of disease occurrence and possible production losses, including abortions and milk production, in order to understand the impact of RVF infection in Mayotte. A better implementation of the animal identification and registration system and tracing of movements would be of benefit for this objective.

The assessment of the probability of persistence of RVF in the department of Mayotte was mainly based on two previously published studies that addressed this question (Cavalerie et al., 2015; Metras et al., 2017) and their predictions were compared in light of the different assumptions made by the models. Both studies considered Mayotte to comprise a single livestock population with no distinction between cattle, sheep and goats in terms of RVFV transmission nor allowance for spatial location of hosts (i.e. the island was treated as a homogeneously mixed population of hosts and vectors). Both studies suggested that the probability of RVFV persisting in Mayotte is low. Indeed, without vertical transmission in the vector or the import of infected animals, persistence is unlikely. In fact, according to the first study, which considered vertical transmission in vectors, the possibility of persistence of RVF infection in Mayotte was estimated at 9.5% and 2.1% for a persistence of 5 and 9 years, respectively. Whereas, for the second study where vertical transmission in vectors was not considered, once importation of RVFV-infected animals stopped, the probability of RVF persistence was 0.26%. Since, in general, the role of vertical transmission in RVF vectors for the persistence of the disease from one year to another or even between inter-epizootic episodes is still poorly understood, long-term studies about the prevalence of viable RVFV in immature stages of mosquitoes are recommended.

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[1] Centre de Coopération Internationale en Recherche Agronomique pour le Développement.

In relation to the risk of RVF spread from Mayotte to other countries, the only identified possible pathways are infected vectors transported in airplanes or by wind currents. For the former, the target countries considered in relation to the number of flights were continental France and Réunion. The risk of introduction of RVF to continental France was $4 \times 10^{-6}$ epidemic per year (median value; 95% CI: $2 \times 10^{-8}$; 0.0007), and 0.001 epidemic per year to Réunion (95% CI: $4 \times 10^{-6}$; 0.16). For spread by wind currents, the HYSPLIT model was used and showed that mosquitoes dispersing on the wind from Mayotte between January and April 2019 could have reached some neighbouring countries, such as the Comoros Islands, Madagascar, Mozambique and, possibly, Tanzania. However, these countries are already endemic for RVF, and an incursion of RVFV-infected mosquitoes would have negligible impact. Considering the risk of spread of RVF from Mayotte, it is recommended to improve actions preventing introduction of infected vectors from Mayotte to other uninfected areas, such as Metropolitan France and Réunion. Particular attention should be given to air traffic connections from Mayotte to exposed areas (Réunion, Comoros, Madagascar, Kenya/France, Tanzania/France) and strengthen the surveillance in neighbouring countries. Existing disinsectisation procedures should be maintained and possibly improved.

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# 1. Introduction

## 1.1. Background and Terms of Reference as provided by the European Commission

**General introduction-background information**

Rift Valley Fever (RVF) is a disease affecting primarily domestic ruminants (cattle, sheep, goats, camels) and some wild ruminants, that is caused by a single stranded RNA virus of the genus Bunyaviridae.

RVF is a vector borne disease, transmitted primarily through various species of vectors (primarily hematophagous mosquitoes). Certain species of vectors (Aedes mosquitoes) may act as reservoirs of the disease during inter-epidemic periods, thanks to their potential for transovarian (vertical) transmission of the virus to their eggs. As a result, new generations of RVF infected mosquitoes may hatch from infected eggs, especially in periods of favourable conditions (e.g. high rainfalls).

Ruminants are infected primarily by vector bites. Clinical signs range from sudden deaths and abortions to mild, non-specific symptoms, depending on the virulence of the strain and the species, breed and age of the affected animals. Mortality may reach 70–100% in lambs and kids and 20–70% in sheep and calves. Abortion rates may reach 85–100% within the affected herds. RVF in camels can cause abortions and neonatal deaths. Infected wild ruminants usually do not demonstrate any clinical signs.

Humans can become infected by RVF, through the bites of vectors, by contact with infected animals and animal materials (blood, discharges, abortion materials etc.) or by consumption of untreated animal products (fresh meat and/or raw milk). No human-to-human transmission has been recorded to date. About 50% of infected humans have no clinical signs while the rest may demonstrate flu-like symptoms. A small percentage, may develop severe clinical forms, involving haemorrhagic fever with hepatic disease, meningoencephalitis or ocular complications. The total case fatality rate varies between different epidemics (overall less than 1% in those documented).

To date no RVF outbreaks in humans or animals have been reported in Europe or countries sharing land borders with the continental areas of the EU. The closest RVF evidence available is limited to serological findings from retrospective studies carried out in Turkey, using blood samples collected from camels, gazelles and buffaloes from 2000 to 2006.

Currently the disease is endemic in large areas of Southern and Eastern Africa, where outbreaks of RVF occur periodically (e.g. every few years), in seasons when weather conditions favour competent vectors. In recent decades large RVF epidemics have occurred in Egypt (1977–1978, 1993, 2003), Mauritania (2010, 2012, 2015), Madagascar (2007–2009), Comoros (2007) and elsewhere in the African continent (Kenya, Somalia, South Africa, Sudan, Senegal etc.). Egypt currently marks the northernmost limit of RVF spread. The disease moved outside the African continent for the first time in 2000, into the Arab peninsula (Saudi Arabia and Yemen).

On 5 April 2017, EFSA, following a request from the Commission, adopted a scientific opinion on 36 vector-borne diseases, including RVF. The opinion, based on a semi quantitative risk assessment, concluded that the risk of introduction of RVF in the EU was estimated to be very low.

In Mayotte, a French department located in the Indian Ocean, close to the Union of the Comoros (Grande Comore, Moheli and Anjouan) islands and Madagascar, human cases of RVF were detected for the first time in 2007. Retrospective serological studies demonstrated the presence of RVF in livestock since 2004 (serological evidence). Until recently the disease appeared to be in remission with no new human cases detected since 2011. However, in 2018, RVF re-emerged in Mayotte and between 22nd November 2018 and 14th March 2019, more than 101 human cases and more than 60 outbreaks in ruminants have been reported.

In response to the RVF resurgence, the competent authorities of Mayotte are implementing surveillance and biosecurity measures, coupled with vector control/protection measures, aiming to limit the overall disease spread and prevent animal-to-human transmission. In addition, movements of ruminants and raw meat and milk thereof, originating from Mayotte, have been prohibited.

The Commission is empowered to adopt delegated acts supplementing the rules laid down in Part III of Regulation (EU) 2016/429 on transmissible animal diseases (Animal Health Law) on disease control measures for listed diseases as referred to in point (a), (b) and (c) of its Article 9 (category A, B and C diseases). Therefore, a draft Commission Delegated Regulation laying down rules for the prevention and control of certain diseases has been developed and the draft is in consultation.

The rules laid down in the abovementioned draft Commission Delegated Regulation are largely replacing the rules currently in force concerning the disease control measures in the event of animal diseases with serious effects on the livestock as they have proven to be effective in preventing the spread of those diseases within the Union. Consequently, animal disease control measures laid down in existing Directive will be, if not already done so by the Animal Health Law, replaced by the rules provided in that Delegated Regulation. This is also the case of Directive 92/119/EEC which currently provides for measures to apply in the event of occurrence of certain diseases. This includes Rift Valley Fever, which is in accordance with Commission Implementing Regulation (EU) 2019/1882, categorised as Category A disease.

In this regard, the existing rules of Directive 92/119/EEC will cease to apply for Rift Valley Fever as from the date of application of the Animal Health Law and its complementing legislation, i.e. from 21 April 2021. The proposed measures for the prevention and control of RVF should be assessed in order to ensure that they are updated based on the latest scientific knowledge in this new set of legislation.

**Terms of Reference**

1 RISK OF ENTRY OF RVF INTO THE CONTINENTAL PARTS OF THE EU

    1.1 Provide an update of the global epidemiological situation in relation to RVF with emphasis on areas posing a higher risk for the EU.

    1.2 Provide an updated assessment of the overall risk of introduction of RVF (combined rate of entry, vector transmission and establishment), separately for each one of the EU regions potentially at risk, as specified in the 2017 EFSA scientific opinion on Vector-borne diseases (VBD).

    1.3 Provide a separate risk assessment of the risk of introduction of RVF for specific Member States that may be at particular risk.

**2 IMPACT OF RVF IN THE DEPARTMENT OF MAYOTTE AND RELEVANT CONTROL MEASURES**

    **2.1 Assess the probability of overwintering of RVF in the department of Mayotte as well as the risk of RVF spreading from Mayotte to other areas including other French departments in the Indian Ocean or Metropolitan France.**

    **2.2 Assess the impact of the disease (as defined in the 'VBD opinion'), with emphasis on animal health and farm production in Mayotte from the time of its initial occurrence to date.**

    2.3 Assess the possible short- and long-term effectiveness, of different control measures, in eliminating or reducing the disease impact in Mayotte (as per TOR 2.2 above), namely:

        2.3.1 Stamping out of RVF outbreaks;

        2.3.2 Establishment of a protection and a surveillance zone around RVF outbreaks;

        2.3.3 Biosecurity measures, as the ones currently in place in Mayotte, coupled with personal sanitary protection measures related to human–animal contact, including measures to prevent consumption of potentially infected meat and milk;

        2.3.4 Vector control and protection measures;

        2.3.5 Vaccination of livestock;

    2.4 Assess the possible effectiveness of different surveillance strategies in animals that may be used for RVF detection and possible prediction of RVF recurrence in Mayotte in the future, in view of the diagnostic methods currently available.

3 SURVEILLANCE AND CONTROL MEASURES FOR RVF [IN CASE OF OCCURRENCE OR HIGH RISK OF RVF INCURSION IN EUROPE]

    3.1 In case of high risk of RVF introduction in Europe, assess and describe the surveillance measures necessary to ensure early detection of the disease.

    3.2 In case of RVF occurrence in Europe, assess the effectiveness of the main available disease prevention and control measures for RVF, including the relevant measures provided for in the draft Commission Delegated Regulation on rules for the prevention and control of certain listed diseases under Part III of Regulation (EU) 2016/429 on transmissible animal diseases (Animal Heath Law9), namely their potential to:

        — limit the geographical spread of the disease

        — reduce the number of outbreaks

— reduce the overall impact of the disease being present in an area for prolonged periods (e.g. in case overwintering is possible)

In particular, assess the feasibility, availability and effectiveness of:

    3.2.1  the general measures set out in the enacting terms of Part I and II of draft Commission Delegated Regulation

    3.2.2  the disease-specific measures set out in Annexes I to X to draft Commission Delegated Regulation

    3.2.3  vaccination of listed species, including assessment of possible:

— risk mitigating measures necessary to be put in place for animals and products of animal origin thereof, following vaccination

— surveillance performed after vaccination.

## 1.2. Interpretation of the Terms of Reference (if appropriate)

It was agreed with the European Commission to address the ToRs in three scientific opinions to be delivered according to the following deadlines:

- January 2020 for the ToRs 1.1, 1.2 and 1.3
- March 2020 for ToRs 2.1 and 2.2
- September 2020 for ToRs 2.3, 2.4 and 3.

The present opinion deals with ToRs 2.1 and 2.2, i.e. the RVF situation in Mayotte, in particular the probability of overwintering of RVF, the risk of RVF spreading from Mayotte to other areas such as other French departments in the Indian Ocean or Metropolitan France, and the assessment of the impact of the disease, with emphasis on animal health and farm production from the time of its initial occurrence to date.

**Probability of overwintering of RVF in the department of Mayotte**

In Mayotte, the tropical climate allows the presence and activity of insect vectors throughout the year, with some difference in mosquito abundance linked to the rainfall in the two main seasons, rainy season or dry season. Given the climate in Mayotte, therefore, the term 'overwintering' must be not interpreted as in temperate areas, where the winter temperature hampers the vector life cycle, but should be interpreted as the possible persistence of RVF virus throughout the year, during the inter-epizootic periods. These aspects are addressed in Section 3.2.

**Risk of RVF spreading from Mayotte to other areas including other French departments in the Indian Ocean or Metropolitan France**.

Concerning the risk of RVF spread from Mayotte to other areas, including other French departments in the Indian Ocean or Metropolitan France, the only French department in that area is Réunion, for where there is no evidence that the livestock has ever been affected by RVFV. Other countries neighbouring Mayotte are Madagascar, Comoros, Kenya, Tanzania, Mozambique, Mauritius, which are not French departments. Apart from Mauritius, all these countries were already affected by RVFV before the emergence of RVF in Mayotte (EFSA AHAW Panel, 2020). The target countries and the related pathways to be considered for the assessment of possible spread from Mayotte are discussed in Section 3.3.

**Impact of the disease (as defined in the 'VBD opinion'), with emphasis on animal health and farm production in Mayotte from the time of its initial occurrence to date:**

In the VBD opinion (EFSA AHAW Panel, 2017), the impact of the disease being present in an area was intended as the combination of the impact on animal health, the production losses in affected farms, and on public health. In this opinion, the impact on animal health due to RVF epidemics in Mayotte is assessed considering the morbidity and mortality registered in outbreaks of RVF in the island, the number of abortions observed and attributable to RVF infection and the occurrence of cases of flu-like syndromes in cattle. For the impact on animal production, the effect on milk production was assessed on the basis of the milk drop observed in 2019 in one study of a bovine dairy farm. The ToRs do not request an assessment on public health impact; thus, this latter aspect is not included in the opinion. The impact of RVF in Mayotte is assessed in Section 3.1.

## 2. Data and methodologies

### 2.1. Data

#### 2.1.1. Epidemiological data

Historical and current data and information on the epidemiology of RVF in Mayotte, in relation to the outbreaks and cases in animals and humans, were obtained from World Organisation of Animal Health (OIE), Animal Disease Notification System (ADNS), French Veterinary Authorities and from the World Health Organisation (WHO)[2] and from Agence Régionale de Santé (ARS) Mayotte (Regional Health Agency of Mayotte)[3] for human cases. In addition, information from publications was used.

Data and information on the RVF laboratory analyses and the results were provided by the French Agricultural Research Centre for International Development (CIRAD, Centre de Coopération Internationale en Recherche Agronomique pour le Développement), which is the French RVF national reference laboratory (NRL) with laboratory facilities located in Réunion.

An animal health surveillance system, named SESAM, has been in place in Mayotte since 2009. It is jointly managed by CIRAD, the French veterinary services DAAF 976 and COOPADEM, a farmer's cooperative. SESAM includes data on RVF seroprevalence, occurrence of flu-like syndromes and abortions in farmed ruminants. Data from SESAM were obtained from COOPADEM and CIRAD. Data on seroprevalence of RVF were also gathered from several studies based on samples collected from 2004 to 2019 as follows, from 2004 to 2015 (Cetre-Sossah et al., 2012a,b; Metras et al., 2016) and from 2016 to 2019 (Direction de l'Alimentation, de l'Agriculture et de la Forêt (DAAF), CIRAD, COOPADEM).

Concerning data on abortions, the number of cases and the results of laboratory investigations were obtained both from SESAM and from the French Departmental laboratory in Mayotte, which routinely tests aborted fetuses in the framework of the brucellosis national surveillance plan.

Since there are no milk processing plants in Mayotte, no data on milk production that would allow the identification of any variation in milk production are available. COOPADEM provided data on milk production losses from a farm affected by RVF that had historical records of milk production.

#### 2.1.2. Data on climate, geographical and demographical characteristic

Data on climate, on temperature and on precipitation in Mayotte were obtained from the website of METEO FRANCE.[4] Demographic data were obtained from Institut national de la statistique et des etudes economiques (INSEE), France.

#### 2.1.3. Data on animal populations

Data on animal populations and farm management that have been used for this Opinion were derived from the websites of the Statistic and Prospective Service of the French Ministry of Agriculture and Food (Le Service de la statistique et de la prospective, Ministère de l' Agriculture et de l' Alimentation[5]) and from the Direction of Food, Agriculture and Forestry (Direction de l' Agriculture de l' Alimentation et la Foret, DAAF) of Mayotte.[6] They include the data from results of the last agricultural census carried out in 2010[7] in Mayotte and other statistical publications and studies carried out by the above-mentioned services.

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[2] WHO, Disease Outbreaks News: https://www.who.int/csr/don/13-may-2019-rift-valley-fever-mayotte-france/en/

[3] ARS Le Reunion hosted the archives of the press releases in relation to the diseases: les archives des communiqués de presse diffusés par l'ARS Océan Indien en 2019: https://www.lareunion.ars.sante.fr/communiques-de-presse-de-lars-ocean-indien-2019

[4] Meteo France : http://www.meteofrance.yt/climat/description-du-climat; and http://www.meteofrance.yt/climat/suivi-climatique-recent/an-2019

[5] Résultats du recensement agricole 2010, Mayotte : Synthèse illustrée du recensement agricole 2010 - Élevage - juin 2011 (PDF: 1.4 Mo) - 13/9/2011; http://agreste.agriculture.gouv.fr/IMG/pdf_D97611A05.pdf

[6] DAAF: http://daaf.mayotte.agriculture.gouv.fr/Statistiques.

[7] Résultats du recensement agricole 2010, Mayotte: L'essentiel du recensement agricole 2010; http://daaf.mayotte.agriculture.gouv.fr/IMG/pdf/RA_2010_Mayotte_Essentiel_cle0d6212.pdf

### 2.1.4. Data on trade and travel activities

Data on outbound flights from Mayotte for 2019 were provided by the Operations and Maintenance Infrastructure of the Mayotte Airport Dzaoudzi – Pamandzi[8] (Opérations et Maintenance Infrastructures de l' Aéroport de Mayotte) at monthly level.[9]

Data from 2015 to 2019 related to the trade movement from Mayotte to metropolitan France, other French departments in the Indian Ocean (Department of Réunion), the Union of Comoros, Madagascar and Mauritius were collected from TRACES, EUROSTAT and UN COMtrade.[10]

### 2.1.5. Data on vectors

The potential vector species of RVFV in Mayotte and Réunion were identified through a literature review. In particular from the risk assessment of AFSSA (2008), the review of Linthicum et al. (2016) on the RVFV species in endemic countries; the role of vectors in the area of the Indian Ocean reviewed by Balenghien et al. (2013) and the only publication on the survey of mosquitoes from Mayotte by Le Goff et al. (2014). In this opinion, field and/or laboratory evidence of RVFV were listed for all the mosquito species reported in Réunion and Mayotte. Abundance and distribution in the territories of concern were also extracted from literature when available to determine main vector species based on vector competence, high abundance and wide distribution in both islands. Information of main vector species was used to assess the possible spread of RVFV to other territories (i.e. Réunion and mainland France). We also assessed the main vector species present in Réunion to compare similarity on vector species to those found in Mayotte. Data on the presence/absence of *Aedes aegypti*, *Aedes albopictus* and *Culex quinquefasciatus* were taken from the survey conducted by CIRAD and are available at https://www.mosquito-maps-oi.fr/ (A. Tran, CIRAD, UMR TETIS).

## 2.2. Methodologies

### 2.2.1. Methodology for assessing the impact of RVF in Mayotte (TOR 2.2)

The impact of RVF in Mayotte was estimated through the descriptive epidemiological analysis of the RVF epidemics focusing on seroprevalence, mortality, morbidity, abortions and production losses.

For the latter, a study on the milk production implemented on one single educational bovine dairy farm, with 10 adult lactating cows on average, was considered. During this study, the amount of milk produced by dairy cows on the farm was monitored from 2015 to 2019. In January 2019, the farm was affected by RVF (laboratory confirmed on 23/1/2019) with abortions. The milk loss was assessed by comparing the production in 2019 with the production of the previous years 2015–2018, as a reference period. As in a quality control process, the milk production anomaly was assessed per each week in 2019 against the reference period. The milk production rate anomaly (MPA) is defined as the relative difference between the actual production of milk and the 95% CI bounds of the long-term milk production rate (considered as a reference). Specifically, $MPA(t) = 0$ for $p2.5 \leq MP(t) \leq p97.5$, $MPA(t) = 100 \times [MP(t)/p2.5 - 1]$ for $MP(t) < p2.5$ and $MPA(t) = 100 \times [MP(t)/p97.5 - 1]$ for $MP(t) > p97.5$, where $MP(t)$ is the milk production at the date t and p2.5 and p97.5 are the 2.5 and 97.5 percentiles of the reference. In other words, the reference or long-term production provides the ranges of production that would be expected; the anomaly is the difference between what is happening and what one would expect. MPA provides the deviation from the 'normal'. A positive anomaly means that the production is higher than normal; a negative anomaly indicates that the production is lower than normal. Likewise, the milk deficit is calculated as the cumulation of the difference between actual quantity of milk produced at the date t in 2019 and the 2.5 and 97.5 percentiles of the milk produced during the reference period.

For the estimation of the total economic losses in Mayotte in 2019 deriving from a drop in bovine milk production due to RVF infection, the following formula was used:

$$Cost_{RVF} = n \times m \times t \times p \times c, \qquad (1)$$

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where:

- n: Number of dairy animals affected by RVF in Mayotte
- t: Period (year)
- m: Amount (litres) of milk produced in 1 year/per cow
- p: Proportion of milk reduction
- c: Cost for 1 litre of milk (euros)

The number of dairy animals affected by RVF (n) is an unknown variable and the data reported in the ADNS for RVF outbreaks occurring in the whole island of Mayotte were considered for its estimation, considering both the number of animals affected by RVF disease and the total number of animals present in the outbreaks, to provide two possible ranges of estimates.

The period of the year (t) considered was 8 months (8/12 = 0.67), from December 2018 to July 2019, during which RVF outbreaks were recorded in Mayotte.

The average milk produced per cow (cross-breeding animal) per year (m) was considered equal to 2400 litres of milk (DAAF976, 2018).

For the proportion of milk reduction (p), the results of the analysis of milk production records in the above-mentioned study farm were used.

The cost of 1 litre of milk (c) sold in Mayotte was on average equal to 4 euros/litre (CIRAD, 2013).

Given the long period of observations, the results of this study are very useful for estimating the indirect effects RVF infection in milk production due to abortions and other perturbations of the reproductive sphere of cows. However, due to the extremely limited number of animals under study (this may be the main source of uncertainty), a careful interpretation of the results is needed, especially when the reduction in milk production in the whole bovine population of the island must be inferred.

In addition, further information is provided on the factors that may be linked with the impact of RVF such as climatic, geographical and demographic factors in Mayotte.

### 2.2.2. Methodology for assessing the probability of RVFV overwintering (TOR 2.1)

The RVF epidemiological cycle of Mayotte consists of animal hosts and mosquito vectors both present all year round. Because of weather conditions in Mayotte, there is no break in both mosquito abundance and mosquito activity, although there are seasonal trends. The transmission of RVF is likely to occur all year round in Mayotte. Therefore, the overwintering question in Mayotte system is posed in terms of how long the RVF infection can persist in such a context in the absence of any introduction.

The probability of RVFV persistence (overwintering, see Section 1.2) in Mayotte was assessed in two previously published modelling studies (Cavalerie et al., 2015; Metras et al., 2017). The results of these studies were used as the basis for the assessment, considering the assumptions underlying the two models, as well as their results and predictions.

For assessing the role of vertical transmission for the persistence of RVFV from one year to another, evidences were retrieved from literature, in particular from the complete review of the role of vertical transmission of RVFV by mosquito vectors conducted by Lumley et al. (2017).

Sources of uncertainty related to the vector's role in the maintenance of the RVFV in Mayotte and Réunion were a lack of data and possible overestimation of current evidences related to vertical transmission.

### 2.2.3. Methodology for assessing the risk of spread from Mayotte to neighbouring countries in the Indian Ocean or to continental France (TOR 2.1)

Concerning the risk of RVF spread from Mayotte to other areas including other French departments in the Indian Ocean or Metropolitan France, the possible pathways of spread of RVF from Mayotte were discussed and the relevant ones selected based on literature and expert knowledge. These are discussed in Sections 3.3.2–3.3.3.

Two pathways were selected for a more in-depth risk assessment: windborne spread of infected vectors and movement of vectors carried in airplanes. The HYSPLIT model[11] (REF) has been used to

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[11] https://www.ready.noaa.gov/HYSPLIT.php

assess the windborne movement of infected vectors, while MINTRISK model (details are provided in first opinion on RVF published under this mandate, EFSA AHAW Panel, 2020) is used to assess the possible spread by movement of vectors by flights (Section 3.3.4).

For the latter pathway, the target countries to be considered are only Metropolitan France and Réunion, which is the only French department in that area that was never affected by RVF. For the former pathway of spread, windborne spread of infected vectors, the countries considered are the ones neighbouring Mayotte, i.e. Madagascar, Comoros, Kenya, Tanzania, Mozambique, which are all countries endemic for RVF and were affected earlier than Mayotte (EFSA AHAW Panel, 2020). Mauritius is quite far away from Mayotte island and there are no direct trade, airplane or other connections with Mayotte. For this reason, Mauritius was excluded from the assessment.

**MINTRISK model**

The MINTRISK model is a tool to assess the level of introduction, transmission and impact of vector-borne diseases. MINTRISK stands for Method to INTegrate all relevant RISK aspects; it is a tool developed in Excel and Visual Basic. A web-based version with a central database and using C-sharp for underlying calculations has been created for practical use and access.[12] This tool allows for a systematic, semi-quantitative risk assessment, which can be used for risk evaluation, risk comparison and risk ranking of possible vector-borne diseases of livestock.

The MINTRISK approach to assess the overall risk of pathogen/disease introduction into the EU involves four steps: worldwide occurrence, risk of entry, level of transmission and probability of establishment.

The probability of each step of the risk pathway was calculated. First, the occurrence, rates of entry (number of entries/year), level of transmission (R0, basic reproduction number) and probability of establishment were calculated separately, and then, these three values were combined into an overall rate of introduction (number of epidemics/year). The calculation of the probability of each step was based on the answers to a set of questions to be addressed. Possible answers were qualitative categories associated with a level of the uncertainty (low, moderate, high[13]). A Monte Carlo simulation was used to determine the overall uncertainty in the probability for each step of the pathway and for the overall probability. For most of the questions, the answer categories were given on a logarithmic scale and the outcomes were always expressed on a logarithmic scale.

**Wind-borne dispersal of mosquitoes**

To explore the potential for RVFV-infected mosquitoes to be transported by wind to or from Mayotte, we used the Hybrid Single-Particle Lagrangian Integrated Trajectory model (HYSPLIT) (Stein et al., 2015; Rolph et al., 2017). HYSPLIT is a complete system for computing simple air parcel trajectories (as used here), as well as complex transport, dispersion, chemical transformation and deposition simulations, and is freely available online (https://ready.arl.noaa.gov/HYSPLIT.php). HYSPLIT has been used previously to investigate long-distance dispersal of other vector species (see, e.g. Durr et al., 2017; Huestis et al., 2019).

When assessing incursions of RVFV-infected mosquitoes to Mayotte backward trajectories of 48 h duration were computed for the 28 days prior to 1 January 2008 (i.e. around when the previous epidemic was predicted to have started) or 1 December 2018 (i.e. around when the first cases were reported in the recent epidemic). Air parcels (which could contain mosquitoes) were released every 6 h over the period of interest at 100 m above ground level from a location near the centre of Mayotte (12.83°S, 45.16°E). Their trajectories were then calculated backwards in time for 48 h to indicate where they had originated. The 100 m was chosen as roughly the midpoint of the atmospheric boundary layer. However, exploratory analysis suggested that the conclusions of the modelling were not particularly sensitive to the choice of release height.

When assessing dispersal of RVFV-infected mosquitoes from Mayotte, forward trajectories of 48 h duration were computed from January to April 2019 (i.e. when the majority of outbreaks were reported). Air parcels were released every 6 h over each month at 100 m above ground level from the same location near the centre of Mayotte. Their trajectories were then simulated for 48 h to indicate

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[12] https://www.wecr.wur.nl/mintrisk/ModelMgt.aspx

[13] Three uncertainty levels can be selected to describe the certainty when answering the questions in the MINTRISK model. The model will sample a value from triangular distributions with different ranges around the answer category according to the chosen uncertainty level for a 'moderate' answer category. The ranges around the answer category are +/0.1 for low, +/0.3 for moderate and +/0.5 for high uncertainty (EFSA AHAW Panel, 2017).

where they had moved to. Meteorological data from the Global Data Assimilation System (GDAS; at 1° resolution) were used in the simulations.

It is important to note this analysis does not consider factors such as mosquito flight behaviour or survival during transport (e.g. because temperatures become too low). It also does not consider the number of mosquitoes dispersing or the proportion of these which are infected with RVFV. Accordingly, it does not provide a detailed risk assessment for the introduction of RVFV via wind-borne dispersal on infected mosquitoes. Rather the HYSPLIT modelling gives an indication of locations which could either be a source of RVFV-infected mosquitoes for Mayotte or be at risk of introduction of RVFV via long-distance dispersal of mosquitoes from Mayotte. Results are presented in Section 3.3.5.

# 3. Assessment

## 3.1. Assessment of the impact of RVF in Mayotte (TOR 2.2)

This section is dealing with the assessment of the RVF impact on animal health and production in Mayotte. Besides the epidemiological analysis, some background information is provided on livestock sector, geography, climate and demography in Mayotte that may influence RVF impact.

### 3.1.1. Geographical and climate characteristics of Mayotte

Mayotte is located in the southern hemisphere, between the equator and the Tropic of Capricorn, at the entrance to the Mozambique Channel, halfway between Madagascar and southeast coast of Africa (Mozambique) and close to Comoros. Mayotte is approximately 100 km from Comoros, 400 km from Mozambique, 600 km from Tanzania, 1,300 km from Réunion, 8,000 km from mainland France (Figure 1).
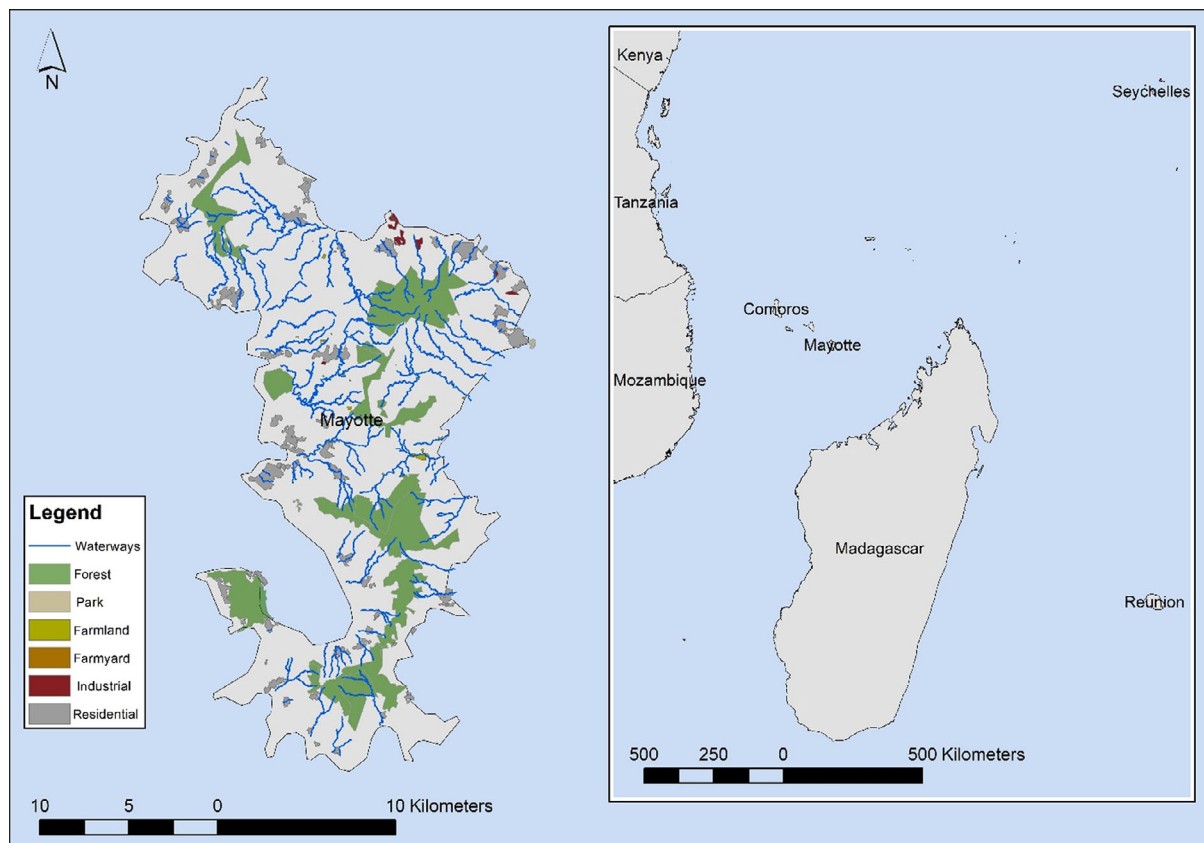


**Figure 1:** Land use and geographical position of Mayotte in the Indian Ocean

The total surface of Mayotte is estimated at 376 square km. It consists of two inhabited islands: the main island, Grande-Terre (or Maore) of 363 square km and a smaller island, Petite-Terre (or Pamanzi) of 11 square km and 30 uninhabited islets around these two (Ministère des Outre-mer).

Information about climatic conditions[14] were retrieved from METEO France[OBJ]. The climate in Mayotte is tropical, hot, humid, maritime characterised by small variations in daily and annual temperatures and significant rainfall (more than 1,500 mm per year). The average temperature in Mayotte is 25.4°C.

The two main wind systems affecting the island are the Monsoon winds that are hot and humid with direction from north to northwest; and the trade winds generated by the anticyclones of Mascareignes,[15] that are cool and dry, with direction from southeast (METEO FRANCE[10]). As a consequence of these two winds in Mayotte, there are two main seasons during the year, separated by two shorter (METEO France):

  i) The hot and rainy season, from December to March; the Australian summer or 'kashkasini'. The temperature regularly ranges around 32°C during the day and 21°C at night while the humidity ranges from 85% to 95% (METEO FRANCE).
  ii) the cold and dry season, from June to September; Australian winter or 'kussini' (METEO France). The minimum temperature can drop to 10°C during the night on the island and it is not uncommon to see several months without rain (METEO FRANCE).

One short season is 'Matulahi', which lasts from April to May, dominated by southeast winds and the other one, the 'M'gnombéni' lasts from October to November with northeast winds.

The maximum and minimum temperatures per month, the monthly mean temperature and precipitation variations during the period of the recent outbreaks (August 2018–August 2019) are presented in Figure 2, based on the data obtained from METEO FRANCE; the temperature variation is limited, and the temperature remains above 15°C all year round.
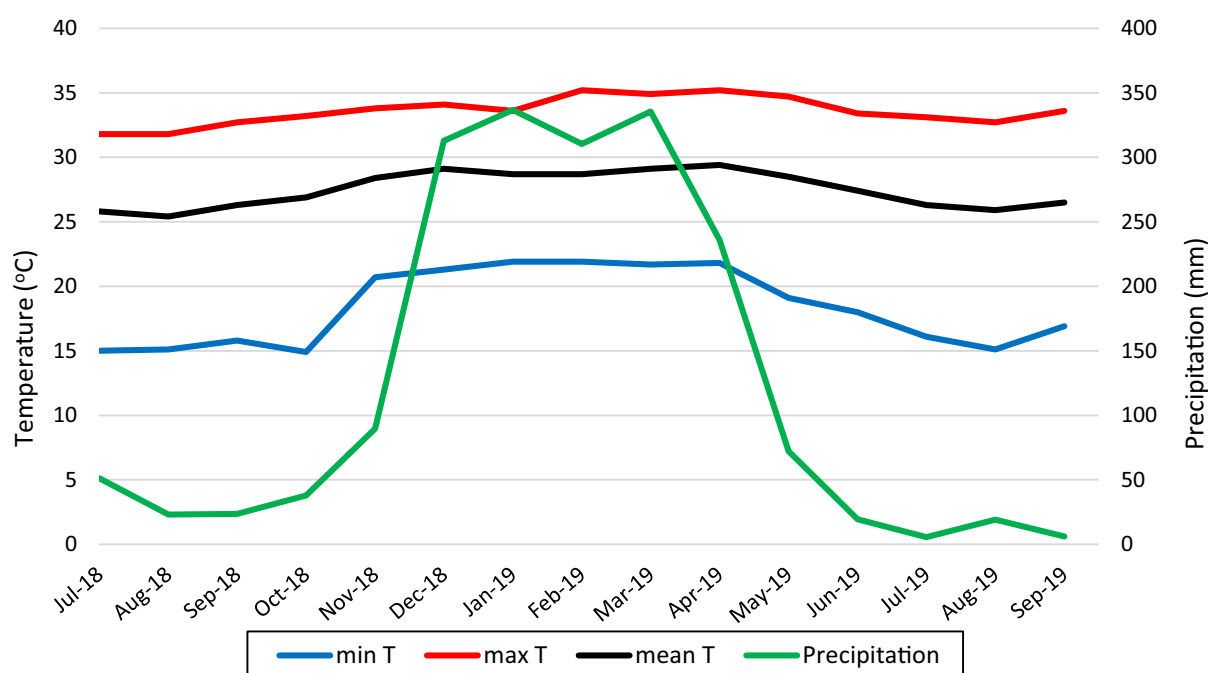


**Figure 2:** The mean, minimum and maximum temperatures and precipitation levels in Mayotte per month, from July 2018 until September 2019. Source of information: METEO France[16]

### 3.1.2. Human demographic characteristics of Mayotte

The population of Mayotte in September 2017 was 256,518 people (INSEE, 2019)[17] and remains the French Department with the greatest demographic growth. Mayotte can be considered as a very

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[14] Meteo France: Mayotte Description of climate, http://www.meteofrance.yt/climat/description-du-climat
[15] Mascarene Islands: Mauritius, Réunion, and Rodrigues.
[16] Meteo France, Climate, Suivi Climatique: http://www.meteofrance.re/climat/suivi-climatique-recent/an-2019
[17] L'Institut national de la statistique et des études économiques (INSEE): https://www.insee.fr/fr/statistiques/3284395

densely populated island with 682 habitants per square km given that it is only overtaken by Paris and five other Departments of Île-de-France.[18] Half of the population of Mayotte does not hold French nationality, but one-third of foreigners were born in Mayotte. In the municipalities of north-east Mayotte around Mamoudzou, many inhabitants arrived from the Comoros Islands (INSEE, 2019). The population of Mayotte is young: half of the inhabitants are under 18 years of age. Mayotte experiences illegal immigration, mainly from the Comoros, and thus, a regional cooperation has been developed with the Union of Comoros to better manage the migratory flows. The dominant religion in Mayotte is Islam, with 95% of the population being Sunni Muslims.

### 3.1.3. Livestock in Mayotte

The last agricultural census of the total animal population in Mayotte was carried out in 2010.[5,19] During the census, all the animals that were present were registered. According to the results, in Mayotte, there were 3,581 bovine herds with a total amount of 17,154 bovines and 4.8 was the average number of heads per herd. The size of the herds was small, since most (60%) of the herds had less than five animals. 36% of the herds had one or two animals, 24% had 3–5 animals, 9% had 6–10 animals and 31% more than 10 animals. Dairy herds accounted for 22% of the bovine herds.

The management of the herds remains traditional and depends on the size of the herd. Approximately 72% of the bovine herds were still raised tethered outside the premises, rather than on pastures belonging to their owners. Only 23% of the herds were known to remain inside the premises.

In relation to small ruminants, there were 2,189 sheep and goat herds, with a total amount of 12,619 animals. 93% of these herds were goat herds with a total of more than 11,500 animals. The size of the sheep population was one-tenth of the goat population, with barely 1,100 animals in total. The size of sheep and goat herds was small, with an average of 5.8 heads per herd. Herds with between 5 and 10 animals constituted 39% of the total number of herds and 45% of the total number of small ruminants. The management system was traditional; food supplements were provided to 21% of the animals. Approximately 51% of the herds were led to areas of free grazing whereas 46% remain in the premises.

More detailed data on animal population in Mayotte, based on the last census of 2010, are presented in Appendix A and an overview of the density of animals and herds in different municipalities ('communes') in Mayotte, based on the proportions on the total number of herds and animals per species., is illustrated in Figures 3 and 4.

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[18] Ministère des Outre-Mer http://www.outre-mer.gouv.fr/mayotte-1.

[19] Résultats du recensement agricole 2010, Mayotte: L'essentiel du recensement agricole 2010 (http://daaf.mayotte.agriculture.gouv. fr/IMG/pdf/RA_2010_Mayotte_Essentiel_cle0d6212.pdf).
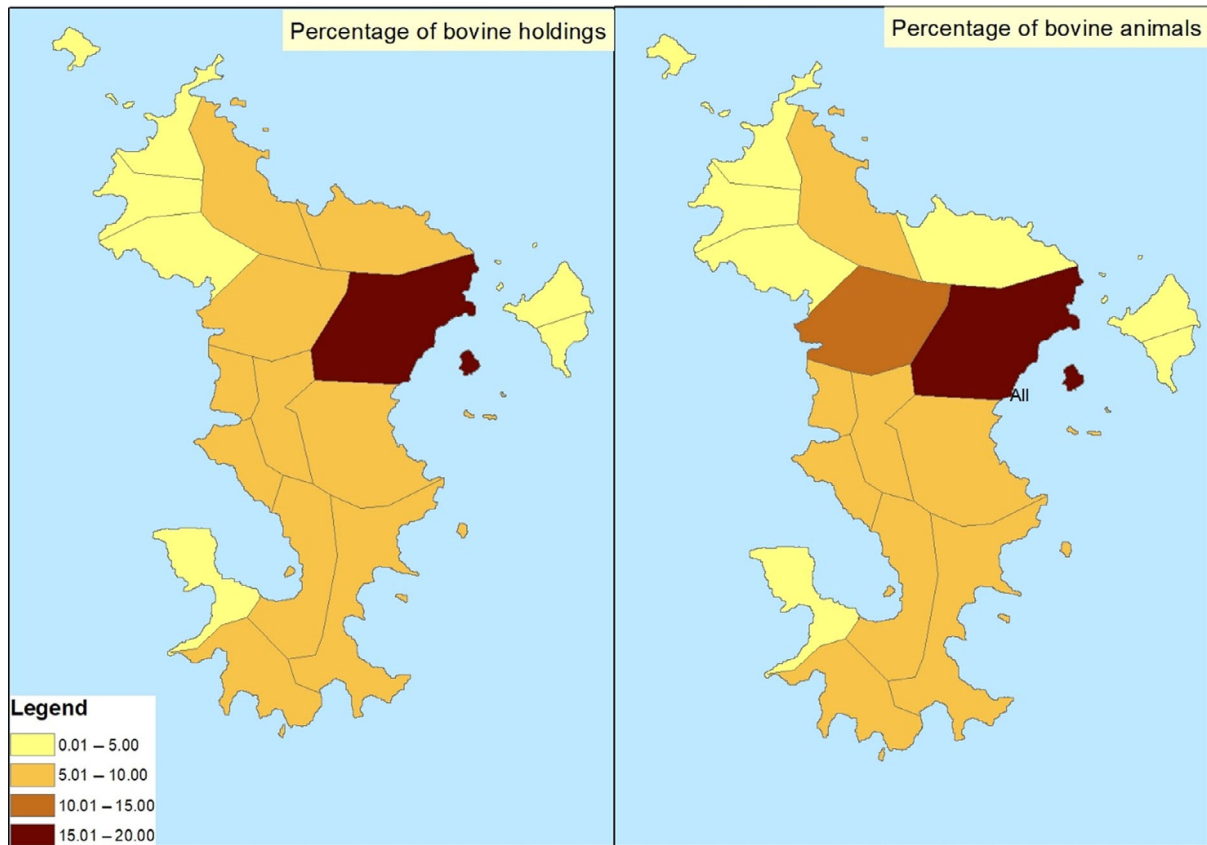
**Figure 3:** Proportional distribution of bovine herds (on the left) and of bovine animals (on the right) per commune (LAU 2) in Mayotte. The percentages were calculated based on the results of the last Agricultural Census having taken place in Mayotte in 2010[19]
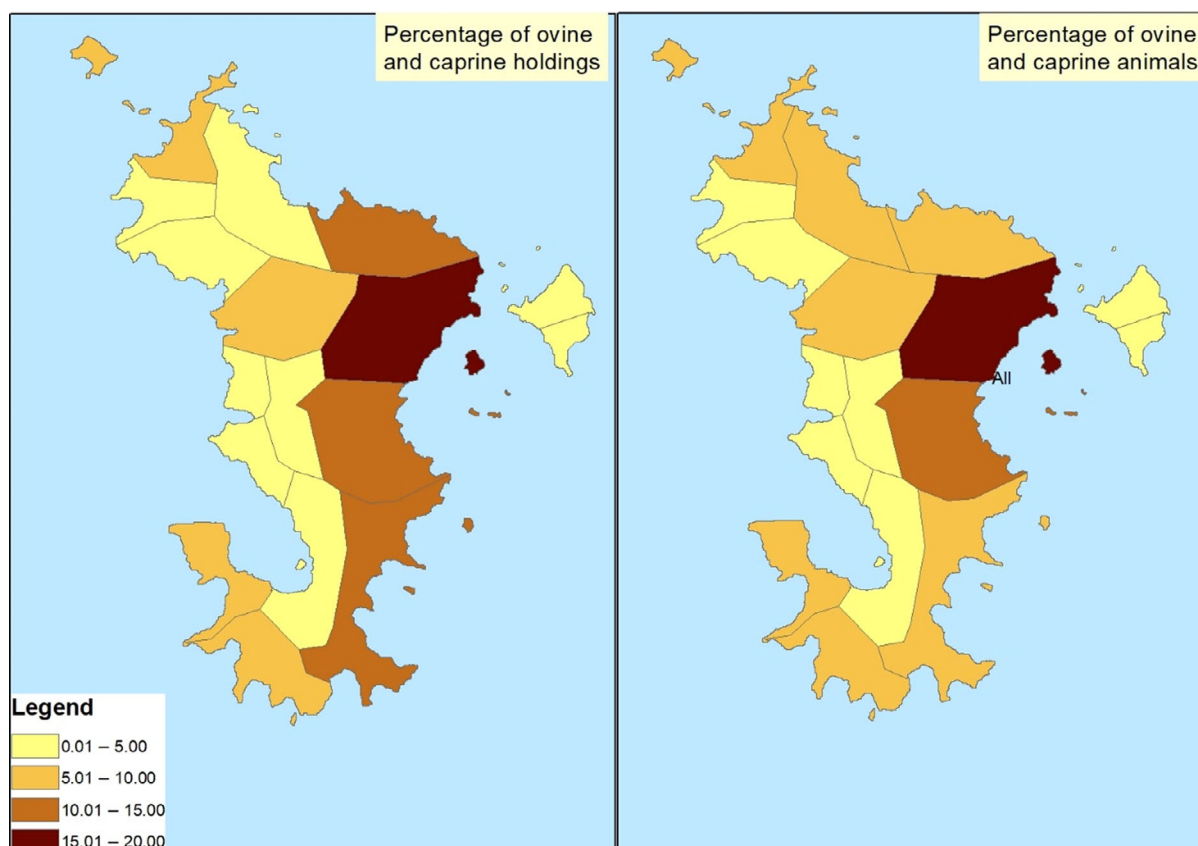
**Figure 4:** Proportional distribution of ovine and caprine herds (on the left) and of ovine and caprine animals (on the right) per each Commune (LAU 2) in Mayotte. The percentages were calculated based on the results of the last Agricultural Census having taken place in Mayotte in 2010

There are some more recent updates of bovine population data, in 2016 and 2017, that can be found in the website of DAAF[20] and according to which the total number of bovines in Mayotte was 20,232 and 20,478, respectively.

The population of small ruminants has not been updated recently and is based on the data from the last census performed in 2010 (French Veterinary Authorities, emails November 2019, January 2020). No camels are present in Mayotte.

**Table 1:** Total number of animals per species and per year, in Mayotte (Source: DAAF Statistiques)

| Species | 2003 | 2010 | 2016 | 2017 |
|---------|------|------|------|------|
| Bovine | 17,235 | 17,152 | 20,232 | 20,478 |
| Caprine | 22,811 | 11,542 | na | na |
| Ovine | 1,499 | 1,077 | na | na |

Na: not available.

According to the information provided by the French Veterinary Authorities, the registration and identification system in Mayotte is not fully in compliance with the EU legislation; there is no detailed information at the farm level, the farms are not geolocated and the data on animal numbers are incomplete and not regularly updated.

No wild ruminant species are present in Mayotte.

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[20] DAAF Direction de l'Alimentation, de l'Agriculture et de la Forêt de Mayotte: http://daaf.mayotte.agriculture.gouv.fr/Memento

## Production

Milk production is only cow milk; 22% of the bovine herds in Mayotte are for milk production. Given the absence of milk processing plants, it is very difficult to come up with precise numbers on production. The estimated dairy cattle population is approximately 2,200. The recent introduction of genetics from the *Montbéliarde* breed has raised the milk production per cow from 1,000 to 1,500 litres per year to 2,500 litres per year. Milk is sold around €4 per litre[5]. The milk consumption per resident is estimated between 35 and 50 litres of milk per year, of which 75% is imported milk (UHT or in powder).[21]

For the meat production, given the absence of slaughterhouses, it is also very difficult to come up with precise numbers. Mostly local zebus are used for meat production, in Mayotte, there are approximately 20,000 cattle in 3,600 herds, of which 4,000 are slaughtered per year with an average carcass weight of 120 kg and an average of 490,000 kg of meat per year. The meat is sold from €10 to €14 per kg.[11]

According to the 2010 census, the meat production from approximately 12,000 small ruminants corresponds to 35,000 kg of caprine and 5,000 kg of ovine meat.

### 3.1.4. Administration and organisation of livestock sector and veterinary diagnostics in Mayotte

Mayotte and Réunion are the two Overseas French Departments *(Départment d'outre mer; DOM)* in the Indian Ocean.[22] Mayotte became officially the 101st Department of France on 31 March 2011 (Ministère de l'Intérieur). In 2014, Mayotte also changed status at European level, becoming an outermost region, and has since become part of the European Union. Mayotte is classified at NUTS 2 and three administrative levels according to the European Legislation and is divided into 17 Municipalities (Communes) (LAU 2 level) (http://www.outre-mer.gouv.fr/mayotte-1).

The French Government exercises the authority in all Overseas Departments through the Ministry of Overseas (Ministère des Outre-Mer). In relation to the field of agriculture, the Departmental Directorate for Food, Agriculture and Forestry (Direction départementale de l'alimentation, de l'agriculture et de la forêt, DAAF[23]) is a decentralised service of the state, with inter-ministerial competence, placed under the authority of the Prefect of Mayotte and reporting to the French Minister of Agriculture. The Veterinary Authority for animal health of Mayotte is based in the Directorate for Food, Agriculture and Forestry: Unit of Animal Health and Welfare (Unite Santé et protection animales) under the Food Service (Service de l' Alimentation, SA) (DAAF Organisation chart[24]).

In Mayotte, there is a public institution named 'Chambre de l'Agriculture, de la Pêche et de l'Aquaculture de Mayotte (CAPAM)', which is a partner of the DAAF. It provides technical support to professionals for agriculture development in the territory. Until the end of 2018, CAPAM was in charge of the animal identification and certification of bovine filiations. However, since the start of the outbreaks of RVF late December 2018 and the peak observed early 2019, DAAF is now the one taking care of both activities.

In 2012, a farmer's cooperative was created in Mayotte from ADEM (a previous farmer's association) named COOPADEM. Since 2013, it is designated by the Veterinary Authorities as the Delegated Health Organisation ('Organisme à Vocation Sanitaire', OVS) of Mayotte. In France, OVS is the regional breeders' organisations to which national authorities may delegate animal health missions like the implementation of control and surveillance programmes. COOPADEM is part of SESAM surveillance system since 2009 and is responsible for the database of RVF in Mayotte since 2012.

In Mayotte, the diagnostic animal health laboratory diagnosis is primarily managed by the Departmental Veterinary Laboratory located in Mamoudzou that can perform some of the conventional and routinely asked analyses. More specific and advanced analyses that involve molecular biology equipment and dedicated reagents essential to confirm the presence of a newly emerged pathogen or its re-occurrence are carried out in the laboratory facilities of CIRAD (UMR ASTRE) (Agricultural Research for the Development namely CIRAD) located in Réunion. The UMR ASTRE of CIRAD is officially mandated by the French Ministry of Agriculture as the French National Reference Laboratory

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[21] AGRESTE Mayotte : ETUDES d'Informations Statistiques agricoles menées en 2017 - janvier 2018 (PDF : 3.9 Mo) - 16/2/2018 http://agreste.agriculture.gouv.fr/IMG/pdf/D97618A02.pdf and http://agreste.agriculture.gouv.fr/en-region/mayotte-665/

[22] Ministere de l' Interieure: https://www.interieur.gouv.fr/fr/Archives/Archives-des-dossiers/2018-Dossiers/Mayotte-le-departement-de-tous-les-defis

[23] Direction départementale de l'alimentation, de l'agriculture et de la forêt of Mayotte http://daaf.mayotte.agriculture.gouv.fr/ and its mission: http://daaf.mayotte.agriculture.gouv.fr/Les-missions-de-la-DAAF,64 and http://daaf.mayotte.agriculture.gouv.fr/IMG/pdf/SA_cle09bb8e.pdf

[24] DAAF Organogram: http://daaf.mayotte.agriculture.gouv.fr/IMG/pdf/Organigramme_general_Services_unites-1_cle85a6b2.pdf

for RVF and is responsible for the confirmation of the animal cases of RVF detected in the samples from clinically suspected animals. Moreover, due to the absence of RVF-specific reagents, consumables and equipment in the Departmental Veterinary Laboratory of Mayotte, most of the samples collected in the framework of the RVF sero-surveillance programme during the 2018–2019 epizootics were analysed by CIRAD in Réunion. Due to the distance between Mayotte and Réunion and flights connections, animal samples are sent on a routine basis of once a week, which may create a short delay in the early diagnosis of the diseases and the implementation of the control measures.

### 3.1.5. Animal trade and animal movements

Livestock production is limited in Mayotte. Farmers replace and renew their livestock with locally born animals or by artificial insemination with semen imported from abroad. Animal import from non-EU neighbouring countries (e.g. Comoros, Madagascar) to Mayotte is forbidden; this raises the demand for animals and animal products; thus, animals are mostly imported to Mayotte rather than exported. This creates a driver for high prices of livestock in Mayotte and consequently for possible illegal introduction of animals. Live animals are not imported to Mayotte from other European territories because of the distances and the consequent high cost. The price at slaughterhouse is between €1,800 and €3,100 for one adult cattle and more than €6,000–7,000 for a dairy cow (DAAF, 2018). A dispatch of 25 cattle was imported from mainland France in 2008 and another one of 45 cattle in 2018 (COOPADEM). Import of live animals to Mayotte from other non-EU neighbouring countries is not permitted. Nevertheless, according to some publications and the information provided by the French Veterinary Authorities, the police regularly intercept boats that illegally transport ruminants, from the surrounding islands. These animals are culled, and the carcases destroyed, but in advance, blood samples are collected and stored, in case of further use. According to the data in Table 4 provided by COOPADEM, it is clear that there is a frequent uncontrolled trade of animals, even in small numbers. Moreover, in June and August 2018, recently infected animals, positive for RVFV-specific IgM antibodies, were found among animals that were illegally moved and seized by the police (Table 4).

**Table 2:** Numbers of ruminants that arrived in Mayotte and were seized by the police between May 2018 and December 2019 (only for months where uncontrolled movements were detected)

| Month year | Cattle | | | Goats | | | Sheep | | |
|---|---|---|---|---|---|---|---|---|---|
| | Seized | Tested for IgG (no. of pos.) | Tested for IgM (no. of pos.) | Seized | Tested for IgG (no. of pos.) | Tested for IgM (no. of pos.) | Seized | Tested for IgG (no. of pos.) | Tested for IgM (no. of pos.) |
| May 2018 | 0 | 0 | 0 | 4 | 4 (0) | 4 (0) | 4 | 4 (0) | 4 (0) |
| June 2018 | 2 | 2 (1) | 2 (0) | 10 | 10 (1) | 10 (1) | 19 | 19 (9) | 19 (9) |
| August 2018 | 1 | 0 | 0 | 10 | 10 (8) | 10 (0) | 8 | 8 (8) | 8 (2) |
| September 2018 | 0 | 0 | 0 | 1 | 1 (0) | 1 (0) | 0 | 0 | 0 |
| October 2018 | 3 | 3 (0) | 3 (0) | 0 | 0 | 0 | 2 | 2 (2) | 2 (0) |
| December 2018 | 1 | 1 (1) | 1 (0) | 2 | 0 | 2 (0) | 2 | 0 | 2 (0) |
| **Total 2018** | **7** | **6 (2)** | **6 (0)** | **27** | **25 (9)** | **27 (1)** | **35** | **33 (19)** | **35 (11)** |
| February 2019 | 1 | 1 (0) | 1 (0) | 8 | 8 (0) | 8 (0) | 1 | 1 (0) | 1 (0) |
| July 2019 | 2 | 0 | 2 (0) | 1 | 0 | 1 (0) | 0 | 0 | 0 |
| August 2019 | 4 | 3 (0) | 4 (0) | 10 | 0 | 10 (0) | 4 | 0 | 4 (0) |
| September 2019 | 1 | 0 | 0 | 5 | 0 | 0 | 1 | 0 | 0 |
| October 2019 | 0 | 0 | 0 | 2 | 0 | 0 | 0 | 0 | 0 |
| November 2019 | 0 | 0 | 0 | 2 | 2 (1) | 2 (0) | 5 | 5 (0) | 5 (0) |
| December 2019 | 0 | 0 | 0 | 6 | 6 (1) | 6 (0) | 0 | 0 | 0 |

| Month year | Cattle | | | Goats | | | Sheep | | |
|---|---|---|---|---|---|---|---|---|---|
| | Seized | Tested for IgG (no. of pos.) | Tested for IgM (no. of pos.) | Seized | Tested for IgG (no. of pos.) | Tested for IgM (no. of pos.) | Seized | Tested for IgG (no. of pos.) | Tested for IgM (no. of pos.) |
| **Total 2019** | **8** | **4 (0)** | **7 (0)** | **34** | **16 (2)** | **27 (0)** | **11** | **6 (0)** | **10 (0)** |

Numbers of tested and numbers of RVFV-specific IgG and IgM-positive antibodies are provided, respectively (Source: COOPADEM).

**Key points:**

- Animals are often illegally transported in Mayotte, thus representing a continuous risk of (re) introduction of RVF and other diseases.
- There is evidence that at least in June and August 2018, small ruminants recently infected with RVFV (IgM antibodies were detected) have been introduced into Mayotte.

### 3.1.6. Historical and recent epidemiological situation of RVF in Mayotte

#### 3.1.6.1. Emergence of RVF in Mayotte in 2007 and surveillance activities

Rift Valley Fever was confirmed for the first time in Mayotte, 7 September 2007, in a 12-year-old boy who was transferred to Mayotte's Hospital with a history of severe encephalitis. The young boy was coming from Moroni (Grande Comore Island, Union of the Comoros) and never travelled outside Comoros. The onset of symptoms started in May 2007 in Comoros and RVF was diagnosed in Mayotte by ELISA that identified the presence of RVFV IgM and IgG antibodies (Sissoko et al., 2009).

Following this initial human case detected in Mayotte, sporadic human cases have been reported in the four islands of the Comoros archipelago in an inter-epidemic or a post-epidemic period, one in March 2008 (AFSSA, 2008), and two other ones confirmed in 2011–2012 after having travelled to the Union of the Comoros, one in Mayotte and one in mainland France (InVS, 2011, 2012).

This first case in Mayotte in 2007 stimulated the Veterinary and Public Health Authorities for further investigation. Several studies were implemented in human and animal populations either retrospectively in stored samples or prospectively (see Appendix B). Surveillance activities were initiated in order to monitor and follow up the epidemiological situation in Mayotte. The results are not strictly comparable because of their different study designs, target populations, laboratory methods. Sometimes, they were based on the availability of resources (reagents, consumables, staff). Nevertheless, they can provide a rough estimation on the presence of RVF in Mayotte.

Since September 2007 until March 2008, samples collected from humans with dengue-like illness who tested negative for *Plasmodium* spp., chikungunya virus (CHIKV) and dengue virus (DENV) were screened for RVFV. Recent RVFV infection was identified in 10 samples out of 220 tested (4.5%), based on the presence of viral RNA detected by RT-PCR (Drosten et al., 2002) or by an in-house IgM-capture enzyme immunoassays ELISA (Sissoko et al., 2009a). None of these patients travelled to RVF endemic countries within 3 weeks interval before the onset of the illness. 50% of the cases were in contact with animals during their work (animal herding, contact with aborted animals, milking, slaughtering and butchering). 70% of the cases occurred from January to April, during the hot rainy season (Sissoko et al., 2009a). RVF viruses isolated from samples from two patients, were sequenced and the results showed that they were related to the 2006–2007 eastern African-Kenya-1 lineage (Sissoko et al., 2009a; Cetre-Sossah et al., 2012b). Therefore, RVF outbreaks of 2007 in Mayotte appear to be an expansion of the eastern Africa outbreaks (Sissoko et al., 2009a).

Lernout et al. (2013) carried out a multistage, cluster sampling survey in humans, in different districts of Mayotte. The individuals were enrolled for a 5-week period (March–April 2011). Serum samples were analysed by using an in-house indirect ELISA prepared by the National Reference Centre for Arboviruses (NRC-Arbo) at the Pasteur Institute in Paris. Of the 1,413 human sera, 58 (4.1%) were detected positive for the presence of RVFV IgG antibodies. The overall weighted seroprevalence of RVFV antibodies in the general population aged more than 5 years old was 3.5% (95% CI 2.6–4.8). No significant differences in prevalence were observed when comparing gender or geographical area. The highest seroprevalences were observed in farmers (32.1%) and persons associated with animal birthing activity or in contact with aborted animal foetuses (27.8%).

Following the first human case in 2007, Cetre-Sossah et al. (2012a) conducted four serological investigations on samples collected in Mayotte during the period 2004–2008. The results of these studies are the following:

- A first set of samples collected from ruminants on a yearly basis from 2004 to 2007 were tested for RVFV-specific IgG antibodies and seroprevalence was estimated at 22.7% (n = 130) in 2004 followed by a large decrease in 2005 reaching 3.07% (n = 130) followed by an increase in 2006 and 2007 with 12.3% (n = 130) and 30.9% (n = 126), respectively. Specific RVFV IgM antibodies were not detectable during this study.
- A second set of samples, consisting of 29 illegally introduced goats and 79 cattle born on Mayotte and living near the introduced goats, was analysed. Among the goats, RVFV-specific IgG antibodies were identified in four goats (13.79%) and IgM (6.89%) in two goats suggesting recent infection. Among the 79 cattle, IgG and IgM against RVFV were found in 29 (37%) and in 3 (4%) cattle, respectively. A third set of 301 cattle serum samples were collected between June 2007 and May 2008 from 104 farms in 17 communes of Mayotte. IgG antibodies identified in 32 cattle (10.6% (95% CI: 7–14%)) indicated the exposure of the animals to RVF. The positive samples were distributed all over the island.
- A last set of samples, originating from a prospective study of 70 seronegative goats distributed in five farms and collected every 6 or 8 weeks between August 2008 and August 2009, was tested for RVF-specific IgM and IgG antibodies. Only one goat (1.43%), located in Bouyouni, seroconverted in February 2009 and IgM antibodies were detected.

Lernout et al. (2013) performed a prospective longitudinal study where 198 seronegative ruminants (131 bovines, 67 small ruminants) from 33 sentinel herds were randomly chosen and monthly bled between March 2010 and August 2011. An overall seroprevalence in the ruminant population was estimated at 25.3% (95% CI: 19.8–32.2). Prevalence at herd level was 61.9% (95% CI: 44.8–79.2). No significant difference (p-values < 0.05) was observed between small ruminants 22.4% (95% CI: 14.1–32.2) and cattle 26.8% (95% CI: 19.1–35.3).

In 2009, a surveillance system for animal diseases was initiated in Mayotte (Système d'épidémiosurveillance animale à Mayotte, SESAM), in order to investigate the presence of RVF.[25] All the samples were tested for IgG, while IgM testing was randomly done on a subset of sera samples when funding was available. Metras et al. (2016) collected the raw data from the studies of Cetre-Sossah et al. (2012a) and additional data from surveillance activities in the framework of SESAM from May 2009 to June 2015, collated them and proceeded with an analysis of RVF seroprevalence for an 11-year period (October 2004 to June 2015). They used a data set of 5,720 samples from 3529 animals of 448 herds. All the samples were tested for IgG, while 26.5% (n = 1,513) were tested for both IgG and IgM. Given the small size of Mayotte, the whole island was considered as a single epidemiological unit. Data were aggregated by 'epidemiological year' (July–June), in order not to split the rainy season which is favourable to vectors abundance and RVF outbreaks (see Table 4).

RVF sero-surveillance is still ongoing in Mayotte. For the purpose of this Opinion, the data from the study of Metras et al. (2016) provided by Dr Metras, Dr Dommergues and Dr Cetre Sossah were combined with the latest data (2015–2020) of the surveillance on RVF generated in the framework of SESAM aggregated per epidemiological year following the Metras et al. (2016) methodology. The results of RVFV IgG and IgM antibodies (estimated sero-prevalence) are presented in Table 4 and in the graph of Figure 5.

The results of Metras et al. (2016) study from May 2009 to June 2015 are included in Table 4 together with the results of the RVF surveillance the following years.

**Table 3:** The sero-prevalence of IgG and IgM antibodies of RVF in ruminants (cattle, sheep and goats), according to the results of the different sero-surveillance activities in Mayotte from 2004 to 2020 per epidemiological year (from July of year y to June of year y + 1). CI, Confidence Intervals

| Epi-year (July–June) | IgG antibodies | | | IgM antibodies | | |
|---|---|---|---|---|---|---|
| | Tested | Positive | Seroprevalence, % (95% CI) | Tested | Positive | Seroprevalence, % (95% CI) |
| 2004–2005 | 243 | 33 | 13.6 (8.5–18.7) | 0 | NA | NA |
| 2005–2006 | 22 | 1 | 4.5 (. 0–18.3) | 0 | NA | NA |
| 2006–2007 | 169 | 20 | 11.8 (7.1–16.6) | 0 | NA | NA |

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[25] https://coatis.rita-dom.fr/osiris/files/BulletinEpidemiologiqueSesamSeptembre2012_fichier_ressource_be-sesam-septembre-2012.pdf

| Epi-year (July–June) | IgG antibodies | | | IgM antibodies | | |
|---|---|---|---|---|---|---|
| | Tested | Positive | Seroprevalence, % (95% CI) | Tested | Positive | Seroprevalence, % (95% CI) |
| 2007–2008 | 647 | 111 | 17.2 (12.09–22.2) | 16 | 3 | 18.725 (0–44.9) |
| 2008–2009 | 142 | 51 | 35.9 (16.7–55.1) | 96 | 39 | 40.6 (24.9–56.4) |
| 2009–2010 | 591 | 154 | 26.1 (26. –19.4) | 77 | 28 | 36.4 (21.5–51.2) |
| 2010–2011 | 182 | 26 | 14.3 (10.3–18.3) | 109 | 4 | 3. 7 (0.1–7.2) |
| 2011–2012 | 500 | 72 | 14.4 (9.4–19.3) | 0 | NA | NA |
| 2012–2013 | 645 | 78 | 12.1 (8.3–15.9) | 0 | NA | NA |
| 2013–2014 | 1,253 | 122 | 9.7 (7.2–12.3) | 576 | 5 | 0.9 (0.0–1.7) |
| 2014–2015 | 462 | 29 | 6.3 (2.8–9. 8) | 462 | 0 | 0 |
| 2015–2016 | 1,798 | 126 | 7.2 (6.4–7.6) | 1,381 | 2 | 0.1 (0.0–0.2) |
| 2016–2017 | 328 | 9 | 2.7 (1.8–3.6) | 0 | NA | NA |
| 2017–2018 | 559 | 12 | 2.1 (1.53–2.8) | 3 | 0 | 0 |
| 2018–2019 | 1,033 | 342 | 33.1 (31.6–34.6) | 886 | 61 | 6.9 (6.0–7.7) |
| 2019–2020 | 378 | 225 | 59.5 (57–62.0) | 207 | 4 | 1.9 |

NA: not tested.
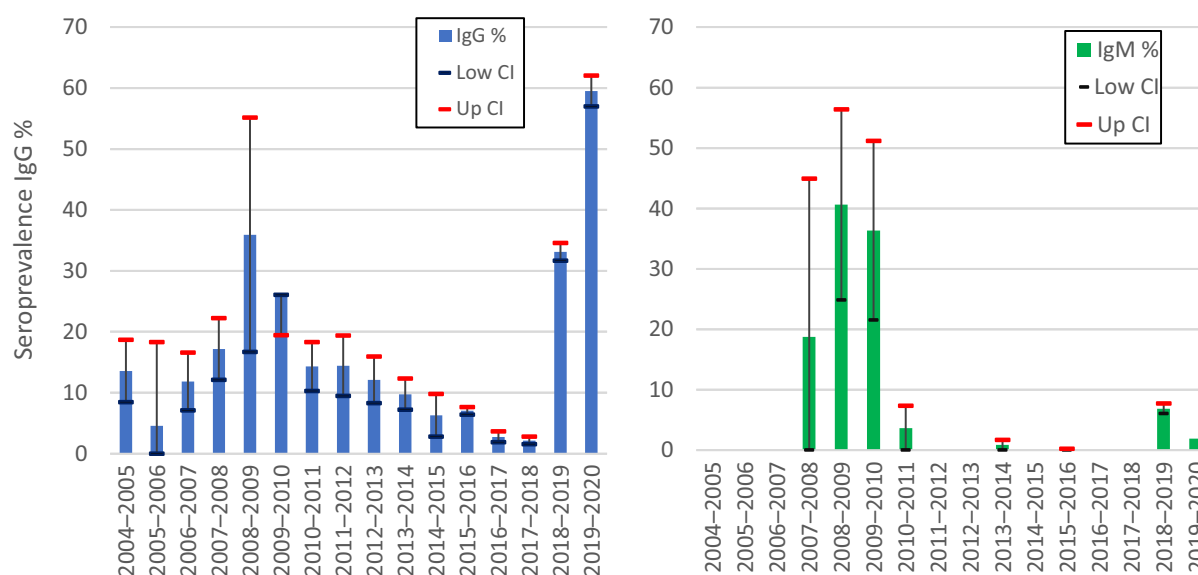


**Figure 5:** The seroprevalence of IgG and IgM antibodies of RVF according to the results of the different sero-surveillance activities in Mayotte from 2004 till 2020 per epidemiological year (from July of year y to June of year y + 1)

In addition, in the Union of Comoros, a longitudinal survey of livestock was set up in the Comorian ruminant population from 2010 to 2011, in order to identify the hypothetical source of RVF. The phylogeographic genomic analysis has shown that RVFV detected in a zebu collected in Anjouan in August 2011 seems to be related to the last known epidemic of RVF that occurred in East Africa and Madagascar (2007–2009) (Maquart et al., 2016). This result highlights the fact that RVF has been maintained within local livestock populations and transboundary animal movements from Eastern continental Africa to Indian Ocean islands likely resulted in RVFV crossover.

**Key points**

- The animal population in Mayotte has been exposed to RVFV at least since 2004 or even earlier, since RVF-specific IgG antibodies were detected in serum samples in 2004. RVFV-specific IgM antibodies were not identified before 2007 and efforts for virus isolation were unsuccessful.
- Illegal animal movements from the Union of the Comoros was the most likely way of introduction of RVFV in Mayotte since IgM (recent infection) and IgG (ever infected in the past)

antibodies were detected in goats illegally introduced to Mayotte from the Union of the Comoros.

- The first documented introduction of RVF in Mayotte was in 2007, and the responsible virus was the eastern African-Kenya-1 lineage circulating in East Africa on 2006–2007. This indicates an expansion of the eastern Africa outbreaks followed by high RVF seroprevalences geographically distributed all over the island (Cetre-Sossah et al., 2012a).
- The seroprevalence in livestock decreased from 2008 to June 2018, and this suggests the absence of new virus incursion into the island in this period.

### 3.1.6.2. Re-emergence of RVF in Mayotte in 2018

The first human case in Mayotte was admitted at the hospital on 22 November 2018, the date considered as the onset of the symptoms, and RVF confirmed in December, one month later.

In January 2019, RVF was confirmed in animals and notified to the Animal Disease Notification System (ADNS). Since Mayotte Department is part of French Territory, French Veterinary Authorities are obliged to notify the RVF outbreaks to the EU ADNS according to the Council Directive 82/894/EEC. The data on ADNS include only the outbreaks that have been officially confirmed and notified by the Veterinary Authorities. An outbreak can refer to more than one affected animal even in different species if they constitute a unique epidemiological unit and are identified at the same location. A confirmed case is an animal with clinical signs and positive results either in IgM detection or PCR or both, official confirmed by CIRAD in La Réunion (French Veterinary Authorities, PAFF Committee). Since then all suspect animals with abortion or flu-like syndrome were tested for RVF.

Two laboratory tests were performed in order to confirm the RVF in ruminants, a commercial IgM ELISA test (ID Screen RVF IgM Capture, IDVet, France) and a quantitative qRT-PCR based on the L segment of RVF (Bird et al., 2007).

Until August 2019, 121 outbreaks in ruminants from Mayotte were reported in ADNS, plus four outbreaks in December 2018 reported by French veterinary services, for a total of 125 outbreaks: 72.8% of the total number of outbreaks concerned only cattle, 14.4% goats, 6.4% cattle and goats, 4% sheep, 0.8% cattle and sheep and 1.6% cattle, sheep and goats. As shown in Figure 6, the outbreaks are distributed across the whole island. The minimum distance from each outbreak to the closest one is 30.1 m and the maximum is 2,664.8 m with the median 531 and 25 and 75 quantiles 304.3 and 1,025.9 accordingly.
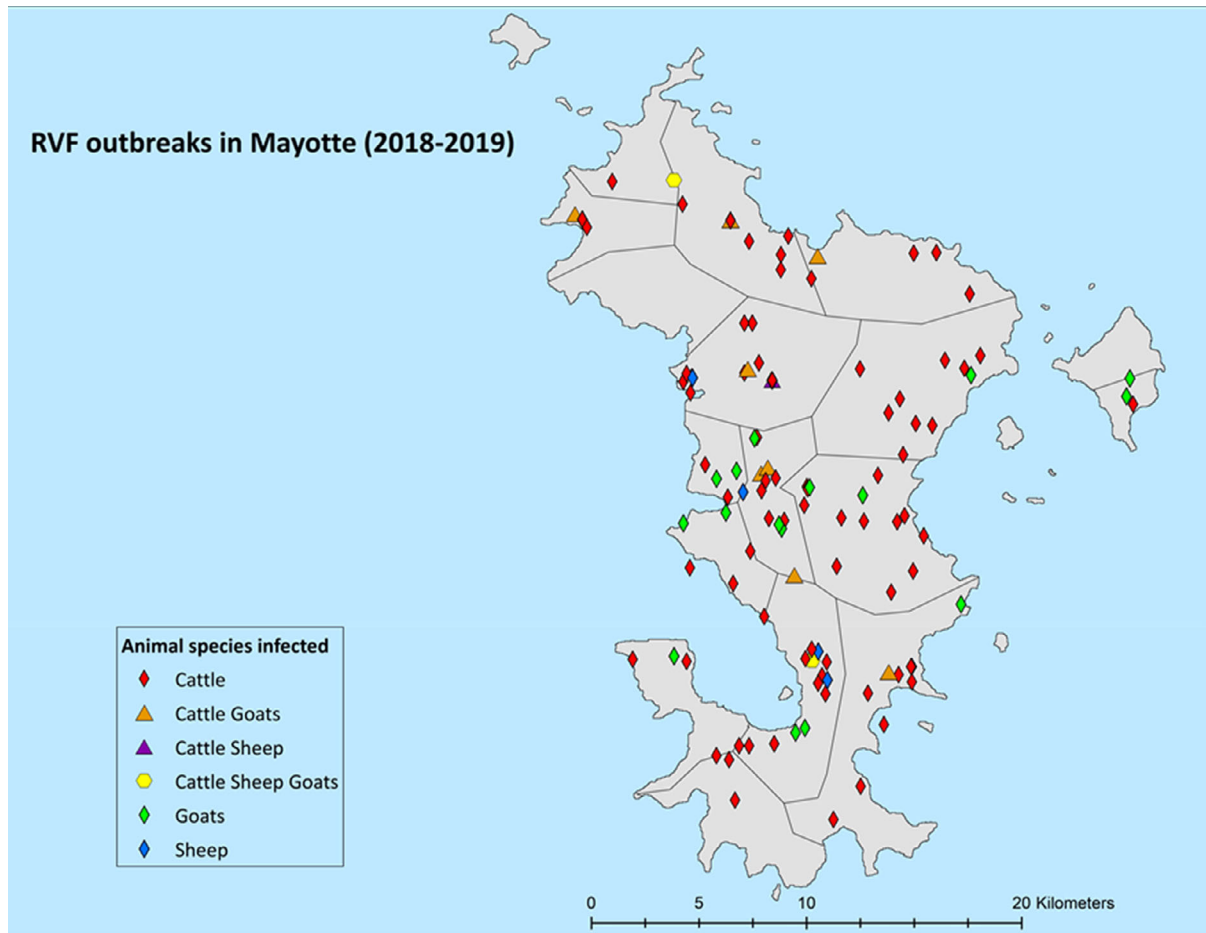
**Figure 6:** Geographical distribution of the outbreaks in the animal population (cattle, sheep, goats) according to the notifications to the ADNS and the additional information of Veterinary Authorities, December 2018–August 2019

The epidemiological investigation into disease introduction revealed the illegal imports of live animals (mainly goats) from the Union of the Comoros during the preparation for the celebration of Eid al Adha[26] of 2018 (22 August 2018) (reported in ADNS, information provided by French Veterinary Authorities).

The Public Health and Veterinary Authorities frequently published information on the evolution of the disease both in human and animal population by press releases that were uploaded on the website of the Regional Agency of Health (Agence Régionale de Santé, ARS)[27] in Mayotte and are available to the public. The information of the evolution of the disease included in these press releases is presented in Appendix C and in the graph of the Figure 6. A total of 143 human cases were confirmed between November 2018 and July 2019 (Youssouf et al., 2020).

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[26] Eid al Adha which means 'feast of the sacrifice' is one of the most important religious Islamic fests when animals usually goats, sheep or cows are sacrificed as an offer to God, and the meat is distributed to the people. https://www.aljazeera.com/news/2019/08/muslims-celebrate-eid-al-adha-religious-holiday-190811073635616.html; https://www.edarabia.com/eid-al-adha/

[27] ARS: les archives des communiqués de presse diffusés par l'ARS Océan Indien en 2019: https://www.lareunion.ars.sante.fr/communiques-de-presse-de-lars-ocean-indien-2019
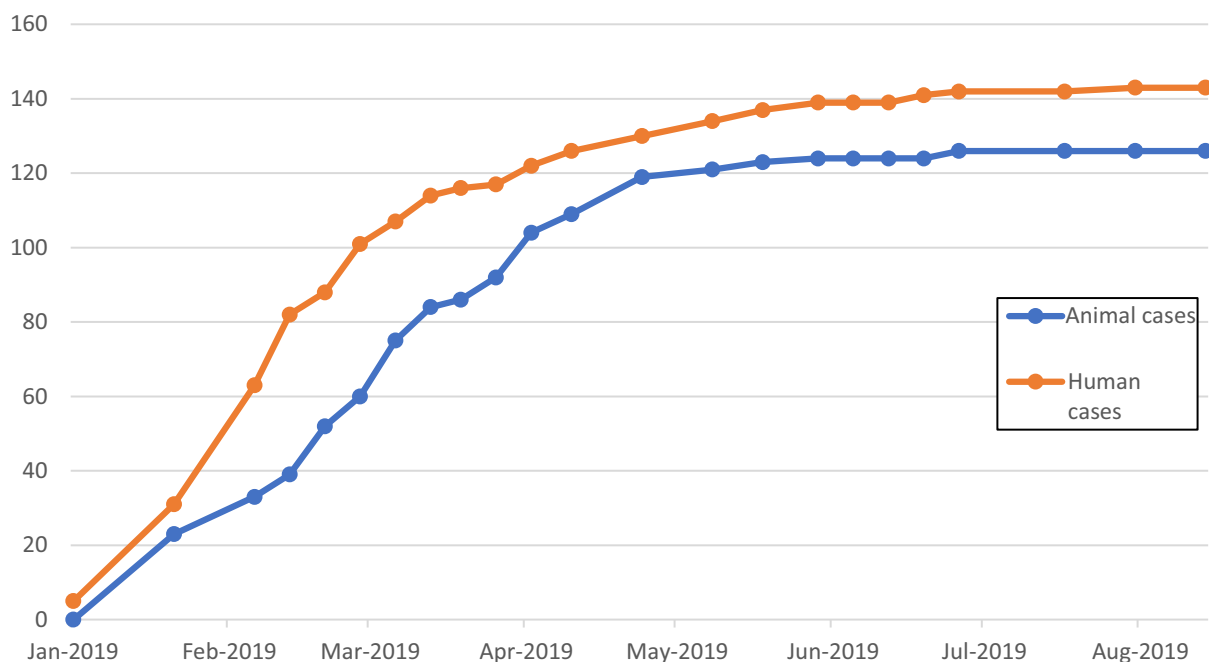
**Figure 7:** Cumulated cases of RVF in humans and animals in Mayotte in 2019. Data Source: **Regional Agency of Health (Agence Régionale de Santé, ARS)**

Given the outbreaks of the 2018–2019 epidemic, the serosurveillance was targeted on selected farms without any clinical signs in cattle. Nevertheless, it is impossible to ensure that the selection of farms was not biased. Commercial kits were used to identify IgG (previously infected) and IgM (recent infected) antibodies (ID Screen RVF multispecies competition kit, RVF ELISA IgM capture IDvet, France). The samples were analysed in the Departmental Veterinary Laboratory of Mayotte when reagents and consumables were available. In 2018 and 2019, due to the lack of resources, the samples were dispatched to Réunion to be analysed by CIRAD. The results of RVF surveillance and the seroprevalence of IgG and IgM antibodies per month in Mayotte are presented in Table 5 and in the graph of the Figure 8 (data from COOPADEM). The animals in which IgM antibodies were identified did not present clinical signs.

**Table 4:** The results of the RVF sero-surveillance per month in cattle and small ruminants just before and after the recent RVF epidemic in Mayotte

| Month | IgG antibodies | | | IgM antibodies | | |
|-------|--------|----------|------------------------|--------|----------|------------------------|
| | Tested | Positive | Prevalence % (95% C.I.) | Tested | Positive | Prevalence % (95% C.I.) |
| Aug-18 | 48 | 6 | 12.5 (7.7–17.3) | NA | NA | NA |
| Sep-18 | 131 | 12 | 9.2 (6.6–11.7) | 1 | 0 | 0 |
| Oct-18 | 0 | NA | NA | NA | NA | NA |
| Nov-18 | 0 | NA | NA | NA | NA | NA |
| Dec-18 | 1 | 1 | 100 | 1 | 0 | 0 |
| Jan-19 | 0 | NA | NA | NA | NA | NA |
| Feb-19 | 443 | 66 | 14.9 (13.2–16.6) | 442 | 31 | 7.01 (5.8–8.2) |
| Mar-19 | 113 | 85 | 75.2 (71.2–79.3) | 144 | 19 | 13.2 (10.4–16.0) |
| Apr-19 | 0 | NA | NA | NA | NA | NA |
| May-19 | 177 | 91 | 51.4 (47.7–55.2) | 176 | 8 | 4.5 (3–6.1) |
| Jun-19 | 120 | 81 | 67.50 (63.22–71.78) | 122 | 3 | 2.46 (1.06–3.86) |
| Jul-19 | 177 | 108 | 61.02 (57.35–64.68) | 180 | 3 | 1.67 (0.71–2.62) |
| Aug-19 | 38 | 25 | 65.79 (58.09–73.49) | 12 | 0 | 0 |
| Sep-19 | 157 | 86 | 54.78 (50.80–58.75) | 15 | 1 | 6.67 (0.23–13.11) |
| Oct-19 | 6 | 6 | 100 (CI) | NA | NA | NA |
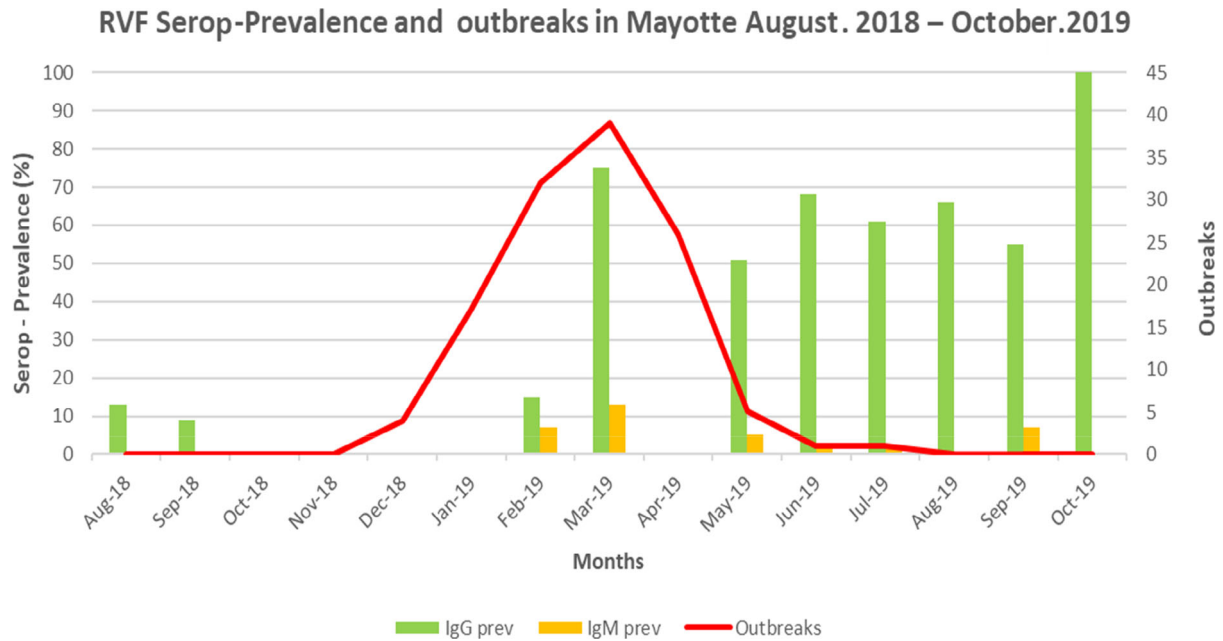
**Figure 8:** Seroprevalence of IgG and IgM RVF antibodies, per month in cattle and small ruminants in Mayotte just before and after the recent RVF epidemics in 2019

Moreover, a recent study on genetic sequencing (Vanhomwegen et al., submitted) has shown that RVFV circulating in the 2018–2019 epidemics is genetically different from the one in 2008 included in clade Kenya-1. The RVFV isolated in 2018–2019 is still part of the Eastern African lineages but considered as reintroduced strains: this supports the fact that the current epidemics is due to re-introduction rather than RVF persisting in the island.

**Key Points**

- The most probable way of RVF re-introduction into Mayotte was indicated by the epidemiological investigations, which revealed illegal imports of live animals (mainly goats) from the Union of the Comoros during the preparation for the celebration of Eid al Adha of 2018 (22 August 2018).
- Recent genetic study has shown that the RVFV in 2018–2019 epidemic is genetically different from the one in 2008, thus dealing with a RVFV re-introduction.
- The recent epidemic of RVF lasted 10 months (November 2018 to August 2019) counting 125 outbreaks in animals and 143 human cases.
- The seroprevalence of RVF was high across the whole island in 2019.
- According to the notifications to the ADNS, the RVF outbreaks in 2018–2019 were distributed all over the island.

### 3.1.7. RVF impact on animal health and farm production in Mayotte

*Morbidity*

According to the data submitted to the ADNS and the supplementary information from the French Authorities, during the recent epizootic 2018–2019, there were 166 cattle, 43 goats and 19 sheep infected. Based on the data in ADNS and using the animal populations of the census of 2010 for small ruminants and the latest update of 2017 for cattle, the morbidity in cattle was 0.81% while in small ruminants was 0.49% (1.89% for sheep and 0.37% for goats).

*Mortality*

From the data on the outbreaks of the recent RVF epidemic that were notified in the ADNS, only two deaths in cattle were reported. Based on this information and considering the whole Department of Mayotte as a unique epidemiological unit, the mortality in the total population of cattle (20,000 heads in 2017) can be estimated at 0.01% and case fatality rate equal to 1.20%.

### Abortions in animal populations

The number of abortions in Mayotte is usually monitored by the national brucellosis surveillance programme. Abortions in animals notified after the first human RVF case in 2018 were also tested for RVF by RT-PCR.

Data on the number of abortions reported by farmers in livestock have been available since 2012 at the Departmental laboratory (Table 6). On average, 36 abortions were reported each calendar year. In 2019, 199 abortions were reported until November, which is more than a fivefold increase (Figure 9). The increase can be attributed to RVF epidemics but also to the increase awareness (an awareness campaign was carried out) due to the recent RVF epidemic.

**Table 5:** Yearly number of reported abortions in livestock. Source: data from COOPADEM

| Year | Cattle | | | Goats | | | Sheep | | | Total tested |
|------|--------------|------------|----------------------|--------------|------------|-----------------|--------------|------------|-----------------|--------------|
| | No abortions | RVF tested | RVF positive in PCR | No abortions | RVF tested | RVF positive | No abortions | RVF tested | RVF positive | |
| 2012 | 9 | 0 | – | 1 | 0 | – | 1 | 0 | – | 11 |
| 2013 | 17 | 0 | – | 10 | 0 | – | 3 | 0 | – | 30 |
| 2014 | 37 | 0 | – | 10 | 0 | – | 0 | 0 | – | 47 |
| 2015 | 32 | 0 | – | 10 | 0 | – | 3 | 0 | – | 45 |
| 2016 | 38 | 0 | – | 5 | 0 | – | 0 | 0 | – | 43 |
| 2017 | 31 | 0 | – | 3 | 0 | – | 1 | 0 | – | 35 |
| 2018 | 32 | 4 | 4 | 3 | 0 | – | 2 | 0 | – | 37 |
| 2019 | 131 | 126 | 79 | 64 | 57 | 32 | 4 | 4 | 4 | 199 |
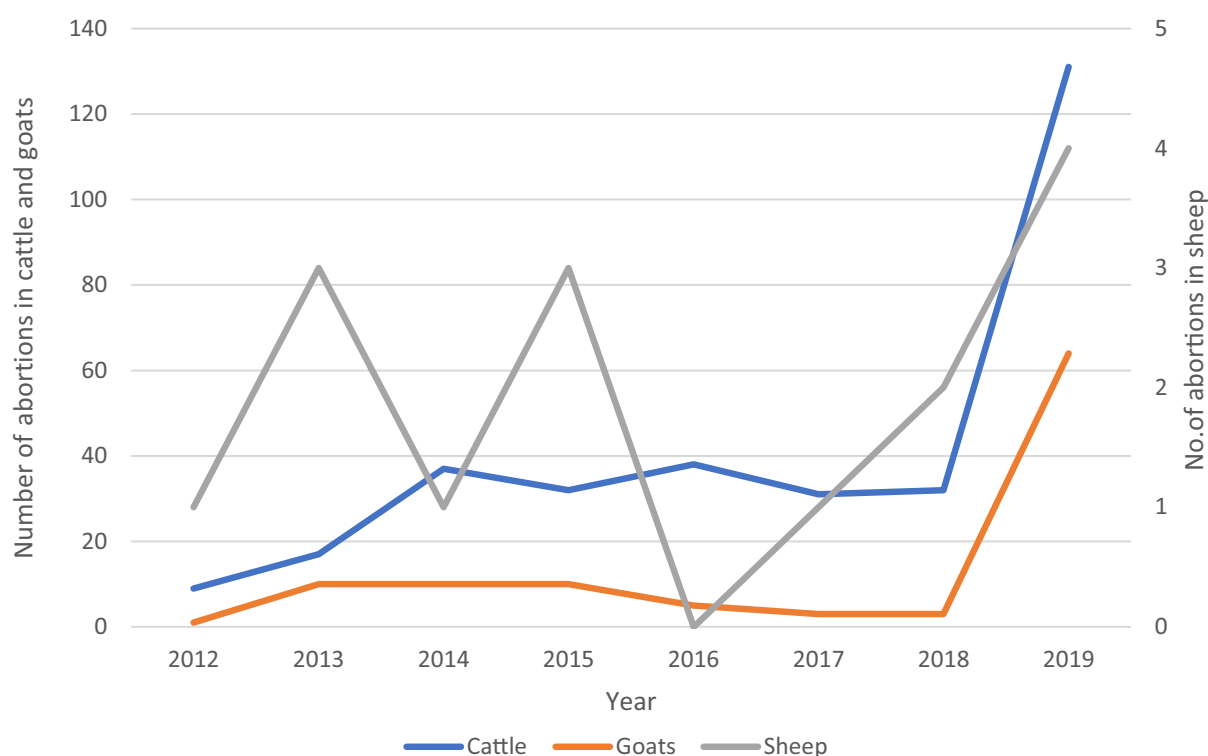


**Figure 9:** Number of abortions reported by the farmers per year in Mayotte in cattle, sheep and goats Source: data from COOPADEM

The number of abortions was:

- for cattle, it was 3.03 times higher than the previous year (2018) and 3.7 times higher compared to the mean of the previous 7 years.

- for goats, it was 20.33 times higher than the previous year (2018) and 10.6 times higher compared to the mean of the previous 7 years.
- for sheep, it was two times higher than the previous year (2018) and 2.58 times higher compared to the mean of the previous 7 years. In any case, the number of sheep (and reported abortions) in Mayotte is very small.

In Figure 10, the number of abortions and related PCR positivity is shown per each week in 2019. As expected, the PCR positives are in the first period of 2019, when the RVF outbreaks were also reported.
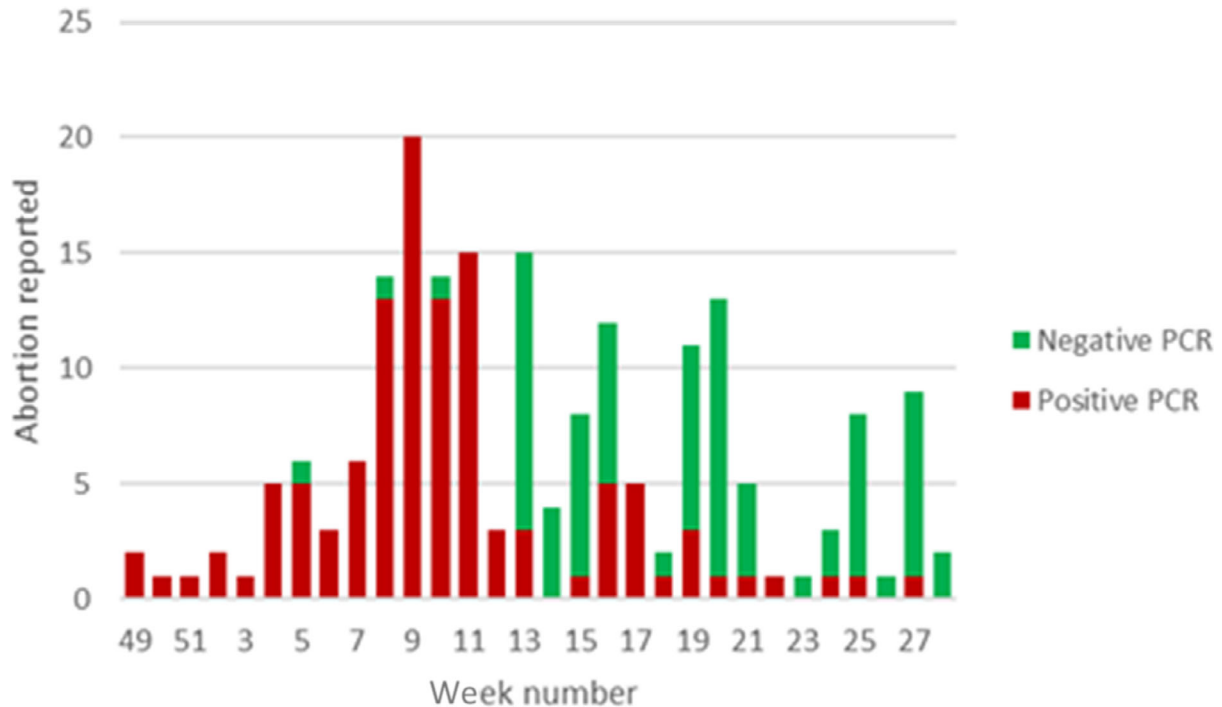


**Figure 10:** Number of reported abortions in livestock since the first human confirmed RVF case with RVF RT-PCR results. Week number 49 starts on 3 December 2018. Week number 28 in 2019 (8–14 July)

### Flu-like syndromes in cattle

The *flu-like syndrome (syndrome grippal or bavite)* is a pathological entity due to a set of different pathogens that has been put under surveillance in Mayotte by private veterinarians since 2011.

It is commonly used to describe several clinical signs mainly associated with the diseases that cause excessive salivation such as Bluetongue (BT), Epizootic Hemorrhagic Disease (EHD) and Bovine Ephemeral Fever (BEF) (known as 3-day sickness) (French Veterinary Authorities). Even without a specific aetiology, flu-like syndrome is the most frequent reason for a farmer to call a veterinarian in Mayotte (Dacheux et al., 2019; Dommergues et al., 2019).

Therefore, COOPADEM implemented a project to investigate the flu-like syndrome in cattle since 2012. The investigation relies on the notification of flu-like syndromes by the vets. From 2015 to 2018, vets reported nasal discharge in 88% of flu-like syndromes, anorexia in 80%, hyperthermia (above 39.5°C) in 43%, excessive salivation in 32%, lameness in 29% and decubitus in 22%.

Some clinical signs of RVF are very similar to those that are described under the flu-like syndrome. During the 2018–2019 epidemics, animals with flu-like syndromes were tested only for RVF. RVF was confirmed positive based either on PCR (Bird et al., 2007) or on RVF-positive IgM antibodies detection (RVF ELISA IgM capture, IDvet) by CIRAD, Réunion in 34 flu-like syndromes samples out of the 117 tested, in 2019 (Table 7 and Figure 11 for reported flu-like syndrome weekly in 2019). Techniques used to diagnose BTV, EHDV and BEFV are detailed in Dommergues et al. (2019) and Dacheux et al. (2019).

**Table 6:** Reported cases of flu-like syndromes in cattle, Mayotte, 2012–2019 including results of bluetongue (BTV), epizootic hemorrhagic disease virus (EHDV), bovine ephemeral fever (BEFV) and RVFV genome detection. NT, Not tested

| Year | Flu-like syndromes | Tested for BTV | Positive BTV no. (%) | Tested for EHDV | Positive EHDV no. (%) | Tested BEFV | Positive BEFV no. (%) | Tested RVFV | Positive RVFV no. (%) |
|---|---|---|---|---|---|---|---|---|---|
| 2012 | 15 | NT | NT | NT | NT | NT | NT | NT | NT |
| 2013 | 14 | NT | NT | NT | NT | NT | NT | NT | NT |
| 2014 | 35 | 15 | 3 (20) | 0 | NT | 0 | NT | 0 | NT |
| 2015 | 48 | 26 | 8 (30.7) | 26 | 8 (30.7) | 0 | NT | 5 | 0 |
| 2016 | 60 | 43 | 12 (27.9) | 43 | 21 (48.8) | 0 | NT | 0 | NT |
| 2017 | 19 | 17 | 4 (23.5) | 17 | 5 (29.4) | 10 | 4 (40) | 0 | NT |
| 2018 | 29 | 27 | 6 (22.2) | 27 | 8 (29.6) | 0 | NT | 1 | 1 |
| 2019 | 122 | 0 | NT | 0 | NT | 0 | NT | 117 | 34 (29) |
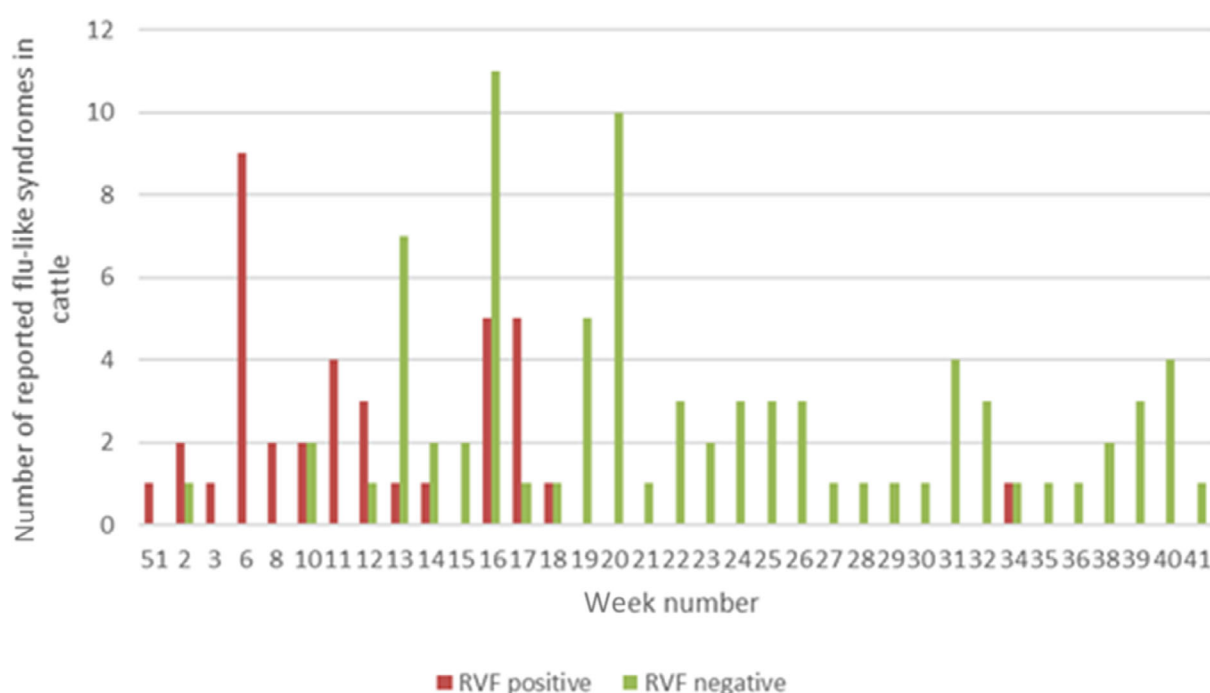


**Figure 11:** Weekly reported cases of flu-like syndromes in cattle in 2019

*Milk production case study in a dairy farm in Mayotte*

Data on milk production for one farm raising mainly crossbred cattle in Mayotte were used. Records on weekly milk production (litres per week) from 2015 to 2019 and the number of lactating cows each week were available.

This farm was affected by RVF in January 2019; RVFV was laboratory confirmed on 23 January 2019. Abortions were reported on 8th, 11th, 13th, 18th of February. In previous years, abortions were recorded in 2016 and 2017, but none in 2018. Flu-like syndrome was reported on 8 February in a different cow than the one which aborted. The previous cases of flu-like syndrome were reported in 2018. Lactating cows were blood sampled on 2 February and three out of five were IgM positive, while four out of five were IgG positive. All cattle present in the farm older than 1-year old were blood sampled on 18 June, 1 out of 38 was IgM positive, while 20 out of 38 were IgG positive (52.6%).

The aim of this analysis was to verify the possible variation of the milk production due to the RVF outbreak in early 2019. To this end, the rate of milk production in 2019 was compared with that observed during the reference period from 2015 to 2018. The Table 7 below summarises the median values of the weekly milk production in the years under study and the mean number of lactating animal present.

**Table 7:** Number of dairy cows (mean with CI 95%) and milk production rate (median with CI 95%)

| Year | No. dairy cows: mean [CI : 2.5%; 97.5%] | Milk production rate (L/cow/week): median [CI: 2.5%; 97.5%] |
|---|---|---|
| 2015 | 10 [8; 12] | 58.9 [40.4; 85.6] |
| 2016 | 10 [8; 11] | 57.3 [46.2; 67.8] |
| 2017 | 9 [8; 11] | 63.8 [47.2; 87] |
| 2018 | 9 [7; 11] | 59.6 [47.9; 80.3] |
| **2015–2018** | **10 [7; 11]** | **60.7 [45.9; 85.8]** |
| 2019 | 8 [6; 9] | 49.6 [29.1; 67.3] |

From Table 7, the production loss per cow per week in 2019 compared to the reference period of 2015–2018 is about 18% (60.7–49.6/60.7 × 100 = 18%).

A rough comparison of Figure 12 shows that the milk production in 2019 follows the same trend over the weeks compared to that in the reference period with weeks of low milk production at the beginning and ¾ of the year. However, the milk production from week 27 to week 41 in 2019 is below the lower bound of the reference period 2015–2018. The detailed milk production in 2015–2018 and in 2019 per each week with related number of dairy cows present each week in the farm studied and the deviation of milk production in 2019 from expected production in the reference period (2015–2018) shown per week is reported in Appendix E.
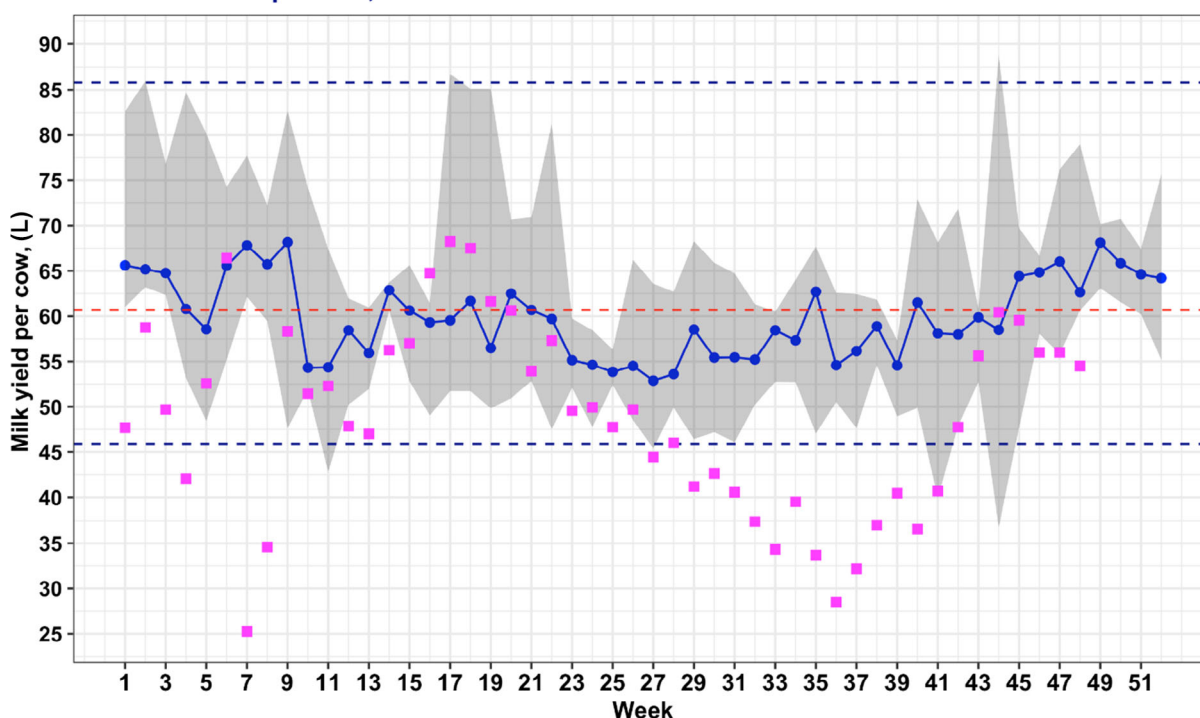


**Figure 12:** Weekly milk production during the reference period 2015–2018 and in 2019. For each week, the blue line represents the median and the grey shadow represents the range given by 2.5% and 97.5% percentiles for the reference period 2015–2018. Purple squares correspond to production rate in 2019. Horizontal dashed lines correspond to the median (red), 2.5% and 97.5% percentiles (blue) of the overall reference period 2015–2018

This finding could be related to the reproductive perturbations given by the RVFV infection, which can be various according to the period of pregnancy during which the mother is infected. Abortions can be expected when the infection occurs in the second half of the pregnancy. Foetal resorption can be observed in case of infection in the first stages of pregnancy. If we consider that the RVF epidemics in Mayotte had a peak between February and April 2019, then according to the pregnancy period in

which animals aborted, a milk drop can be expected from 2 to 4 months after the infection (animals aborted in mid-late stage of pregnancy) until almost 9 months for animals infected in the early stages of pregnancy.

Considering the value of milk reduction due to RVFV infection as assessed by the above study (18%), two possible estimates of the total economic losses in Mayotte in 2019 due to milk drop may be calculated:

- Considering that all animals present in the outbreaks (n = 1,060) experienced an effect on the milk production, the total loss would be equal to €1,221,120.
- Considering that only animals affected by the disease as notified in ADNS (n = 166) experienced an effect on the milk production, the total loss would be equal to €191,232.

**Key points:**

- The official mortality rate in RVF outbreaks, as notified to ADNS, was equal to 0.01%.
- In 2019, the number of abortions reported in ruminants was fivefold greater than years before. The majority of the aborted foetuses tested for RVF was positive by PCR.
- Weekly milk production rate, as recorded in one study dairy farm, showed in 2019 from week 29 to week 41 levels of production below the lower bound (2.5% percentile of the production), as calculated for 2015–2018 period and a general milk loss of 18%. In monetary terms, this corresponds to €191,232 lost, if only the affected animals as notified in ADNS (n = 166) are considered. Nevertheless, this result is affected by a large limitation given that it comes from extrapolating data from one single farm to the whole country.

## 3.2. Assessment of the probability of RVF overwintering in Mayotte

Mayotte system for RVFV circulation consists of animal hosts and mosquito vectors both present all year round. Because of weather conditions in Mayotte, the transmission of RVFV is likely to occur all year round in Mayotte, with differences in vector abundance linked to the rainy and dry season. Therefore, the overwintering question in Mayotte system is posed in terms of how long the RVFV infection can persist in such a context in the absence of any introduction. In the following section, the persistence mechanisms of RVF in Mayotte are assessed.

RVF can persist and overwinter either (i) in the host populations due to a low level circulation of the virus, or due to additional mechanisms, such as transplacental transmission or the permanence of live virus in organs or tissues of animal hosts (i.e. the establishment of a long-lasting carrier state) or (ii) in the vector population through vertical transmission.

### 3.2.1. Persistence in animal hosts

In the case of RVF, the permanence of the infection through transplacental transmission in animal hosts is considered rare and there is no known carrier state in mammals (EFSA, 2005). Also, the quite short viraemic period does not allow the virus to survive and be infectious for a prolonged time in animal hosts (EFSA AHAW Panel, 2020).

However, susceptible hosts, domestic or wild, can support a low-level virus circulation during the inter-epidemic periods, especially in the climatic conditions of Mayotte, which allow the presence of active mosquitoes all through the year.

The persistence of the infection in wild ruminant populations, like springbok, wildebeest and impala, with sporadic spill over into domestic species, had been observed in some countries of eastern and southern Africa (Evans et al., 2008; Olive et al., 2012; Rostal et al., 2017). However, the role of wild population in the maintenance of the infection during the inter-epizootic periods has been proved only in those African areas with relevant numbers of these animals, like the Kruger or the Etosha Parks in South Africa and Namibia, respectively (Dondona et al. 2011; Beechler et al., 2015). The absence of any significant wild ruminant population in Mayotte indicates the possibility of the persistence of the infection in the wild hosts as very unlikely.

Evidence of virus circulation at low levels in the domestic ruminant population was observed in West and East Africa (Sumaye et al., 2013; Rissmann et al., 2017). It is not possible to directly assess the importance of this persistence mechanism for Mayotte, although the progressive reduction of serological prevalence observed after the 2007–2008 epidemic, until 2018, is suggesting the absence of any detectable virus circulation in the domestic ruminants during the inter-epizootic period. This possible persistence mechanism, however, is analysed more in detail in the section 3.2.3.

### 3.2.2. RVF persistence through vectors

Information of main vector species was used to assess the possible spread of RVFV to other territories (i.e. Réunion and mainland France). We also assessed the main vector species present in Réunion to compare the similarity of vector species to those found in Mayotte.

#### 3.2.2.1. Vector abundance and activity in Mayotte and Réunion

In the following section, we summarised information for each of the potential vector species in Réunion and Mayotte Islands on mosquito presence, abundance, evidences for RVFV transmission, host preference and breeding sites.

The mosquito systematics follow Wilkerson et al., 2015 (genera taxa; subgenera is not included intentionally in the species name for simplification). For field or laboratory evidence of RVFV transmission, we followed the review of Linthicum et al. (2016), updated when new evidence was available from recent literature.

In general, 50 species of mosquitoes have been related to the transmission of or competence for RVFV either by field or laboratory evidences (see (Linthicum et al., 2016)). Most of the species belong to *Culex* and *Aedes* genera.

According to the assessment, there are 47 species of mosquitoes in Mayotte and 13 in Réunion belonging to five genera (*Aedes, Anopheles, Culex, Eretmapodites and Mansonia)* (Balenghien et al., 2013; Le Goff et al., 2014; AFSSA, 2008)) (Table 8).

For the abundance of vector species in Mayotte, we followed the information provided by Le Goff et al. (2014) and AFSSA (2008). In Le Goff et al. (2014), only immature stages were sampled in different habitats. Authors categorised abundance of the mosquito species of Mayotte according to its frequency of presence in the different breeding habitats sampled in the island. The so-called 'Principal Species' were those that were present in ≥ 20% of the habitat that were sampled. Those species were *Ae. aegypti*, *Ae. albopictus*, *An. gambiae* and *E. subsimplicies*. Only the three former ones have been so far related to RVFV transmission either by field or laboratory evidence, but it is known that *An. gambiae* play a minor role. For assessing the abundance in Réunion, we followed the information provided by AFSSA (2008) and Balenghien et al. (2013). In this case, *Ae. albopictus*, *Cx. pipiens*, *Cx. quinquefasciatus* are considered the most abundant species. In the case of *Ae. albopictus* and *Ae. aegypti*, current control methods after chikungunya and dengue epidemics in Réunion contributed to limiting its abundance.

#### Genus Aedes

**Ae. aegypti:** this species is found in Réunion and Mayotte. It is considered as one of the major vectors of RVFV since the virus has been isolated from field specimens in Kenya (1956) and Sudan (2007–2008) and in laboratory transmission assays. This species is found in the rural and urban environments and is highly anthropophilic. Due to current control programmes after epidemics of dengue and chikungunya in Réunion, it is considered to play a minor role in epizootic/epidemic episodes of RVFV since the current population of *Ae. aegypti* in Réunion is restricted to sylvatic areas (AFSSA, 2008). In Mayotte, it is considered a widespread and abundant species (AFSSA, 2008). The breeding sites in Mayotte for this species are diverse, such as holes in rocks, vegetal debris, large artificial containers and man-made containers. The species included in subgenus *Aedimorphus*, *Neomelaniconion* and *Stegomyia* are considered to be capable of transmitting RVFV by vertical transmission (Tantely et al., 2015; Linthicum et al., 2016), however, this phenomenon still requires confirmation for most of the species involved in RVFV transmission (Lumley et al., 2017). This species is frequently found in airplanes (Ibañez-Justicia et al., 2017a,b; Le Maitre and Chadee, 1983; Ammar et al., 2019). It is considered a mammalophilic and a highly anthropophilic species (REF).

**Ae. albopictus:** this species is present in Mayotte and Réunion. It is present in urban and rural areas, associated with small containers where females oviposit (Medlock et al., 2012). It is considered a potential vector for epizootic/epidemic episodes of RVFV according to the risk assessment conducted by AFSSA (2008) (EFSA, 2013); however, there is no data of the isolation of RVFV from adults collected at field level. The rate of infection for *Ae. albopictus* in laboratory was found to be between 19% and 37% (AFSSA, 2008). According to the survey conducted by CIRAD on mosquito species in Mayotte and Réunion,[28] it is present in the three locations of Mayotte (Figure 14) and widespread in

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[28] https://www.mosquito-maps-oi.fr/index.php/view/map/?repository=troi&project=projet

Réunion (Figure 15) where it was the major vector of Chikungunya (Delatte et al., 2008). It is considered a mammalophilic and a highly anthropophilic species (Delatte et al., 2010).

*Ae. circumluteolus:* This species is a vector for RVFV in East Africa and Southern Africa. According to AFFSA (2008), this species has a small presence in Mayotte and is absent in Réunion. This species belongs to the subgenus *Neomelaniconion* that includes several species of African origin and major vectors of RVFV such as *Ae*. (*Neo*.) *palpalis* s.l. and *Ae*. (*Neo*.) *macintoshi*. *Ae. circumluteolus* is considered a major vector for epizootic episodes in other RVFV endemic African countries, confirmed by field and laboratory evidence of its role in the transmission of RVFV. This species is known to breed in temporary grassland depressions (dambos) particularly after heavy rains in other parts of Africa (i.e. Kenya) (Davies et al., 1985). It is considered a mammalophilic species (Jupp and McIntosh, 1987).

*Ae. fowleri:* This species is present in Mayotte and Réunion. *Ae. fowleri* is included in the subgenus *Aedimorphus* that includes *Ae. dalzieli*, *Ae. ochraceus* and *Ae. vexans* that are field vectors of RVFV in mainland Africa. There are RVFV field isolations that incriminate this species as vector of the disease (Table 8). There is little information about this species in Mayotte according to Le Goff et al. (2014) and in Réunion is considered a very rare species (AFSSA, 2008). Its breeding is mainly restricted to water ponds and pools. It is not considered as an abundant species (Le Goff et al., 2014) and therefore, plays a minor role in epizootic/epidemic episodes. It is known to be a mammalophilic species (Fontenille et al., 1998).

### Genus *Anopheles:*

*An. coustani*: This species is present in Réunion and Mayotte. RVFV have been isolated from field specimens in Zimbabwe 1969; Kenya 1978; Sudan 2007 and Madagascar 2008, 2009 (Ratovonjato et al., 2010) (Linthicum et al., 2016) and from laboratory infections. Its abundance is considered medium–high. The breeding sites for this species in Mayotte are slow flowing water, holes in ground and marsh and swamp water (Le Goff et al., 2014). This species feed predominantly in mammals, including humans (Tantely et al., 2013a). Long-distance migration (i.e. active movement not just passive movement favoured by wind streams) has been attributed to *An. coustani* in the Sahel area (Huestis et al., 2019). From a study conducted in Sudan, one larva resulted positive to RVFV (Seufi and Galal, 2010); however, its role in maintenance of the virus is uncertain.

*An. gambiae*: This species is present in Mayotte but not in Réunion. There are few references that link this species with the transmission of RVFV, basically one isolation of the virus from field specimens in Sudan (Seufi and Galal, 2010; Linthicum et al., 2016), and it is not considered a potential vector of RVFV in Mayotte (AFSSA, 2008). RVFV has been isolated from larvae and males of this species, but its possible role in the maintenance of the virus is unclear. This species has been found in ships and airplanes and has colonised other areas apart from Africa, such as Brazil (Tatem et al., 2006; AFSSA, 2008). Preferred hosts of this species are mammals, including humans, and it is one of the major vectors of malaria in Africa.

### Genus *Culex*

*Cx. pipiens:* this species is present in Mayotte and Réunion and according to Balenghien et al. (2013) is located at North latitudes of Mayotte. It is a species known to be very abundant in urban and rural areas (it is one of the most important vectors for transmission to humans, including urban/peri-urban areas) and therefore is commonly related to RVFV epizootic episodes, e.g. in Egypt (Meegan et al., 1980; Turell et al., 1996). The role of *Cx. pipiens* in the transmission of RVFV has been confirmed both in the field and laboratory (Table 8). *Culex pipiens* is considered to include two ecoforms *Cx. pipiens* form *pipiens* considered to be highly ornithophilic, and *Cx. pipiens* form *molestus* considered to be mammalophilic and ornithophilic (Brugman et al., 2018). Recently, it was showed that the two forms of *Cx. pipiens* and even the hybrid forms are susceptible to RFVF infection (Brustolin et al., 2017). Differently to *Aedes* species, its contribution for the overwintering of the virus is considered to be nil due to the incapacity of eggs to stand long periods of desiccation. This species breeds in a wide type of habitats, from artificial ponds to water flooded areas, including natural and agriculture ones (Becker and Weitzel, 2012).

*Cx. quinquefasciatus:* this species is present in Réunion and Mayotte. According to Balenghien et al. (2013) is located at the South latitudes of Mayotte. It is mainly located in urban and peri-urban habitats in high abundance (AFSSA, 2008) and it is also considered as the principal vector of Bancroft filaria on Mayotte (Le Goff et al., 2014). There is field and laboratory evidence (Moutailler et al., 2007) of RVFV transmission by this species, e.g. in Madagascar in 1979 (Clerc et al., 1980); however, it is

considered to have a moderate vector competence for RVFV. Due to its widespread distribution and abundance, it is considered a major vector of epizooties of RVFV. This species is also one of the most frequently found in planes coming from Africa (AFSSA, 2008). *Cx. quinquefasciatus* is an opportunistic blood feeder and was one of the most abundant species collected on humans and sheep (Balenghien et al., 2013).

**Cx. antennatus:** this species is present in Mayotte but not in Réunion. It has been related to RFVF transmission with both field and laboratory evidence and it is considered a very susceptible species to RVFV (Hanafi et al., 2011). *Cx. antennatus* is known to be a vector species of RVFV in Madagascar (Ratovonjato et al., 2010) and in general when present, it is a very abundant and widely distributed mosquito (Hanafi et al., 2011). It is considered an anthropophilic mosquito (Gad et al., 1995), and according to Balenghien et al. (2013), it is abundant in mammal host-baited traps in Mayotte; therefore, it is considered a bridge species between animals and humans. Breeding habitats of this species are flooded areas, rice fields and irrigation channels, and tolerant of brackish conditions. Is also considered a frequent species in airplanes (Ibañez-Justicia et al., 2017a,b).

**Cx. bitaeniorhynchus:** this species is only present in Mayotte in low abundance and is absent from Réunion. It has been related to RVFV field transmission in Kenya (Linthicum et al., 2016). It is a mammalophilic mosquito including feeding on humans (Sahu et al., 2019). This species breeds in water bodies, such as ponds and pits.

**Cx. simpsoni:** this species is found in Mayotte but not in Réunion. RVFV was isolated from a pool of this species and others in Madagascar in 1979 and Kenya in 1982 (Balenghien et al., 2013; Linthicum et al., 2016). According to Le Goff et al. (2014), this species breeds in water ponds, pools, marsh and swamp water in Mayotte.

**Cx. tritaeniorhynchus:** this species is found in Réunion but not in Mayotte. It is an abundant species, e.g. in Madagascar. This species has been related to field transmission of RVFV in Madagascar (Jean Jose Nepomichene et al., 2015) and the Arabic peninsula, as well as to laboratory transmission (Linthicum et al., 2016). *Cx. tritaeniorhynchus* shows feeding preference for mammals, including humans and can be considered one of the major vectors due to its abundance (Tantely et al., 2015). It is also a mosquito species that has been intercepted in airplanes (Haseyama et al., 2007). In Mayotte, this species is known to breed in marsh and swamp water.

**Cx. univittatus:** this species is found in Réunion but not in Mayotte. The transmission of RVFV for this species has been shown from field-collected specimens, for example in Madagascar (Balenghien et al., 2013), and Kenya (Linthicum et al., 2016; Sang et al., 2017) and it is considered as a secondary vector (Tantely et al., 2015) due to its medium–high abundance (Tantely et al., 2013b). Rice fields are the breeding habitat for this species (Nicolas et al., 2014). Its feeding preferences include mammals, humans and birds.

## Genus *Eretmapodites*

**E. quinquevittatus:** this species is reported in Mayotte but not in Réunion. There is field evidence of transmission of RVFV in South Africa in 1971 and in Kenya in 1981–1984 (Linthicum et al., 2016). Laboratory evidence showed that this species develops low to moderate rates of infection of RVFV. It is a mammalophilic species that was found to be abundant in mosquito collections made by using humans and sheep baited traps (Balenghien et al., 2013). Breeding habitats for this species in Mayotte are snail shells and disposed solid waste (Le Goff et al., 2014).

## Genus *Mansonia*

**M. uniformis:** this species is present in Mayotte but not in Réunion. RVFV has been isolated from specimens and/or pools in Kenya (1997–1998, 2006), Madagascar (1979), Mauritania (1987–1988 and 2003), Uganda (1959), Senegal (2003) (Linthicum et al., 2016). There is no experimental information for this species. It is considered abundant in Madagascar showing preference for mammals, including humans and being a potential vector of RVFV (Tantely et al., 2015). The breeding habitats for this species are extensive swamps but differ from other mosquito species since the larvae are generally submerged and anchored by the siphon to aquatic plant roots from where they obtain oxygen (Appleton and Sharp, 1985; Le Goff et al., 2014).
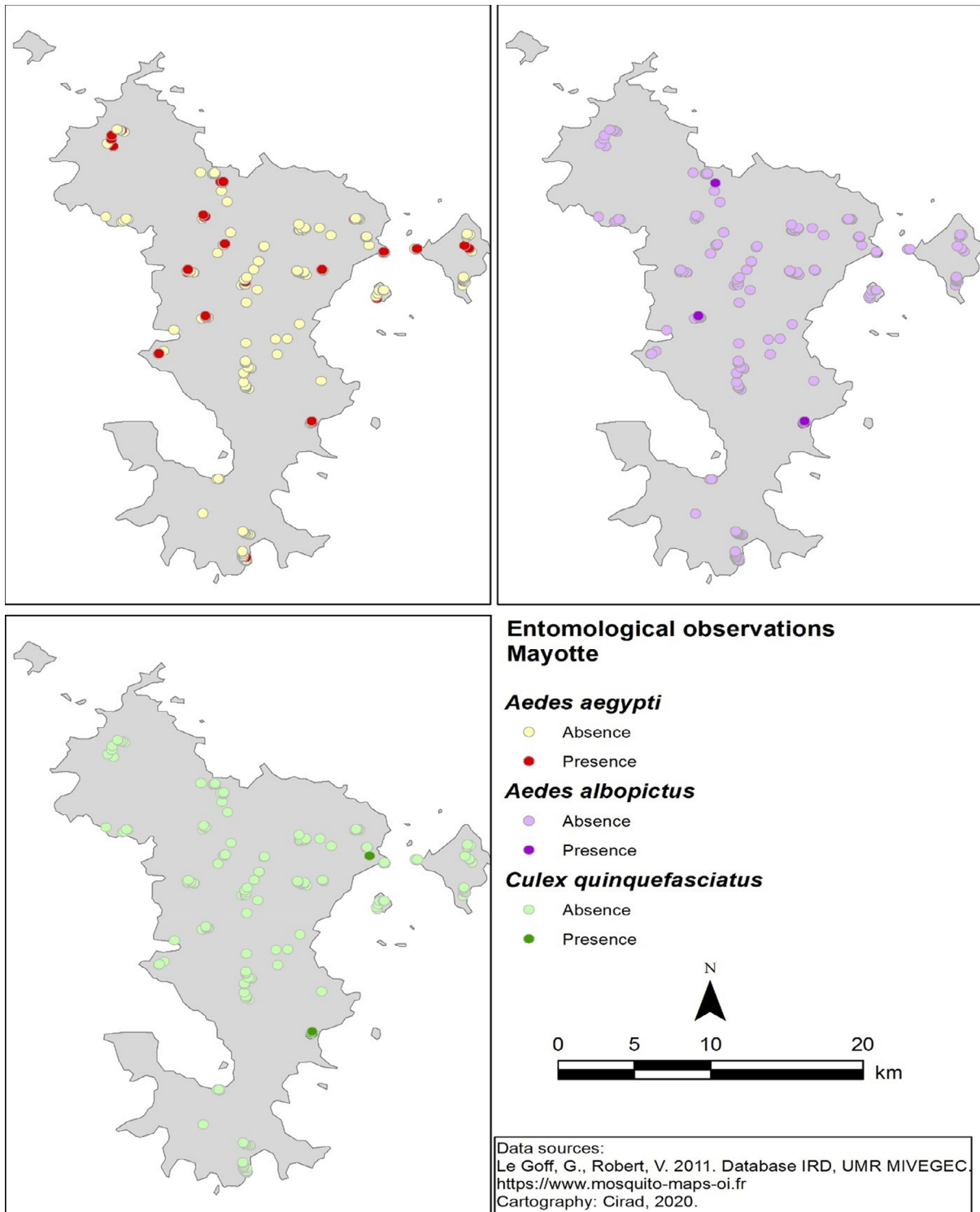
**Figure 13:** Spatial distribution of *Aedes aegypt*i and *Culex quinquefasciatus* in Mayotte.
Source https://www.mosquito-maps-oi.fr
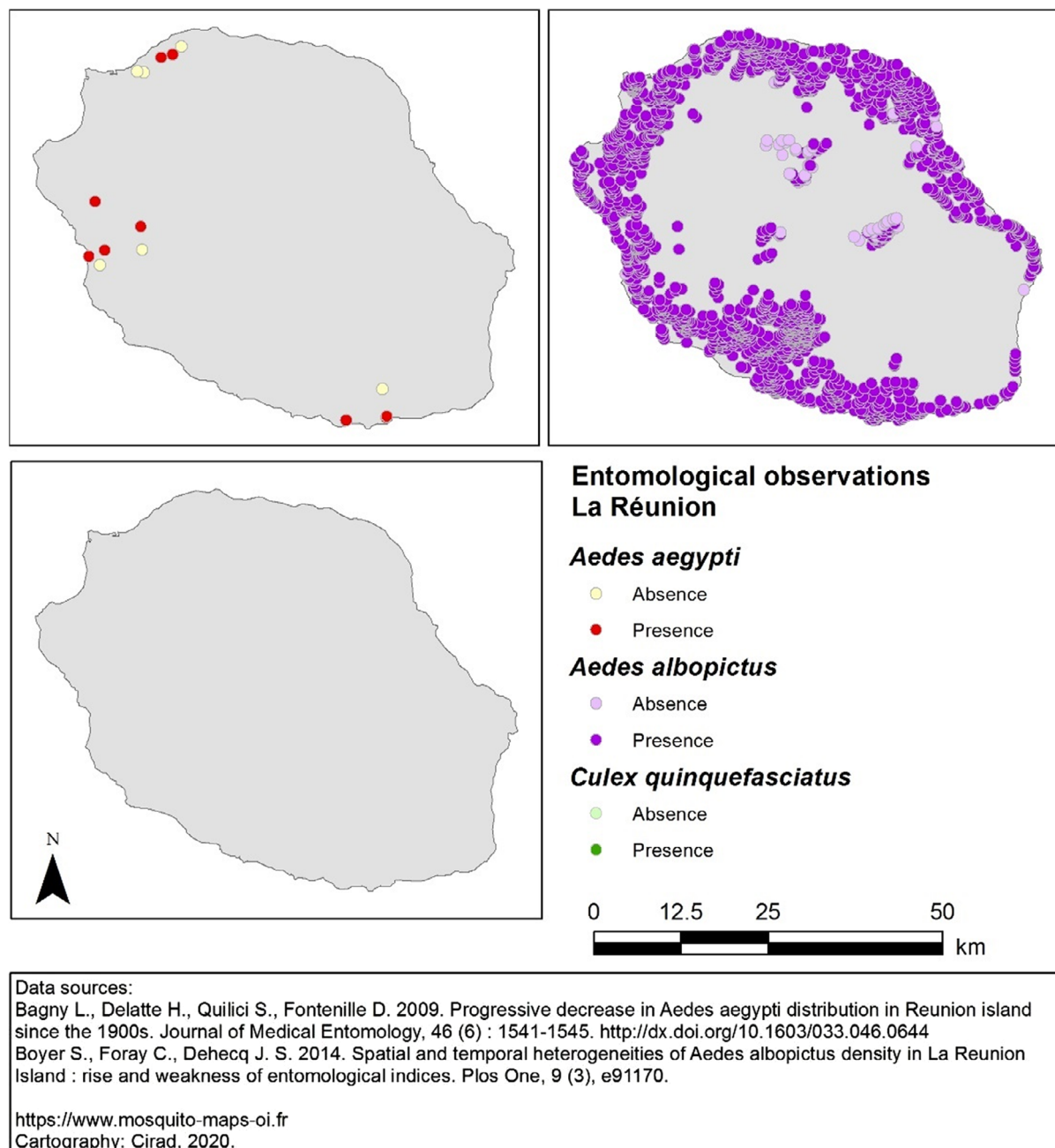
**Figure 14:** Spatial distribution of *Aedes aegypti* and *albopictus* in Réunion. Source https://www.mosquito-maps-oi.fr

**Table 8:** Species of mosquitoes present in Mayotte and Réunion

|  | **Mayotte** | **Réunion** | **RVFV Vector** |
|---|---|---|---|
| *Aedes* |  |  |  |
| *Ae. aegypti* | + | + | FI, LI, LT, MT |
| *Ae. albocephalus* | + |  |  |
| *Ae. albopictus* | + | + | LI, LT |
| *Ae. bromeliae* | + |  |  |
| *Ae. cartroni* | + |  |  |
| *Ae. circumluteolus* | + |  | FI, LI |
| *Ae. dufouri* |  | + |  |

| | Mayotte | Réunion | RVFV Vector |
|---|---|---|---|
| *Ae. fowleri* | + | + | FI |
| *Ae. monetus* | + | | |
| *Ae. pia* | | | |
| *Ae. simpsoni* | + | | |
| *Ae. vittatus* | + | | |
| Anopheles | | | |
| *An. arabiensis* | | + | |
| *An. comorensis* | + | | |
| *An. coustani* | + | + | FI, LI |
| *An. funestus* | + | | |
| *An. gambiae* | + | | FI |
| *An. maculipalpis* | + | | |
| *An. merus* | + | | |
| *An. mascarensis* | + | | |
| *An. pretoriensis* | + | | |
| Culex | | | |
| *Cx. antennatus* | + | | FI, LI |
| *Cx. bitaeniorhynchus* | + | | FI |
| *Cx. carleti* | + | | |
| *Cx. cinerellus* | + | | |
| *Cx. comorensis* | + | | |
| *Cx. decens* | + | | |
| *Cx. horridus* | + | | |
| *Cx. insignis* | | + | |
| *Cx. pipiens* | + | + | FI, LI, LT, MT |
| *Cx. quinquefasciatus* | + | + | FI, LT |
| *Cx. nebulosus* | + | | |
| *Cx. simpsoni* | + | | FI |
| *Cx. tritaeniorhynchus* | | + | FI, LI |
| *Cx. univittatus* | | + | FI, LT |
| *Cx. wiggleworthi* | + | | |
| Eretmapodites | | | |
| *E. quinquevittatus* | + | | FI, LI, LT |
| *E. subsimplicipes* | + | | |
| Ficalbia | | | |
| *F. grjebinei* | + | | |
| Lutzia | | | |
| *L. tigripes* | + | + | |
| Mansonia | | | |
| *M. uniformis* | + | | FI, LI |
| Mimomyia | | | |
| *M. grjebinei* | + | | |
| Orthopodomyia | | | |
| *O. arboricollis* | | + | |
| *O. comorensis* | + | | |
| *O. joyoni* | + | | |
| Uranotaenia | | | |
| *U. alboabdominalis* | + | | |
| *U. andavakae* | + | | |

| | Mayotte | Réunion | RVFV Vector |
|---|---|---|---|
| *U. comorensis* | + | | |
| *U. douceti* | + | | |
| *U. laffosseae* | + | | |
| *U. mayottensis* | + | | |
| *U. pandani* | + | | |
| *Zavortinkius* | | | |
| *Z. brunhesi* | + | | |
| *Z. monetus* | + | | |

It is indicated whether RVFV was isolated in any country from field collected specimens (FI); infected in laboratory conditions (LI); transmitted in laboratory conditions (LT) and transmitted mechanically (MT). Adapted from AFFSA (2008), Le Goff et al. (2014), Linthicum et al. (2016) and Brustolin et al. (2017). Subgenus is not included. Genus and Species are listed in alphabetical order without considering Subgenus.

**Key messages:**

- RVFV vectors are abundant in Mayotte and Réunion and adults can survive all year round.
- There are 47 spp. of mosquitoes recorded in Mayotte, from which 13 are considered vectors or potential vectors.
- There are 13 spp. of mosquitoes recorded in Réunion, from which 8 are considered vectors or potential vector of RVFV.
- There are no studies conducted in Mayotte and Réunion about field isolation of RVFV from potential vector species.
- The most important species for potential RVFV transmission in Mayotte and Réunion according to its wide distribution, abundance and vector competence for RVFV are *Cx. antennatus*, *Cx. pipiens*, *Cx. quinquefasciatus*, *Cx. tritaeniorhynchus*, *An. coustani* and *E. quinquevittatus*.
- There is evidence that current control measures against *Ae. aegypti* and *Ae. albopictus* in Réunion limit their population and as a consequence, its role as vectors of RVFV.

### 3.2.2.2. Persistence of RVFV in the vectors via vertical transmission

Vertical transmission is defined as the transmission of an arbovirus from an infected female mosquito to its offspring (Lequime and Lambrechts, 2014). The most effective mechanism of vertical transmission is transovarial transmission (TOT) where the germinal tissues of the female mosquito are infected by the virus, and therefore, the laid eggs contain virus particles that can viably persist. The next generation of adults will be infective since the virus persisted during the whole development from egg, larva, pupa and finally adult. Therefore, vertical transmission is a natural mechanism of overwintering that allows persistence of the virus from one year to another, when vectors or hosts are absent or in low abundance. Vertical transmission is present in many public health significance arbovirus (i.e. Dengue); however, prevalence is usually low (< 0.1%) and cannot be considered a common phenomenon (Lequime and Lambrechts, 2014), in addition to that, negative results of vertical transmission are in general under reported and this can drive a general overestimation of vertical transmission.

Some species of mosquitoes overwinter as adults, such as *Culex* spp. and *Anopheles* spp., while for other species, as for example *Aedes* spp., the diapause eggs are the stage that survives winters or harsh periods such as drought. The diapause eggs can allow the persistence of pathogens through vertical transmission. This phenomenon depends on the pathogen and the vector species, e.g. Chikungunya virus is considered to be poorly transmitted to eggs and available data about vertical transmission are variable, including positive and negative detection of vertical transmission in eggs (Mourya, 1987; Hailin et al., 1993; Vazeille et al., 2009; Bellini et al., 2012; Delatte et al., 2008a). Dengue virus is known to be vertically transmitted, but its role for the persistence of the virus at local and regional level is also considered to be less important than asymptomatic and viraemic humans (Grunnill and Boots, 2016). In addition, species in the *Culex* genus are associated with significantly lower rates of vertical transmission compared to species of the *Aedes* genus (Lequime et al., 2016). The pathogenic effect of the virus in the females and/or eggs is considered as a possible explanation of the difference of vertical transmission among insect-transmitted viruses (Bellini et al., 2012).

It is acknowledged that RVFV-infected eggs can resist for several years until favourable environmental conditions, usually related to heavy rains, allow hatching. Therefore, Aedine species

start RVFV endemic transmission among mammal hosts (including domestic and wild fauna). Epidemics occur when *Culex* spp. proliferate in high density in the same flood areas and increase transmission of RVFV to animals and/or humans (Linthicum et al., 2016).

Up to now, vertical transmission of RVFV has been reported only three times: from Kenya in *Ae. mcintoshi* (Linthicum et al., 1985, originally reported as *Ae. lineatopennis*) from a total of 31,844 pooled field collected specimens. It was also reported in the same species from five specimens after inoculating RVFV intrathoracically. Finally, in Sudan, RVFV was detected in males of *Aedes vexans* and *Culex quinquefasciatus* by RT-PCR but not virus isolation (Mohamed et al., 2013) from a total of 398 and 1,200 specimens, respectively (Table 9). From the above-mentioned species, only *Cx. quinquefasciatus* is present in Mayotte and Réunion; however, *Culex* spp. are not considered the best candidates for vertical transmission of RVFV since their eggs are not able to resist long periods of desiccation.

From the potential vector species of RVFV present in Mayotte and Réunion from the genera *Aedes*, *Culex* and *Eretmapodites* (Table 9), vertical transmission of RVFV has not been detected in any of those species when present in other RVFV endemic countries in Africa (i.e. Sudan, Kenya, South Africa) (Table 9). Detection of vertical transmission was negative either from 4,762 field collected specimens (including males, eggs, larvae and pupae) and from 7,186 specimens used for laboratory trials (Lumley et al., 2017) in those countries for the above-mentioned RVFV vector genera.

Sumaye et al. (2019) used the field values of vertical transmission of *Ae. mcintoshi* obtained from Linthicum et al., 1985 in Kenya (i.e. range of vertical transmission 0–8.5%) to model the transmission dynamics of RVF with data collected in the Kilombero Valley in Tanzania. Simulations indicated that the vertical transmission role of two vector species, *Ae. aegypti* and *Ae. mcintoshi*, was not sufficient to explain inter-epidemic transmission of RVFV in the area. Authors suggested that the role of vertical transmission is underestimated considering the only reference data available.

Based on the available evidence, it is not possible to confirm the role of the potential species of Mayotte and Réunion for the persistence of RVFV from one year to another. There is a lack of data of the possible vertical transmission of RVFV mosquito vector species in Mayotte and Réunion. Furthermore, none of the species of vectors present in the islands and also in the African continent have shown vertical transmission, despite the number of specimens from field or laboratory trials analysed. The majority of the main potential vectors species identified in Mayotte belong to the genus *Culex* (see Section 3.2.2.1), from which vertical transmission of RVFV is assumed to be very low (if present), since *Culex* spp. eggs are not able to withstand long periods of drought. In addition, transmission dynamics models also confirmed that the limited evidence available about vertical transmission of RVFV in mosquitoes does not support an inter-epidemic transmission with the prevalence of vertical transmission known from countries such as Kenya. Therefore, it can be concluded that if present, the role on persistence of RVFV in Mayotte and Réunion due to vertical transmission seems to be of minor relevance compared to other pathways of re-introduction, such as animal movement from RFVF-infected areas. However, there is high uncertainty since analysis of vertical transmission in large numbers of some of the major vector species (i.e. *Aedes* spp.) remains mostly unexplored in Africa and the territories of concern for this opinion.

**Table 9:** Species of mosquito vectors of RVFV present in Mayotte and Réunion and for which vertical transmission (transovarial transmission – TOT) has been tested, in RVFV endemic countries either in specimens collected from the field or in lab (The technique used for virus detection is also indicated: AM: orally infected animal model, PA: plaque assay; RT-PCR: real-time polymerase chain reaction. Information extracted from Lumley et al., 2017)

|  | Countries | # Field specimens tested | # Lab specimens tested | Technique and (+)/(−) to RVFV |
|---|---|---|---|---|
| *Aedes* |  |  |  |  |
| *Ae. aegypti* | Kenya | 745 |  | AM (−) |
|  | Kenya |  | 759 | PA (−) |
|  | South Africa |  | 2,811 | AM (−) |
| *Ae. fowleri* | Senegal |  | 721 | AM (−), PA (−) |
| *Total* |  | 745 | 4,291 |  |

| | Countries | # Field specimens tested | # Lab specimens tested | Technique and (+)/(−) to RVFV |
|---|---|---|---|---|
| *Culex* | | | | |
| *Cx. antennatus* | Kenya | | 112 | AM (−) |
| *Cx. pipiens* | Kenya | 114 | | AM (−) |
| *Cx. quinquefasciatus* | Sudan | 1,200 | | RT-PCR (+) |
| *Cx. univittatus* | Kenya | 44 | | AM (−) |
| | South Africa | | > 218 | AM (−) |
| *Total* | | 1,358 | 330 | |
| *Eretmapodites* | | | | |
| *E. quinquevittatus* | Kenya | 2,659 | | AM (−) |
| | South Africa | | 1,280 | AM (−) |
| | South Africa | | 1,285 | PA (−) |
| *Total* | | 2,659 | 2,565 | |

### 3.2.3. Epidemiological models explaining RVF persistence in Mayotte

Two modelling studies have explored the persistence of Rift Valley fever virus (RVFV) in Mayotte (Cavalerie et al., 2015; Metras et al., 2017). Here, persistence is defined as the virus being present over time in any hosts or vectors. Both studies considered Mayotte to comprise a single livestock population, so they did not distinguish between cattle, sheep and goats in terms of RVFV transmission nor allow for the spatial location of hosts (i.e. the island was treated as a homogeneously mixed population of hosts and vectors).

The first study used a stochastic compartment model to describe the dynamics of RVF in livestock and in the aquatic larval and adult stages of the mosquito vectors (treating all mosquito species as a single population) (Cavalerie et al., 2015). Seasonality in vector abundance was incorporated using a sinusoidal function for adult emergence with a period of 1 year to capture the wet and dry seasons on Mayotte. The model was parameterised primarily using estimates from the published literature. However, the probabilities of transmission from host to vector, of transmission from vector to host and of vertical transmission in the vector were calculated based on the estimated values for potential RVFV vector species weighted according to their relative abundance in mosquito catches at five farms on Mayotte. In addition, the transmission rates were fine-tuned by fitting the model to IgG prevalence data. The results of the model indicated that the probability of RVFV persisting (defined as virus being present in any livestock host or larval or adult vector) in Mayotte for 1 year was 25.5%, for 5 years was 9.5% and for 9 years (the maximum simulated) was 2.1% (see Figure 8 in Cavalerie et al. (2015)).

The second study used an age-structured stochastic compartment model to describe the dynamics of RVF in livestock (Metras et al., 2017). The normalised difference vegetation index (NDVI) was used as a proxy for the vector dynamics, with the transmission rate between hosts being a function of NDVI. The model also explicitly included the introduction of RVFV to Mayotte through importation of infected animals. Parameters related to host demography were computed from data on the livestock population in Mayotte, while those related to RVFV transmission were estimated by fitting the model to age-specific IgG prevalence data. The results of their model suggest that RVF cannot be sustained in the ruminant population in Mayotte and the disease dies out by 2010 in almost all replicates once imports stop in 2009 (see Figure 4 in Metras et al. (2017)). More precisely, once importation of RVFV-infected animals stopped, the virus was predicted to persist (defined as virus being present in any hosts) until 2016 in only 0.26% of simulations. This may be because of natural fade out in a relatively small population, but neither study explicitly shows this.

The two studies came to contrasting conclusions about the probability of RVFV persisting in Mayotte. Cavalerie et al. (2015) concluded that their results supported the hypothesis (proposed by Lernout et al., 2013) that RVF is endemic in Mayotte. It is worth noting, however, that the authors predicted that around 75% of epidemics would last less than 1 year and 90% of epidemics would last less than 5 years. By contrast, Metras et al. (2017) concluded that there was a very low probability of RVFV persisting in Mayotte, if it is treated as a closed population (i.e. there are no imports of infected livestock or vectors). The key difference between the two studies is that Cavalerie et al. (2015) assumed there was vertical transmission of RVFV in mosquitoes, while Metras et al. (2017) did not

include this route of transmission in their model. This most likely accounts for the probability of persistence over 5 years being over 30 times higher (9.5% vs 0.26%) in Cavalerie et al. (2015) compared to Metras et al. (2017).

Sources of the uncertainty related to vector role in the maintenance of the RVFV in Mayotte and Réunion were lack of data and possible overestimation of current evidences related to vertical transmission.

**Key Points:**

- In summary, both studies suggest that the probability of RVFV persisting in Mayotte for 5 or more years is < 10% but could be much lower if vertical transmission does not occur.
- Different sources of uncertainty may affect the models developed by Cavalerie et al. (2015) and Metras et al. (2017). According to the sensitivity analyses performed on both models, predictions are most sensitive to the biotic and abiotic factors influencing the transmission rate. In particular, those parameters influencing vector abundance and competence are the most difficult to estimate from field data compared with laboratory trials. On the other hand, both models were calibrated using serological data to better fit the model outcomes to the situation in Mayotte.
- Persistence of RVFV by vertical transmission in Mayotte and Réunion appears to be of minor relevance compared to other pathways of re-introduction (i.e. animal movement) since in general it is considered a rare phenomenon with low prevalence in the mosquito population. However, there is a high uncertainty since there is limited information about the vertical transmission of some of the major species of vector species of RVFV in Mayotte and Réunion, as well as the lack of evidences in other RVF endemic countries.

## 3.3. Assessment of the risk of RVF spread from Mayotte to other areas including other French departments in the Indian Ocean or to continental France (TOR 2.1)

In this section, the risk of spread of RVF from Mayotte to other countries is assessed. The target countries and possible pathways are described and selected, and only for those ones the assessment of risk of spread is carried out.

### 3.3.1. Target countries of RVF spread from Mayotte

Among the target countries for possible RVF spread from Mayotte, Metropolitan France and Réunion are considered, the latter as the only French department in the area, which was never affected by RVF. Both France and Réunion are also connected by direct flights with Mayotte.

Other countries neighbouring Mayotte, i.e. Tanzania, Kenya, Mozambique, Comoros, Madagascar and Mauritius, are not French departments; moreover, they are all affected by RVF and are considered RVF endemic (apart from Mauritius). These countries have to be considered as sources of infection for Mayotte rather than target countries for spread from Mayotte, and thus, an assessment of the latter aspect is not relevant. The two introductions (2007/2008 and 2018/2019) of RVFV to Mayotte originated from mainland East Africa (in Tanzania of animals coming from the surrounding countries) through Comoros islands and then to Mayotte. In Madagascar, RVFV was introduced in 2008–2009 through ruminant trade, and subsequent movement of cattle between trade hubs caused its long-distance spread within the country, from Comoros islands. Informal surveys conducted in 2009 and 2010 in the main Comoros harbours and in the northwest of Madagascar (Mahajanga and Antsiranana) revealed the frequent presence of cattle and small ruminants on board freighters and botry (dhows) travelling from the Comoros Islands to Madagascar and from port to port (Lancelot et al., 2017). Moreover, there is no direct flight or sea connection from Mayotte to Mauritius.
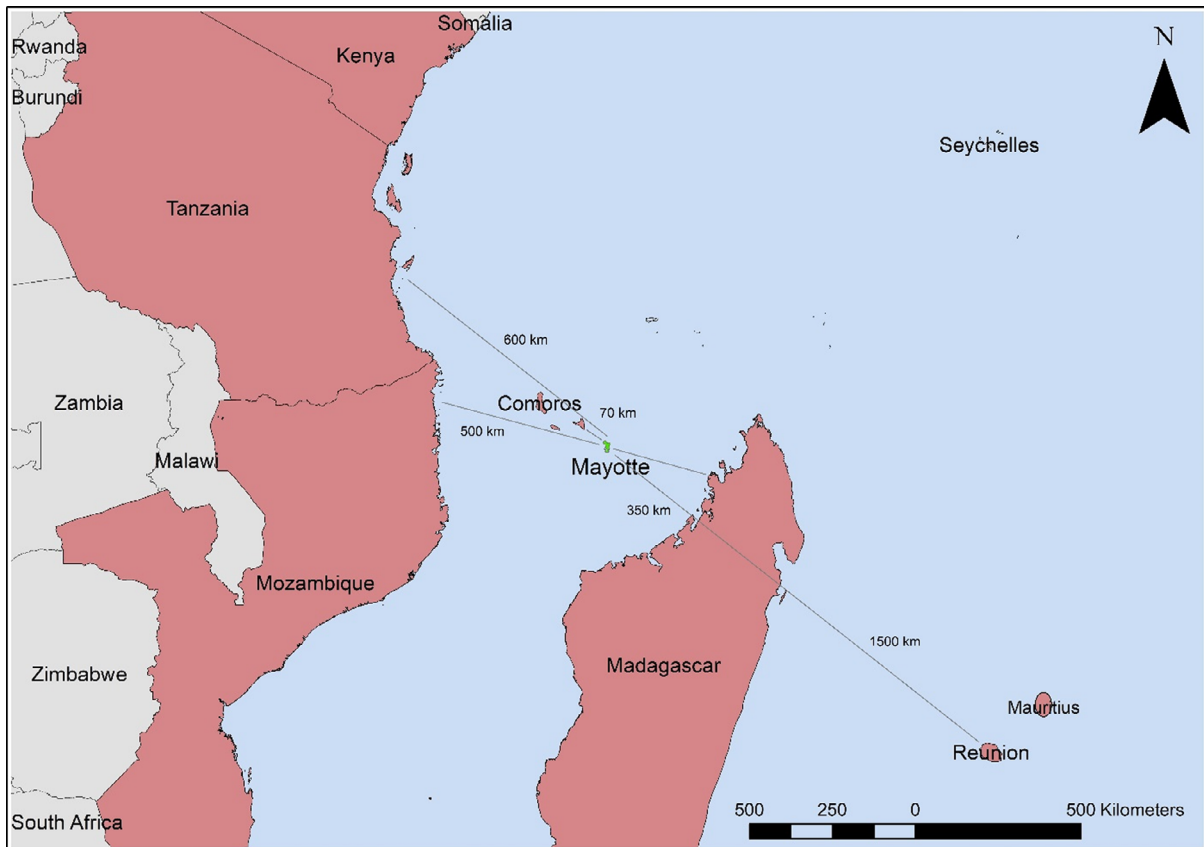
**Figure 15:** Geographical position of Mayotte and distance from the main neighbouring countries

### 3.3.2. Possible pathways of RVF spread from Mayotte

The possible pathway of spread of RVF from Mayotte to other areas including other French departments in the Indian Ocean or in continental France are: i) live animals illegally or legally transported, ii) vectors actively or passively transported through wind currents, flights, boats or ship and iii) non-processed animal products like raw milk and meat legally or illegally transported iv) human travellers.

#### 3.3.2.1. Live Animals and Animal Products

According to the information provided by the French Veterinary Authorities, there is no commercial trade of animals or animal products from Mayotte to other French departments or to European countries. Mayotte is an importer country of live ruminants, so the trade driver is to import live animals to Mayotte, this may lead also to illegal movement towards Mayotte and not from Mayotte. Furthermore, the high price of cattle in Mayotte is a disincentive for exports (see Section 3.1.5).

Therefore, this pathway of spread of RVF from Mayotte through live animals is not plausible and therefore excluded from the assessment.

Consumption of fresh animal products such as raw milk or raw fresh meat can be a way to transmit RVFV to humans (LaBeaud et al., 2011). Nevertheless, since RVFV is highly sensitive to low pH and is thus quickly inactivated in matured meat or dairy products, and no fresh meat or raw milk is exported from Mayotte (in Mayotte, milk is consumed raw but fermented so at lower pH), this pathway of possible spread of RVFV from Mayotte is excluded as well from the assessment (EFSA AHAW Panel, 2020).

#### 3.3.2.2. Vectors Pathway

##### _Vectors moved by wind currents_

As described in EFSA AHAW Panel (2020), the range of windborne transfer was from 97 km for _Ae. vigilax_ to 850 km for _Cx. pipiens pipiens._ For other potential RVFV vectors such as _An. pharoensis, Cx. tritaeniorhynchus_ and _Ae. vexans,_ there are reports of windborne transportation over 280, 500 and

740 km, respectively. The assessment of the risk of spread of RVF from Mayotte to neighbouring countries such as Tanzania, Kenya, Mozambique, Comoros, Réunion, Madagascar and Mauritius was carried out by HYSPLIT model; results are presented in Section 3.3.5.

*Vectors moved through flights*

As described in EFSA AHAW Panel, 2020, mosquitoes can be detected in air cabins and gangways (EFSA AHAW Panel, 2020). There is a probability that RVFV vectors (i.e.: *Culex* species) may also be introduced by plane and therefore to transmit the virus in the surroundings of airports. This also depends not only on the number of flights connecting RVFV-infected countries to target countries but also on the epidemiological status of the originating country, the closeness of infected areas to the airport, etc. In the table below Table 10, the number of outbound direct flights from Mayotte in 2019 is reported. Further details about flights from Mayotte are reported in Appendix D.

**Table 10:** Number of flights per destination country departing from Mayotte Dzaoudzi – Pamandzi airport (DZA) in 2019 (the data for the Seychelles are not included). The flights to France include technical stopovers (passengers stay on the plane in Kenya)

| Destination country | No. of flights arriving from Mayotte airport (DZA) in 2019 |
|---|---|
| France | 228 |
| Comoros | 777 |
| Kenya | 149 |
| Madagascar | 612 |
| Réunion | 453 |
| Saudi Arabia | 1 |
| Tanzania | 29 |
| **Total flights** | **2,249** |

According to the assessment of RVFV vectors introduction to EU conducted by Vectornet (Van Bortel et al., 2020), the probability of importation of infected vectors through airplanes was driven by the number of direct flights from all at-risk African countries to the respective EU Member State. Only for the Netherlands, France and Germany, with several thousands of flights per year from some RVF-affected countries, the value assigned in the MINTRISK model for the average numbers of vectors moved along the pathway per year was the second lowest category, 100–1,000 vectors per year; for all the other countries the values assigned corresponded to the lowest category, i.e. < 100 vectors ('minimal'), which would be the case also for all the countries listed in Table 9. This would also be the case for the spread to France and Réunion.

*Vectors moved by sea transport*

As described in EFSA, 2020, introduction and worldwide expansion of invasive Aedine species such as *Ae. albopictus* has been related to ports with high traffic volumes that increase the risk of invasion from areas that share similar eco-climate conditions.

From Mayotte, there are very limited numbers of ship movement, or on a very small scale, both for transport of passengers (up to 10 boats per week to Comoros and individual people with private boats travelling to Madagascar, Comoros or Mozambique) and for container ship (Table 11). In fact, Mayotte is a small island with very limited export activity (see Section 3.1.5).

**Table 11:** Containers transported from Mayotte to MSs

| | 2015 | | 2016 | | 2017 | | 2018 | | 2019 | |
|---|---|---|---|---|---|---|---|---|---|---|
| | **Total** | **Empty** | **Total** | **Empty** | **Total** | **Empty** | **Total** | **Empty** | **Total** | **Empty** |
| Belgium | | | | | 13 | 4 | 8 | 0 | 19 | 0 |
| Spain | 32 | 0 | 17 | 0 | 16 | 0 | 31 | 0 | 19 | 0 |
| France | 131 | 30 | 183 | 2 | 412 | 0 | 810 | 98 | 289 | 241 |

Data source: Database of Eurostat: Transport/Maritime Transport/Volume of containers transported to/from main ports. Twenty-foot equivalent unit (TEU).

This amount is very limited compared to the number of containers moved from other RVF-affected countries to MS, 20–100 thousand containers moved yearly (EFSA AHAW Panel, 2020), and for which the risk of introduction of RVFV in EU was already found to be low. Given the very low number of containers moved from Mayotte per year, this pathway of spread of vectors is excluded from the assessment.

### 3.3.2.3. Human Pathway

The great majority of cases of infection with RVFV in humans is asymptomatic. For the small proportion with clinical signs, the majority presents with a self-resolving influenza-like syndrome.

Although sick people can develop significant levels of viraemia for a few days (EFSA, 2005; Maurice et al., 2018), humans are considered dead-end hosts in the epidemiological cycle of RVF and human–human transmission of the virus has never been described (EFSA AHAW Panel, 2020). Therefore, this pathway of spread is not further considered.

### 3.3.3. Selection of relevant pathways of RVF spread from Mayotte and target countries

Considering the information presented in the section above, the pathways of spread from Mayotte coupled with the target countries to be further considered are:

- movement of infected vectors by passive movements when shipped by flight to metropolitan France and to Réunion (French Department), to be assessed by MINTRISK model;
- movement of infected vectors by wind currents to countries neighbouring Mayotte.

### 3.3.4. Risk of spread of RVF from Mayotte to metropolitan France and Réunion by vectors transported by flights

The assessment of the risk of spread of RVF from Mayotte to France and to Réunion via vectors moved by flights is carried out by MINTRISK model and it is structured in four components, i.e. occurrence of the disease in Mayotte, rate of entry, level of transmission and probability of establishment. Then, the model computes the overall risk of introduction. As in EFSA AHAW Panel, 2020 RVF 1ST Opinion, for each component, a set of questions need to be answered with a value chosen from a scale given by the model and a related level of uncertainty (low, moderate, high). The values for each MINTRISK question and the reasoning to assign the different values are given in Table 12.

**Table 12:** Steps, question and values assigned with related reasoning for MINTRISK model applied to risk of introduction of RVFV from Mayotte to France and Réunion by movement of vectors shipped by flights

| Step | Question | Value | Reasoning | Uncertainty level |
|---|---|---|---|---|
| **RVF occurrence in Mayotte** | Relative size of the infected area to the total area addressed | > 0.3, very large | Outbreaks all over the island, see Figure 5 | Low |
| | How likely is it that the disease will not be notified to OIE | Very unlikely, < 0.2 | See EFSA AHAW Panel (2020) | Low |
| | What is the duration of undetected spread | Short (0.1–0.3 year) | This was observed in 2018 in Mayotte, the disease entered in summer and was detected by the end of 2018 | Moderate |
| | What is the frequency with which the epidemic occurs in the addressed area | Moderate, 0.3–1 per year | One epidemic per year in 2018 and 2019 | Low |
| | How high is the prevalence of the infection in vectors in the region in the end of high-risk period | High, > 0.1 | In 2018 and 2019, there was an active epidemic, see EFSA AHAW Panel, (2020) | Moderate |

| Step | Question | Value | Reasoning | Uncertainty level |
|---|---|---|---|---|
| **Rate of Entry** | Average numbers vectors moved along the pathway per year | Minimal, < 100, both for France and Réunion | Number of flights per year from Mayotte to France and Réunion is very limited (< 500 per year, see above) compared to yearly number of flights to France from all African affected countries (7–9,000 flights). Mosquito survival is close to 1, see EFSA AHAW Panel (2020) | Low |
| | Probability of passing through the preventive/control measures before/at transport | Moderate, 0.01–0.1 | See EFSA AHAW Panel (2020) | High |
| | Probability that a viable VBD-agent is still present upon arrival in the area at risk | Very high, > 0.8 | RVFV is viable in a surviving vector and the survival of mosquitos depends on the length of trip, few hours for flight to France, less to Réunion, survival is close to 1 | Low |
| **Transmission** | Distribution of the vector in the area at risk | Present | RVF vectors are present both in France and in Réunion | Low |
| | Estimated value of the basic reproduction ratio | 2.3–6.8 (*moderate to high*) | See EFSA AHAW Panel (2020) | Moderate |
| | Fraction of the host population is susceptible | Very high, > 0.8 | France and Réunion are RVF free (EFSA, 2020; Balenghien et al., 2013) | Low |
| **Establishment** | Probability of infecting a first local (indigenous) host, given the pathway of entry and the expected region and time of entry? [1st transmission step] | Very high for Réunion moderate for France | This is calculated as the geometric mean of temperature (number of days above 9.6°C, EFSA AHAW Panel, 2020, which is 1 for Réunion (Figure 1) and 0.667 for France, EFSA AHAW Panel, 2020) and host density, which is moderate for France (EFSA AHAW Panel, 2020) and very high for Réunion (170 ruminant/sq.km of agricultural land). The categories for MINTRISK have been assigned according to 20th, 40th, 60th, 80th percentiles of the distribution of the geometric means | Low |
| | Probability of infecting a first local vector (given first infection of an indigenous host)? [2nd transmission step] | Very high for Réunion Moderate for France | This is calculated as the geometric mean of temperature (see above) and proportion of the country with vector presence, moderate for France (EFSA AHAW Panel, 2020) and very high for Réunion (close to 1, see Figure 15). The categories for MINTRISK have been assigned according to 20th, 40th, 60th, 80th percentiles of the distribution of the geometric means | Low |

The results of the assessment by MINTRISK are reported in Table 13.

**Table 13:** MINTRISK results of rate of entry, transmission, probability of establishment and risk of introduction of RVFV in Réunion and France

| Steps | Réunion | | France | |
|---|---|---|---|---|
| | Values (median and CI) | Qualitative assessment | Values | Qualitative assessment |
| **Rate of entry (number of entry/year)** | 3.55E-05 (1.58E-07, 0.007) | Very low | 3.55E-05 (1.58E-07, 0.01) | Very low |
| **Level of transmission (R0)** | 1.78 (0.47; 6.68) | Moderate | 1.78 (0.47; 6.68) | Moderate |
| **Probability of establishment** | 0.28 (0.11; 0.70) | Very high | 0.0001 (2.51E-05; 0.0004) | Low/moderate |
| **Overall risk of introduction (number of epidemics per year)** | 0.001 (4.47E-06; 0.16) | Very low/low | 3.55E-06 (1.78E-08; 0.0007) | Very low |

**Key messages:**

- The overall risk of RVFV introduction from Mayotte to metropolitan France is 3.55E-06 (1.78E-08; 0.000708) per year (very low) with 95% certainty, corresponding to one epidemic every 1400 years in the worst-case scenario. Likewise, the overall rate of RVFV introduction from Mayotte to la Réunion island is 0.001122 (4.47E-06; 0.158489) per year (from very low to low) with 95% certainty, corresponding to one epidemic every 6.3 years at the maximum (upper bound as worst case scenario).

- The very low values of introduction risk originate from very low rates of importation of infected vectors from Mayotte because of very small number of direct flights connecting Mayotte to metropolitan France and la Réunion island. Therefore, the number of direct flights as a proxy represents a bottleneck to the introduction of RVFV from Mayotte into target areas.

- The risk of RVFV introduction from Mayotte to la Réunion is greater than that from Mayotte to metropolitan France mainly because the probability of establishment in la Réunion (median: 0.282; 95%CI: 0.112–0.708) is much higher than that in metropolitan France (median: 0.0001; 95%CI: 2.51E-05–0.000398). Although quite similar in terms of entry rate (median: 3.55E-05; 95%CI: 1.59E-07–0.0071) and level of transmission (median: 1.78; 95%CI: 0.47–6.68), la Réunion exhibits more favourable conditions (higher host density and weather conditions) for RVF establishment than metropolitan France.

### 3.3.5. Dispersal of RVFV-infected mosquitoes between Mayotte and neighbouring countries by wind

Analysis of wind trajectories using the HYSPLIT model suggests that mosquitoes could potentially have been transported on wind to Mayotte from the Comoros Islands or Madagascar in both January 2008 and December 2018 (**Figure 16**). Consequently, either country could be a possible source for a wind-borne incursion of RVFV-infected mosquitoes to Mayotte in 2008 or 2018. Because no trajectories originate from Mozambique, Tanzania or Kenya, it is unlikely that these countries were direct sources for a wind-borne incursion to Mayotte in either year.
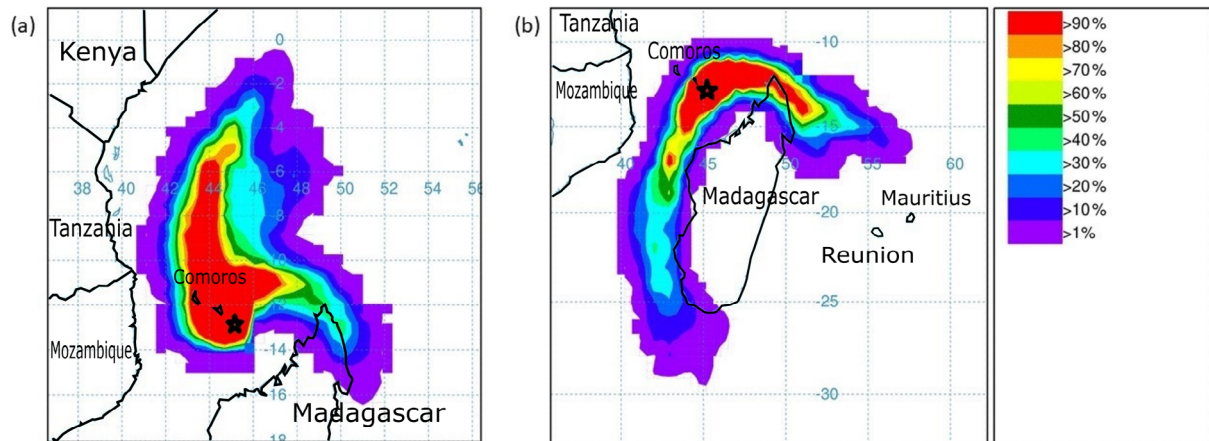
The colour scale indicates the proportion (%) of wind trajectories from the Comoros Islands or Madagascar passing through each 1° by 1° grid square which reach Mayotte (indicated by the star) within 48 h.

**Figure 16:** HYSPLIT backwards trajectories of 48 h duration for wind-borne dispersal of mosquitoes to Mayotte in January 2008 (a) or December 2018 (b)

During the most recent epidemic of RVF on the island in 2019, analysis of wind trajectories using the HYSPLIT model indicates that mosquitoes from Mayotte dispersing on the wind could have reached the Comoros Islands, Madagascar, Mozambique and, possibly, Tanzania after 48 h (Figure 17). However, these four countries report endemic disease (EFSA AHAW Panel, 2020), and an incursion of RVFV-infected mosquitoes would have negligible impact. Trajectories from Mayotte did not reach any other countries and so no other countries are likely (since none of trajectories reached targets) to have been at risk of RVFV being introduced by the long-distance dispersal of mosquitoes from Mayotte between January and April 2019. The trajectories reaching Mauritius (approximately 20.5°S, 57.5°E) in February 2019 (Figure 17) should be interpreted with caution. More detailed examination of the trajectories indicated that these were > 10,000 m above ground level, so no mosquitoes would be expected to survive.
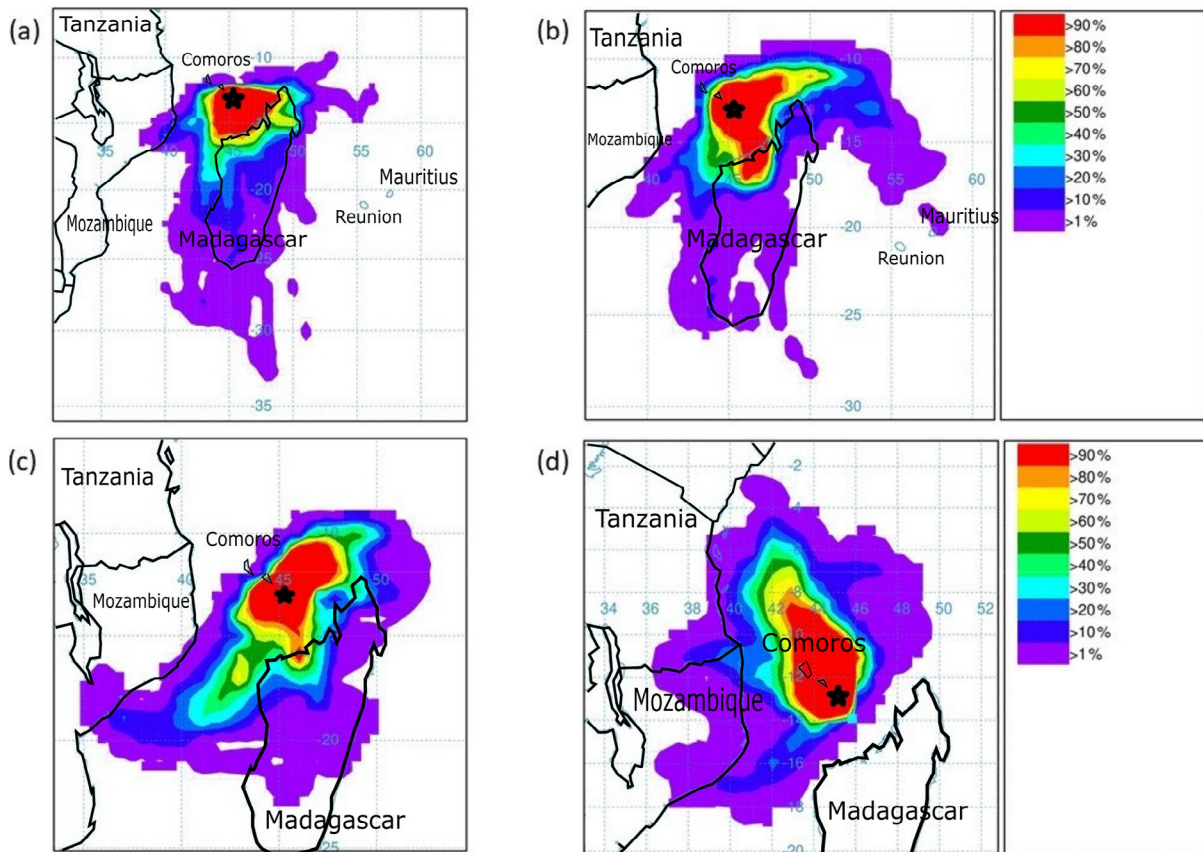
The colour scale indicates the proportion (%) of wind trajectories from Mayotte (indicated by the star) passing through each square of a 1° by 1° grid.

**Figure 17:** HYPSLIT forward trajectories of 48 h duration for wind-borne dispersal of mosquitoes from Mayotte in (a) January, (b) February, (c) March or (d) April 2019

Analysis of wind trajectories from Mayotte using HYPSLIT indicates that RVF could be introduced into neighbouring countries by wind-borne dispersal of mosquitoes from Mayotte. The reverse (i.e. RVF introduction from Comoros and Madagascar to Mayotte) is possible as well. This finding suggests the potential for a pendulum or ping-pong movement of RVF between Mayotte and the neighbouring countries.

## 4.  Conclusions

- The tropical climate in Mayotte provides favourable conditions for the presence of mosquitoes all year round; the temperature remains high (25.4°C average, 15°C min, 31°C max) and rainfall is present throughout the year (high peaks from late November to March).
- Regular illegal introductions of animals into Mayotte, represent a continuous risk of (re) introduction of RVF and other diseases.
- The size of the herds is small, with 4.8 and 5.8 ruminants per farm on average for bovines and small ruminants, respectively. The farming system in both bovines and small ruminants is traditional, mainly based on tethered grazing, with low levels of biosecurity.
- Animal registration and identification systems are not fully implemented, with consequent uncertainties on the real demographic data of farmed ruminants in Mayotte.
- The animal population of Mayotte has been continuously exposed to RVFV at least since 2004 or even earlier, given that RVVF-specific IgG antibodies were detected in sera samples collected in 2004. RVF-specific IgM antibodies were not identified before 2007, when RVFV-infected ruminants were illegally introduced from the Union of the Comoros.
- After a decade (2007–2018) of decrease in the RVF sero-prevalence, RVFV was re-introduced in 2018, most probably through illegal imports of live animals (mainly goats) from the Union of

the Comoros during the preparation for the celebration of Eid al Adha. Up to the end of October 2019, 126 outbreaks of RVF in ruminants, distributed all over the island, were reported in Mayotte.

### ToR 2.1a. Probability of RVF persistence in Mayotte

- The probability of persistence of RVF in Mayotte in animal hosts is considered low, since transplacental transmission in ruminants is considered rare, there is no known carrier state in mammals and there are no wild ruminants in Mayotte, in which RVFV could persist;
- Vertical transmission via vectors in Mayotte appears to contribute less to persistence of RVF compared to the re-introduction via pathways such as animal movement from RFVF-infected areas. Firstly, persistence is considered a rare phenomenon of low prevalence in the mosquito population. Secondly, vertical transmission of RVFV has not been detected in any of potential vector species of RVFV present in Mayotte and Réunion. However, there is a high uncertainty regarding the existence of vertical transmission, given the limited information available in other RVF endemic countries.
- Two published mathematical models assessed the probability of RVF persistence in Mayotte. The first suggests that, assuming vertical transmission in vectors occurs, the probability of RVFV persisting in Mayotte was 9.5% and 2.1% for a persistence of 5 and 9 years, respectively. A second model did not consider vertical transmission in vectors and the study based on this indicates that, once importation of RVFV-infected animals stopped, the virus was predicted to persist in only 0.26% of simulations. Indeed, without vertical transmission in the vector or the continuous re-introduction of the virus through infected animals or vectors, persistence is unlikely.
- The progressive decrease of serological positivity after RVF introduction in 2007 indicates that probably the virus circulation did not persist after that year, until the re-introduction in 2018.
- The low chance of RVF persistence in Mayotte can be due to the small number of susceptible hosts in the island and the slow turnover of the ruminant population.
- Moreover, a recent study on genetic sequencing has shown that RVFV circulating in the 2018–2019 epidemics is different from the one in 2007, thus this supports the fact that the current epidemics are due to re-introduction rather than RVF persisting in the island.

### ToR 2.1b. Risk of spread from Mayotte to other countries including other French departments in the Indian Ocean or to continental France

- In relation to the risk of RVF spread from Mayotte to other countries including other French departments in the Indian Ocean or to continental France, various possible pathways have been analysed:

  o According to the information provided by the French Veterinary Authorities, there is no commercial trade of animals or animal products from Mayotte to other French departments or to other European countries. Moreover, the sale of raw milk is banned. Therefore, the possible spread of RVF form Mayotte through live animals and animal products is deemed non-existent.

  o Concerning the possibility of spreading the infection through infected vectors carried by airplanes, there are few direct flights connections from Mayotte to continental France and other French departments in Indian Ocean (Réunion). The overall risk of introduction of RVF through this pathway was assessed by MINTRISK model as 'Very low' for continental France (median of $4 \times 10^{-6}$ epidemic per year (95%CI: 2E-08; 0.0007), corresponding to one resulting epidemic every 1,400 years, based on the upper bound of the confidence interval as worst-case scenario) and 'Very low to low' for Réunion (median of 0.001 epidemics per year (95%CI: 4.47E-06; 0.16), corresponding to one resulting epidemic every 6.3 years, based on the upper confidence level as worst-case scenario).

  o In relation to the possibility of spread of RVF through infected vectors carried by sea cargo, the limited number of containers annually departing from Mayotte suggests that the probability of RFV spread from Mayotte through this pathway is very low.

  o Simulations with the HYSPLIT model suggest that mosquitoes dispersing on the wind from Mayotte between January and April 2019 could have reached the Comoro Islands, Madagascar, Mozambique and, possibly, Tanzania after 48 h. However, these four countries report endemic disease, and an incursion of RVFV-infected mosquitoes would not change

the prevalence noticeably. No other countries were at risk of RVFV being introduced by the long-distance dispersal of mosquitoes from Mayotte during this same time period. The same model shows also that the backward spread may also occur, while Comoro Islands and Madagascar have been possible sources for a wind-borne incursion of RVFV-infected mosquitoes to Mayotte in 2008 or 2018.

**ToR 2.2. Impact of RVF in Mayotte**

- The animal population in Mayotte has been exposed to RVF virus at least since 2004 or even earlier, since RVF-specific IgG antibodies were detected in serum samples in 2004. RVF-specific IgM antibodies were not identified before 2007, when RVFV-infected ruminants were illegally introduced from the Union of the Comoros.

- Since 2007, after a decade during which the sero-prevalence of RVF was decreasing, in 2018 RVFV was re-introduced, most probably through illegal imports of live ruminants (mainly goats) from the Union of the Comoros during the preparation for the celebration of Eid al Adha. Up to the end of October 2019, 125 outbreaks of RVF, distributed all over the island, were reported in Mayotte domestic ruminants.

- In the 2018–2019 epidemic, according to official notifications, RVF caused low mortality (0.01%). However, in 2019, the number of abortions reported in ruminants was fivefold greater than the years before. The majority of the aborted foetuses tested had RVFV.

- According to the only available data, originating from one farm affected by the 2018–2019 outbreak, the weekly milk production in weeks 29–41 of 2019 was at lower levels than expected based on the period 2015–2018. This drop in the milk production from week 29 to week 41 would be temporally compatible with the reproductive perturbations (abortions, foetal resorptions) caused by RVFV infection, which occurred in late 2018 and early 2019. In addition, albeit the dairy farm under study was infected by RVFV, it cannot be concluded with certainty that the infection was the main cause of the observed milk drop. Milk loss in 2019 compared to previous years 2015–2018 is estimated to be 18%, which would correspond to an economic loss of around €191,000 in the entire Mayotte.

## 5.    Recommendations

- Considering the risk of spread of RVF from and towards Mayotte, it is recommended to maintain and even to improve actions preventing introduction of infected vectors from and towards Mayotte from infected areas and to other uninfected areas, such as Metropolitan France and Réunion. Particular attention should be given to air traffic connections from Mayotte to exposed areas (Réunion, Comoros, Madagascar, Kenya/France, Tanzania/France) and improve the surveillance in neighbouring countries.

- Considering the likely repeated introduction of RVFV in Mayotte from Comoros through illegal movement of live animals, it is recommended to strengthen and support surveillance and border control measures in Mayotte to reduce this event.

- Considering the risk of Mayotte to be exposed to introduction of RVFV, it is of paramount importance to strengthen and improve the surveillance in order to follow the evolution of RVF occurrence in both Mayotte and neighbouring countries.

- Although the data available do not allow a solid estimation of the impact of RVF on animal health and production in Mayotte, it is recommended to implement a more structured system for the recording of disease occurrence and possible production losses, including abortions and milk production in order to understand the impact of RVF in Mayotte. A better implementation of the animal identification and registration system and tracing of movements would be of benefit for such objective.

- In general, the role of vertical transmission in RVFV vectors for the persistence of the disease from one year to another or even between inter-epizootic episodes is still poorly understood. Long-term studies about the prevalence of viable RVFV in immature stages of mosquitoes are recommended.

## References

AFSSA, 2008. Avis de l'AFSSA sur le risque de propagation de la fiévre de la Vallée du Rift (FVR) dans un department et une collective departementale fançais de l'Ocean Indien (la Reunion et Mayotte). Maison-Alfort, France. 156 pp.

Ammar SE, McIntyre M, Swan T, Kasper J, Derraik JGB, Baker MG and Hales S, 2019. Intercepted mosquitoes at New Zealand's ports of entry, 2001 to 2018: current status and future concerns. Tropical Medicine and Infectious Disease, 4. https://doi.org/10.3390/tropicalmed4030101

Appleton CC and Sharp BL, 1985. Preliminary study on the emergence of Mansonia uniformis (Diptera: Culicidae) from swamps at Richards Bay, Natal, South Africa. Journal of the Entomological Society of Southern Africa, 48, 179–184.

Balenghien T, Cardinale E, Chevalier V, Elissa N, Failloux AB, Jean Jose Nipomichene TN, Nicolas G, Rakotoharinome VM, Roger M and Zumbo B, 2013. Towards a better understanding of Rift Valley fever epidemiology in the south-west of the Indian Ocean. Veterinary Research, 44, 78. https://doi.org/10.1186/1297-9716-44-78

Becker J and Weitzel T, 2012. The Culex pipiens Complex in Europe. Journal of the American Mosquito Control Association, 28(4s), 53–67. https://doi.org/10.2987/8756-971x-28.4s.53

Beechler BR, Paweska JT, Kemp A, van Vuren P, Ezenwa VO, Joubert J, Ezenwa VO and Jolles AE. 2015. Rift Valley fever in Kruger National Park: do buffalo play a role in the interepidemic circulation of virus? Transboundary and Emerging Diseases, 62, 24–32.

Bellini R, Medici A, Calzolari M, Bonilauri P, Cavrini F, Sambri V and Dottori M, 2012. Impact of chikungunya virus on Aedes albopictus females and possibility of vertical transmission using the actors of the 2007 outbreak in Italy. PLoS ONE, 7. https://doi.org/10.1371/journal.pone.0028360

Bird BH, Bawiec DA, Ksiazek TG, Shoemaker TR and Nichol ST, 2007. Highly sensitive and broadly reactive quantitative reverse transcription-PCR assay for high-throughput detection of Rift Valley fever virus. Journal of Clinical Microbiology, 45, 3506–3513. https://doi.org/10.1128/JCM.00936-07

Brugman VA, Hernandez-Triana LM, Medlock JM, Fooks AR, Carpenter S and Johnson N, 2018. The role of Culex pipiens L. (Diptera: Culicidae) in virus transmission in Europe. The International Journal of Environmental Research and Public Health, 15. https://doi.org/10.3390/ijerph15020389

Brustolin M, Talavera S, Nunez A, Santamaria C, Rivas R, Pujol N, Valle M, Verdun M, Brun A, Pages N and Busquets N, 2017. Rift Valley fever virus and European mosquitoes: vector competence of Culex pipiens and Stegomyia albopicta (= Aedes albopictus). Medical and Veterinary Entomology, 31, 365–372. https://doi.org/10.1111/mve.12254

Cavalerie L, Charron MV, Ezanno P, Dommergues L, Zumbo B and Cardinale E, 2015. A stochastic model to study rift valley fever persistence with different seasonal patterns of vector abundance: new insights on the endemicity in the tropical island of mayotte. PLoS ONE, 10, e0130838. https://doi.org/10.1371/journal.pone.0130838

Cetre-Sossah C, Pedarrieu A, Guis H, Defernez C, Bouloy M, Favre J, Girard S, Cardinale E and Albina E, 2012a. Prevalence of Rift Valley Fever among ruminants, Mayotte. Emerging Infectious Diseases, 18, 972–975. https://doi.org/10.3201/eid1806.111165

Cetre-Sossah C, Zeller H, Grandadam M, Caro V, Pettinelli F, Bouloy M, Cardinale E and Albina E, 2012b. Genome analysis of Rift Valley fever virus, Mayotte. Emerging Infectious Diseases, 18, 969–971. https://doi.org/10.3201/eid1806.110994

CIRAD. 2013. Un développement de l'élevage bovin à Mayotte, mèlant tradition et innovation.Available online: https://reunion-mayotte.cirad.fr/actualites/archives/elevage-bovin-a-mayotte

Clerc Y, Coulanges P, Ratsirahonana S and Locheron P, 1980. Epidemic of influenza in Antananarivo (with isolation of virus A/Texas/77 (H3N2)). Archives de l'Institut Pasteur de Madagascar, 47, 101–120.

DAAF (Direction de l'alimentation, de l'agriculture et de la foret), 2018. Bovins lait: systems de production et analyse technico-èconomique. Available online: http://agreste.agriculture.gouv.fr/IMG/pdf/D97618A08.pdf

Dacheux L, Dommergues L, Chouanibou Y, Domeon L, Schuler C, Bonas S, Luo D, Maufrais C, Cetre-Sossah C, Cardinale E, Bourhy H and Metras R, 2019. Co-circulation and characterization of novel African arboviruses (genus Ephemerovirus) in cattle, Mayotte island, Indian Ocean, 2017. Transboundary and Emerging Disease, 66, 2601–2604. https://doi.org/10.1111/tbed.13323

Davies FG, Linthicum KJ and James AD, 1985. Rainfall and epizootic Rift Valley fever. Bulletin of the World Health Organization, 63, 941–943.

Delatte H, Paupy C, Dehecq JS, Thiria J, Failloux AB and Fontenille D, 2008. Aedes albopictus, vecteur des virus du chikungunya et de la dengue à la Réunion: biologie et contrôle. Parasite, 15, 3–13.

Delatte H, Desvars A, Bouétard A, Bord S, Gimonneau G, Vourc'h G and Fontenille D, 2010. Blood-feeding behavior of Aedes albopictus, a vector of Chikungunya on La Réunion. Vector-Borne and Zoonotic Diseases, 10, 249–258.

Dommergues L, Vilarouge C, Metras R, Youssouffi C, Sailleau C, Zientara S, Cardinale E and Cétre-Sossah C, 2018. Evidence of Bluetongue and Epizootic Haemorrhagic Disease circulation on the island of Mayotte. Acta Tropica, 191. https://doi.org/10.1016/j.actatropica.2018.12.037

Dondona AC, Aschenborn O, Pinoni C, Di Gialleonardo L, Maseke A, Bortone G and Monaco F, 2016. Rift valley fever virus among wild ruminants, Etosha National Park, Namibia, 2011. Emerging Infectious Diseases, 22, 128.

Drosten C, Göttig S, Schilling S, Asper M, Panning M, Schmitz H and Günther S, 2002. Rapid detection and quantification of RNA of Ebola and Marburg viruses, Lassa virus, Crimean-Congo hemorrhagic fever virus, Rift Valley fever virus, dengue virus, and yellow fever virus by real-time reverse transcription-PCR. Journal of Clinical Microbiology, 40, 2323–2330.

Durr PA, Graham K and van Klinken RD, 2017. Sellers' revisited: a big data reassessment of historical outbreaks of bluetongue and african horse sickness due to the long-distance wind dispersion of culicoides midges. Frontiers in Veterinary Science, 4, 98. https://doi.org/10.3389/fvets.2017.00098

EFSA (European Food Safety Authority), 2005. The risk of a Rift Valley fever incursion and its persistence within the community. EFSA Journal 2005; 3(10):238, 130 pp. https://doi.org/10.2903/j.efsa.2005.238

EFSA (European Food Safety Authority), 2013. Scientific Opinion on Rift Valley fever. EFSA Journal 2013;11 (4):3180, 48 pp. https://doi.org/10.2903/j.efsa.2013.3180

EFSA (European Food Safety Authority), 2017. Vector-borne diseases. EFSA Journal 2017; 15(5):4793, 91 pp. https://doi.org/10.2903/j.efsa.2017.4793

EFSA AHAW Panel (EFSA Panel on Animal Health and Welfare), 2020. Rift Valley Fever – epidemiological update and risk of introduction into Europe. EFSA Journal 2020;18(3):6041, 72 pp. https://doi.org/10.2903/j.efsa.2020.6041

Evans A, Gakuya F, Paweska JT, Rostal M, Akoolo L, Van Vuren PJ, Manyibe T, Macharia JM, Ksiazek TG, Feikin DR, Breiman RF and Kariuki Njenga M, 2008. Prevalence of antibodies against Rift Valley fever virus in Kenyan wildlife. Epidemiology and Infection, 136, 1261–1269. https://doi.org/10.1017/S0950268807009806

Fontenille D, Traore-Lamizana M, Diallo M, Thonnon J, Digoutte JP and Zeller HG, 1998. New vectors of Rift Valley fever in West Africa. Emerging Infectious Diseases, 4, 289–293. https://doi.org/10.3201/eid0402.980218

Gad AM, Riad IB and Farid HA, 1995. Host-feeding patterns of Culex pipiens and Cx. antennatus (Diptera: Culicidae) from a village in Sharqiya Governorate, Egypt. Journal of Medical Entomology, 32, 573–577. https://doi.org/10.1093/jmedent/32.5.573

Grunnill M and Boots M, 2016. How important is vertical transmission of dengue viruses by mosquitoes (Diptera: Culicidae)? Journal of Medical Entomology, 53, 1–19. https://doi.org/10.1093/jme/tjv168

Hailin Z, Yunzhi Z and Zhuqing M, 1993. Transovarial transmission of Chikungunya virus in Aedes albopictus and Aedes aegypti mosquitoes. Chinese Journal of Virology, 9, 222–227.

Hanafi HA, Fryauff DJ, Saad MD, Soliman AK, Mohareb EW, Medhat I, Zayed AB, Szumlas DE and Earhart KC, 2011. Virus isolations and high population density implicate Culex antennatus (Becker) (Diptera: Culicidae) as a vector of Rift Valley Fever virus during an outbreak in the Nile Delta of Egypt. Acta Tropica, 119, 119–124. https://doi.org/10.1016/j.actatropica.2011.04.018

Haseyama M, Iizuka S, Omae H and Tsuda Y, 2007. Results of mosquito collection from international aircrafts arriving at Narita International Airport, Japan and mosquito surveillance at the airport. Medical Entomology and Zoology, 58, 191–197. https://doi.org/10.7601/mez.58.191

Huestis DL, Dao A, Diallo M, Sanogo ZL, Samake D, Yaro AS, Ousman Y, Linton YM, Krishna A, Veru L, Krajacich BJ, Faiman R, Florio J, Chapman JW, Reynolds DR, Weetman D, Mitchell R, Donnelly MJ, Talamas E, Chamorro L, Strobach E and Lehmann T, 2019. Windborne long-distance migration of malaria mosquitoes in the Sahel. Nature, 574, 404–408. https://doi.org/10.1038/s41586-019-1622-4

Ibañez-Justicia A, Gloria-Soria A, den Hartog W, Dik M, Jacobs F and Stroo A, 2017a. The first detected airline introductions of yellow fever mosquitoes (Aedes aegypti) to Europe, at Schiphol International airport, the Netherlands. Parasites & Vectors, 10, 603. https://doi.org/10.1186/s13071-017-2555-0

Ibañez-Justicia A, Gloria-Soria A, Den Hartog W, Dik M, Jacobs F and Stroo A, 2017b. The first detected airline introductions of yellow fever mosquitoes (Aedes aegypti) to Europe, at Schiphol International airport, the Netherlands. Parasites and Vectors, 10. https://doi.org/10.1186/s13071-017-2555-0

INSEE (Institute National de la statistique et des etudes economiques), 2019. Government of France. "Estimation de population par région, sexe et grande classe d'âge - Années 1975 à 2019" (XLS) (in French). Retrieved 13 December 2019.

InVS (Institut de veille sanitaire, French Institute for Public Health Surveillance), 2011. Bulletin Hebdomadaire International N°318.

InVS (Institut de veille sanitaire, French Institute for Public Health Surveillance), 2012. Bulletin Hebdomadaire International N°372.

Jean Jose Nepomichene TN, Elissa N, Cardinale E and Boyer S, 2015. Species diversity, abundance, and host preferences of mosquitoes (Diptera: Culicidae) in two different ecotypes of Madagascar with recent RVFV transmission. Journal of Medical Entomology, 52, 962–969. https://doi.org/10.1093/jme/tjv120

Jupp PG and McIntosh BM, 1987. A bionomic study of adult Aedes (Neomelaniconion) circumluteolus in northern Kwazulu, South Africa. Journal of the American Mosquito Control Association, 3, 131–136.

LaBeaud AD, Muiruri S, Sutherland LJ, Dahir S, Gildengorin G, Morrill J, Muchiri EM, Peters CJ and King CH, 2011. Postepidemic analysis of Rift Valley fever virus transmission in northeastern Kenya: a village cohort study. PLoS Neglected Tropical Diseases, 5, e1265.

Lancelot R, Beral M, Rakotoharinome VM, Andriamandimby SF, Heraud JM, Coste C, Apolloni A, Squarzoni-Diaw C, de la Rocque S, Formently PB, Bouyer J, Wint GR and Cardinale E, 2017. Drivers of Rift Valley fever epidemics in Madagascar. Proceedings of the National Academy of Sciences of the United States of America, 114, 938–943.

Le Goff G, Goodman SM, Elguero E and Robert V, 2014. Survey of the mosquitoes (Diptera: Culicidae) of Mayotte. PLoS ONE, 9, e100696. https://doi.org/10.1371/journal.pone.0100696

Le Maitre A and Chadee DD, 1983. Arthropods collected from aircraft at Piarco International Airport, Trinidad, West Indies. Mosquito News, 43, 21–23.

Lequime S and Lambrechts L, 2014. Vertical transmission of arboviruses in mosquitoes: a historical perspective. Infection, Genetics and Evolution, 28, 681–690. https://doi.org/10.1016/j.meegid.2014.07.025

Lequime S, Paul RE and Lambrechts L, 2016. Determinants of Arbovirus Vertical Transmission in Mosquitoes. PLoS Pathogens, 12, e1005548. https://doi.org/10.1371/journal.ppat.1005548

Lernout T, Cardinale E, Jego M, Despres P, Collet L, Zumbo B, Tillard E, Girard S and Filleul L, 2013. Rift valley fever in humans and animals in Mayotte, an endemic situation? PLoS ONE, 8, e74192. https://doi.org/10.1371/journal.pone.0074192

Linthicum KJ, Davies FG, Kairo A and Bailey CL, 1985. Rift Valley fever virus (family Bunyaviridae, genus Phlebovirus). Isolations from Diptera collected during an inter-epizootic period in Kenya. Journal of Hygiene, 95, 197–209. https://doi.org/10.1017/S0022172400062434

Linthicum KJ, Britch SC and Anyamba A, 2016. Rift Valley Fever: an emerging mosquito-borne disease. Annual Review of Entomology, 61, 395–415. https://doi.org/10.1146/annurev-ento-010715-023819

Lumley S, Horton DL, Hernandez-Triana LLM, Johnson N, Fooks AR and Hewson R, 2017. Rift valley fever virus: strategies for maintenance, survival and vertical transmission in mosquitoes. Journal of General Virology, 98, 875–887. https://doi.org/10.1099/jgv.0.000765

Maurice AdS, Harmon J, Nyakarahuka L, Balinandi S, Tumusiime A, Kyonodo J, Mulei S, Namutebi A, Knust B and Shoemaker T, 2018. Rift Valley fever viral load correlates with the human inflammatory response and coagulation pathway abnormalities in humans with hemorrhagic manifesttions. Plos Neglected Tropical Diseases, 12, e0006–6460. https://doi.org/10.1371/journal.pntd.0006460

Maquart M, Pascalis H, Abdouroihamane S, Roger M, Abdourahime F, Cardinale E and Cetre-Sossah C, 2016. Phylogeographic reconstructions of a rift valley fever virus strain reveals transboundary animal movements from eastern continental africa to the union of the comoros. Transbound Emerging Diseases, 63, e281–e285. https://doi.org/10.1111/tbed.12267

Medlock JM, Hansford KM, Schaffner F, Versteirt V, Hendrickx G, Zeller H and Bortel WV, 2012. A review of the invasive mosquitoes in Europe: ecology, public health risks, and control options. Vector-Borne and Zoonotic Diseases, 12, 435–447. https://doi.org/10.1089/vbz.2011.0814

Meegan JM, Khalil GM, Hoogstraal H and Adham FK, 1980. Experimental transmission and field isolation studies implicating Culex pipiens as a vector of Rift Valley fever virus in Egypt. American Journal of Tropical Medicine and Hygiene, 29, 1405–1410. https://doi.org/10.4269/ajtmh.1980.29.1405

Metras R, Jewwll C, Porphyre T, Thompson PN, Pfeiffer DU, Collinc LM and White RG, 2015. Risk factors associated with Rift Valley fever epidemics in South Africa in 2008-11. Scientific Reports, 5, 9942.

Metras R, Cavalerie L, Dommergues L, Merot P, Edmunds WJ, Keeling MJ, Cetre-Sossah C and Cardinale E, 2016. The epidemiology of Rift Valley Fever in Mayotte: insights and perspectives from 11 years of sata. PLoS Neglected Tropical Diseases, 10, e0004783. https://doi.org/10.1371/journal.pntd.0004783

Metras R, Fournie G, Dommergues L, Camacho A, Cavalerie L, Merot P, Keeling MJ, Cetre-Sossah C, Cardinale E and Edmunds WJ, 2017. Drivers for Rift Valley fever emergence in Mayotte: a Bayesian modelling approach. PLoS Neglected Tropical Diseases, 11, e0005767. https://doi.org/10.1371/journal.pntd.0005767

Mohamed RAEH, Abdelgadir DM and Bashab HM, 2013. Transovarian transmission of Rift Valley fever virus by two species of mosquitoes in Khartoum state (Sudan): Aedes vexans (Meigen) and Culex quinquefasciatus (Say). Sudan Journal of Public Health, 8, 164–170.

Mourya DT, 1987. Absence of transovarial transmission of Chikungunya virus in Aedes aegypti & Ae. albopictus mosquitoes. Short Research Communication. Indian Journal of Medical Research, 85, 593–595.

Moutailler S, Bouloy M and Failloux AB, 2007. Short report: efficient oral infection of Culex pipiens quinquefasciatus by Rift Valley fever virus using a cotton stick support. American Journal of Tropical Medicine and Hygiene, 76, 827–829.

Nicolas G, Chevalier V, Tantely LM, Fontenille D and Durand B, 2014. A spatially explicit metapopulation model and cattle trade analysis suggests key determinants for the recurrent circulation of rift valley Fever virus in a pilot area of madagascar highlands. PLoS Neglected Tropical Diseases, 8, e3346. https://doi.org/10.1371/journal.pntd.0003346

Olive MM, Goodman SM and Reynes JM, 2012. The role of wild mammals in the maintenance of Rift Valley fever virus. Journal of Wildlife Diseases, 48, 241–266. https://doi.org/10.7589/0090-3558-48.2.241

Ratovonjato J, Olive M-M, Tantely LM, Andrianaivolambo L, Tata E, Razainirina J, Jeanmaire E, Reynes J-M and Elissa N, 2010. Detection, Isolation, and Genetic Characterization of Rift Valley Fever Virus from Anopheles (Anopheles) coustani, Anopheles (Anopheles) squamosus, and Culex (Culex) antennatus of the Haute Matsiatra Region, Madagascar. Vector-Borne and Zoonotic Diseases, 11, 753–759. https://doi.org/10.1089/vbz.2010.0031

Rissmann M, Eiden M, El Mamy BO, Isselmou K, Doumbia B, Ziegler U and Groschup MH, 2017. Serological and genomic evidence of Rift Valley fever virus during inter-epidemic periods in Mauritania. Epidemiology & Infection, 145, 1058–1068.

Rolph G, Stein A and Stunder B, 2017. Real-time Environmental Applications and Display sYstem: READY. Environmental Modelling & Software, 95, 210–228. https://doi.org/10.1016/j.envsoft.2017.06.025

Rostal MK, Liang JE, Zimmermann D, Bengis R, Paweska J and Karesh WB, 2017. Rift Valley Fever: does Wildlife play a role? ILAR Journal, 58, 359–370.

Sahu SS, Sonia T, Dash S, Gunasekaran K and Jambulingam P, 2019. Insecticide resistance status of three vectors of Japanese encephalitis in east central India. Medical and Veterinary Entomology, 33, 213–219. https://doi.org/10.1111/mve.12352

Sang R, Arum S, Chepkorir E, Mosomtai G, Tigoi C, Sigei F, Lwande OW, Landmann T, Affognon H, Ahlm C and Evander M, 2017. Distribution and abundance of key vectors of Rift Valley fever and other arboviruses in two ecologically distinct counties in Kenya. PLoS Neglected Tropical Diseases, 11, e0005341. https://doi.org/10.1371/journal.pntd.0005341

Seufi AM and Galal FH, 2010. Role of Culex and Anopheles mosquito species as potential vectors of rift valley fever virus in Sudan outbreak, 2007. BMC Infectious Diseases, 10, 65. https://doi.org/10.1186/1471-2334-10-65

Sissoko D, Giry C, Gabrie P, Tarantola A, Pettinelli F, Collet L and Pierre V, 2009. Rift valley fever, Mayotte, 2007–2008. Emerging Infectious Diseases, 15, 568.

Stein AF, Draxler RR, Rolph GD, Stunder BJB, Cohen MD and Ngan F, 2015. NOAA's HYSPLIT atmospheric transport and dispersion modeling system. Bulletin of the American Meteorological Society, 96, 2059–2077. https://doi.org/10.1175/bams-d-14-00110.1

Sumaye RD, Geubbels E, Mbeyela E and Berkvens D, 2013. Inter-epidemic transmission of Rift Valley fever in livestock in the Kilombero River Valley, Tanzania: a cross-sectional survey. PLoS Neglected Tropical Diseases, 7, e2356.

Sumaye R, Jansen F, Berkvens D, De Baets B, Geubels E, Thiry E and Krit M, 2019. Rift Valley fever: an open-source transmission dynamics simulation model. PLoS ONE, 14. https://doi.org/10.1371/journal.pone.0209929

Tantely ML, Rakotoniaina J-C, Tata E, Andrianaivolambo L, Razafindrasata F, Fontenille D and Elissa N, 2013. Biology of mosquitoes that are potential vectors of rift valley fever virus in different biotopes of the central highlands of madagascar. Journal of Medical Entomology, 50, 603–610. https://doi.org/10.1603/me12069

Tantely LM, Boyer S and Fontenille D, 2015. A review of mosquitoes associated with Rift Valley fever virus in Madagascar. The American Journal of Tropical Medicine and Hygiene, 92, 722–729.

Tatem AJ, Hay SI and Rogers DJ, 2006. Global traffic and disease vector dispersal. Proceedings of the National Academy of Sciences, 103, 6242–6247. https://doi.org/10.1073/pnas.0508391103

Turell MJ, Presley SM, Gad AM, Cope SE, Dohm DJ, Morrill JC and Arthur RR, 1996. Vector competence of Egyptian mosquitoes for Rift Valley fever virus. American Journal of Tropical Medicine and Hygiene, 54, 136–139. https://doi.org/10.4269/ajtmh.1996.54.136

Van Bortel W, Petric D, Ibanez Justicia A, Wint W, Krit M, Marien J, Vanslembrouck A and Braks M, 2020. Assessment of the probability of entry of Rift Valley fever virus into the EU through active or passive movement of verctors. EFSA supporting publication 2020;EN-1801, 24 pp. https://doi.org/10.2903/sp.efsa.20202.en-1801

Vanhomwegen J, Caro V, Batéjat C, Kwasiborski A, Vandenbogaert M, Hourdel V, Feher M, Grassin Q, Hoinard D, Flamand M, Côtre-Sossah C, Cardinale E, Collet L and Manuguerra JC, 2020. Ongoing Rift Valley fever outbreak in Mayotte, Indian Ocean, submitted.

Vazeille M, Mousson L and Failloux AB, 2009. Failure to demonstrate experimental vertical transmission of the epidemic strain of Chikungunya virus in Aedes albopictus from La Réunion, Indian Ocean. Mem Inst Oswaldo Cruz, Rio de Janeiro, 104, 632–635.

Wilkerson RC, Linton YM, Fonseca DM, Schultz TR, Price DC and Strickman DA, 2015. Making mosquito taxonomy useful: a stable classification of tribe Aedini that balances utility with current knowledge of evolutionary relationships. PLoS ONE, 10. https://doi.org/10.1371/journal.pone.0133602

Youssouf H, Subiros M, Dennetiere G, Collet L, Dommergues L, Pauvert A, Rabarison P, Vauloup-Fellous C, Le Godais G, Jaffar-Bandjee MC, Jean M, Paty MC, Noel H, Oliver S, Filleul L and Larsen C, 2020. Rift Valley Fever Outbreak, Mayotte, France, 2018–2019. Emerging Infectious Disease, 26, 769–772.

## Abbreviations

| | |
|---|---|
| ADNS | Animal Disease Notification System |
| BEF | Bovine Ephemeral Fever |
| BT | Bluetongue |
| CIRAD | Centre de Coopération Internationale en Recherche Agronomique pour le Développement |
| COOPADEM | farmer s cooperative in Mayotte |
| ELISA | enzyme-linked immunosorbent assay |
| EHD | Epizootic Hemorrhagic Disease |
| HYSPLIT | Hybrid Single-Particle Lagrangian Integrated Trajectory model |
| MPA | milk production rate anomaly |
| OIE | World Organisation of Animal Health |
| MPA | milk production rate anomaly |
| NDVI | normalised difference vegetation index |
| NRL | national reference laboratory |
| PCR | polymerase chain reaction |
| RVF | Rift Valley fever |

## Appendix A – Population data of ruminants in each commune in Mayotte according to the last agricultural census of 2010

| Commune/Municipality in Mayotte | Cattle | | Sheep and Goats | |
|---|---|---|---|---|
| | Herds N (%) | Animals N (%) | Herds N (%) | Animals N (%) |
| Acoua | 90 (2.51) | 236 (1.38) | 92 (4.20) | 367 (2.91) |
| Bandraboua | 234 (6.53) | 880 (5.13) | 93 (4.25) | 836 (6.62) |
| Bandrele | 355 (9.91) | 1,432 (8.35) | 207 (9.46) | 1,100 (8.72) |
| Bouéni | 97 (2.71) | 289 (1.68) | 154 (7.04) | 777 (6.16) |
| Chiconi | 291 (8.13) | 1,363 (7.95) | 62 (2.83) | 314 (2.49) |
| Chirongui | 248 (6.93) | 1,013 (5.91) | 94 (4.29) | 389 (3.08) |
| Dembeni | 314 (8.77) | 1,690 (9.85) | 212 (9.68) | 1,294 (10.25) |
| Dzaoudzi | 98 (2.74) | 474 (2.76) | 76 (3.47) | 545 (4.32) |
| Kani-Kéli | 213 (5.95) | 1,114 (6.49) | 116 (5.30) | 676 (5.36) |
| Koungou | 188 (5.25) | 641 (3.74) | 253 (11.56) | 1,235 (9.79) |
| Mamoudzou | 596 (16.64) | 3,106 (18.11) | 380 (17.36) | 2,196 (17.40) |
| Mtsamboro | 77 (2.15) | 325 (1.89) | 114 (5.21) | 649 (5.14) |
| M'Tsangamouji | 124 (3.46) | 649 (3.78) | 45 (2.06) | 264 (2.09) |
| Ouangani | 222 (6.20) | 875 (5.10) | 98 (4.48) | 458 (3.63) |
| Pamandzi | 22 (0.61) | 184 (1.07) | 13 (0.59) | 117 (0.93) |
| Sada | 180 (5.03) | 1,158 (6.75) | 69 (3.15) | 525 (4.16) |
| Tsingoni | 232 (6.48%) | 1,725 (10.06) | 111 (5.07) | 877 (6.95) |
| Total | **3,581** | **17,154** | **2,189** | **12,619** |

Source: DAAF Mayotte.

## Appendix B − Publications with sero-surveillance studies of RVF in Mayotte

| Sampling period | Animal species | N tested | Diagnostic method | Positive results (% on the samples) | Seroprevalence with CI | Method | Publication |
|---|---|---|---|---|---|---|---|
| 2004 | Cattle | 130 | In house IgG ELISA; confirmed by neutralisation tests | 29 (22.66%) | | Retrospective study in stored samples | Cetre-Sossah et al. (2012a) |
| 2005 | | 130 | In house IgG ELISA; confirmed by neutralisation tests | 4 (3.07%) | | | |
| 2006 | | 130 | In house IgG ELISA; confirmed by neutralisation tests | 16 (12.31%) | | | |
| 2007 | | 126 | In house IgG ELISA; confirmed by neutralisation tests | 39 (30.95%) | | | |
| September 2007 to March 2008 | Humans | 220 | In-house IgM-capture enzyme immunoassays ELISA | 3 | | Retrospective study in patients | Sissoko et al. (2009a) and Cetre-Sossah et al. (2012b) |
| | | | RT-PCR by Drosten et all 2002 | 7 | | | |
| | | | Virus isolation | 2 | | | |
| November 2007 to April 2008 | Goats (Illegally introduced) | 29 | In-house competitive IgG ELISA | 4 (13.79%) | | | Cetre-Sossah et al. (2012a) |
| | | | In-house IgM-capture ELISA | 2 (6.89%) | | | |
| | Cattle close to goats | 79 | In-house competitive IgG ELISA | 29 (37%) | | | |
| | | | In-house IgM-capture ELISA | 3 (4%). | | | |
| Jun 2007 to May 2008 | Cattle | 301 | In-house competitive IgG ELISA | 32 (10.6% (95% CI 7%−14%) | | | Cetre-Sossah et al. (2012a) |
| Aug. 2008 to Aug. 2009 | Goats | 70 | Seroconversion (IgG) | 1 (1.43%) | | | Cetre-Sossah et al. (2012a) |
| | | | IgM Identification | | | | |

| Sampling period | Animal species | N tested | Diagnostic method | Positive results (% on the samples) | Seroprevalence with CI | Method | Publication |
|---|---|---|---|---|---|---|---|
| March 2010 to August 2011 | Cattle | 131 | ELISA kits for IgG RVFV antibodies | | | Prospective, monthly sampling, seronegative sentinels, randomly selected farms | Lernout et al. (2013) |
| | Small ruminants | 67 | | | | | |
| March–April 2011 | Humans | 1,413 | IgG in-house indirect ELISA test (Pasteur, Paris) | 58 (4.1%) | | | |
| October 2004 to April 2013 | Ruminants | 2,342 | Competitive Elisa Kit | This study incudes also data from other published studies | | | Cavalerie et al. (2015) |
| October 2004 to June 2015 | Cattle | 5,720 | IgG | This study includes the samples already used in some of the studies mentioned above, and the results per epidemiological year are included in Table 3 | | | Metras et al. (2015) |
| | Goats | | | | | | |
| | Cattle | 1,513 | IgM | | | | |
| | Goats | | | | | | |

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## Appendix C – Cumulated number of RVF affected herds and human cases and number of new confirmed herds and human cases in 2019 in Mayotte

| Date of press release | Cumulated number of herds | Cumulated number of human cases | New herds confirmed | New human cases confirmed |
|---|---|---|---|---|
| 17/1/2019 | 0 | 5 | 0 | 5 |
| 6/2/2019 | 23 | 31 | 23 | 26 |
| 22/2/2019 | 33 | 63 | 10 | 32 |
| 1/3/2019 | 39 | 82 | 6 | 19 |
| 8/3/2019 | 52 | 88 | 13 | 6 |
| 15/3/2019 | 60 | 101 | 8 | 13 |
| 22/3/2019 | 75 | 107 | 15 | 6 |
| 29/3/2019 | 84 | 114 | 9 | 7 |
| 4/4/2019 | 86 | 116 | 2 | 2 |
| 11/4/2019 | 92 | 117 | 6 | 1 |
| 18/4/2019 | 104 | 122 | 12 | 5 |
| 26/4/2019 | 109 | 126 | 5 | 4 |
| 10/5/2019 | 119 | 130 | 10 | 4 |
| 24/5/2019 | 121 | 134 | 2 | 4 |
| 3/6/2019 | 123 | 137 | 2 | 3 |
| 14/6/2019 | 124 | 139 | 1 | 2 |
| 21/6/2019 | 124 | 139 | 0 | 0 |
| 28/6/2019 | 124 | 139 | 0 | 0 |
| 05/7/2019 | 124 | 141 | 0 | 2 |
| 12/7/2019 | 126 | 142 | 2 | 1 |
| 2/8/2019 | 126 | 142 | 0 | 0 |
| 16/8/2019 | 126 | 143 | 0 | 1 |
| 30/8/2019 | 126 | 143 | 0 | 0 |
| **Total** | **126** | **143** | | |

## Appendix D – Number of flights per destination country departing from Mayotte Dzaoudzi – Pamandzi airport (DZA) per month in 2019

| Destination Country | Destination City | Number of flights arriving from Mayotte airport (DZA) in 2019 | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | Jan | Feb | Mar | Apr | May | Jun | Jul | Aug | Sep | Oct | Nov | Dec | Total |
| Comoros/ Madagascar | MORONI/ ANTANANARIVE | 4 | 4 | 5 | 1 | 0 | 0 | 8 | 0 | 0 | 0 | 0 | 0 | **22** |
| Comoros | ANJOUAN | 53 | 36 | 34 | 9 | 20 | 22 | 27 | 27 | 9 | 14 | 2 | 22 | **275** |
| Comoros | ANJOUAN/MOHELI | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | **1** |
| Comoros | ANJOUAN/MORONI | 0 | 0 | 21 | 21 | 27 | 24 | 26 | 29 | 25 | 26 | 26 | 27 | **252** |
| Comoros | MOHELI | 8 | 5 | 3 | 5 | 9 | 8 | 9 | 9 | 5 | 8 | 9 | 9 | **87** |
| Comoros | MORONI | 17 | 11 | 10 | 8 | 9 | 10 | 23 | 26 | 12 | 9 | 5 | 17 | **157** |
| Comoros | MORONI/ANJOUAN | 0 | 0 | 1 | 4 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | **5** |
| France | PARIS-CDG | 0 | 0 | 0 | 4 | 15 | 23 | 13 | 14 | 2 | 1 | 2 | 3 | **77** |
| Greece/France | ATHENS/PARIS-CDG | 0 | 0 | 0 | 0 | 0 | 0 | 3 | 0 | 0 | 0 | 0 | 0 | **3** |
| Kenya | NAIROBI | 13 | 15 | 13 | 13 | 14 | 9 | 13 | 9 | 14 | 11 | 13 | 12 | **149** |
| Kenya/France | MOMBASSA/PARIS-CDG | 0 | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 0 | 0 | 0 | 0 | **2** |
| Kenya/France | NAIROBI/PARIS-CDG | 14 | 10 | 11 | 12 | 0 | 1 | 0 | 0 | 5 | 17 | 10 | 18 | **98** |
| Madagascar | ANTANANARIVE | 10 | 8 | 8 | 7 | 9 | 9 | 1 | 9 | 9 | 9 | 8 | 9 | **96** |
| Madagascar | DIEGO-SUAREZ | 7 | 5 | 8 | 7 | 5 | 5 | 9 | 13 | 3 | 11 | 3 | 10 | **86** |
| Madagascar | DIEGO-SUAREZ/NOSY BE | 5 | 4 | 4 | 3 | 2 | 3 | 7 | 5 | 7 | 9 | 6 | 6 | **61** |
| Madagascar | MAJUNGA | 22 | 17 | 19 | 17 | 18 | 17 | 26 | 24 | 14 | 17 | 13 | 24 | **228** |
| Madagascar | NOSY BE | 6 | 4 | 5 | 7 | 8 | 6 | 10 | 9 | 3 | 11 | 3 | 10 | **82** |
| Madagascar | NOSY BE/DIEGO-SUAREZ | 5 | 4 | 3 | 7 | 4 | 2 | 1 | 1 | 0 | 3 | 3 | 4 | **37** |
| Mayotte | DZAOUDZI | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | **1** |
| Reunion | REUNION | 40 | 29 | 36 | 31 | 34 | 39 | 52 | 52 | 34 | 32 | 30 | 44 | **453** |
| Seychelles | MAHE | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 3 | 1 | 0 | 0 | 0 | **4** |
| Tanzania | DAR-ES-SALAAM | 3 | 2 | 3 | 2 | 2 | 2 | 4 | 3 | 2 | 3 | 0 | 3 | **29** |
| Tanzania/France | DAR ES SALAAM/PARIS-CDG | 0 | 0 | 0 | 0 | 0 | 0 | 14 | 17 | 17 | 0 | 0 | 0 | **48** |
| Tanzania/Saudi Arabia | DAR ES SALAAM/JED | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | **1** |
| | **Total** | **207** | **154** | **184** | **158** | **176** | **182** | **248** | **250** | **163** | **181** | **133** | **218** | **2,254** |

Some of the flights have stopovers e.g. there are 98 flights to Paris CDG airport that have a stopover in Nairobi.

## Appendix E – Milk production in 2015–2018 and in 2019 per each week in the study farm

The detailed milk production in 2015–2018 and in 2019 per each week with related number of dairy cows present in each week in the study farm is shown in Figure E.1.
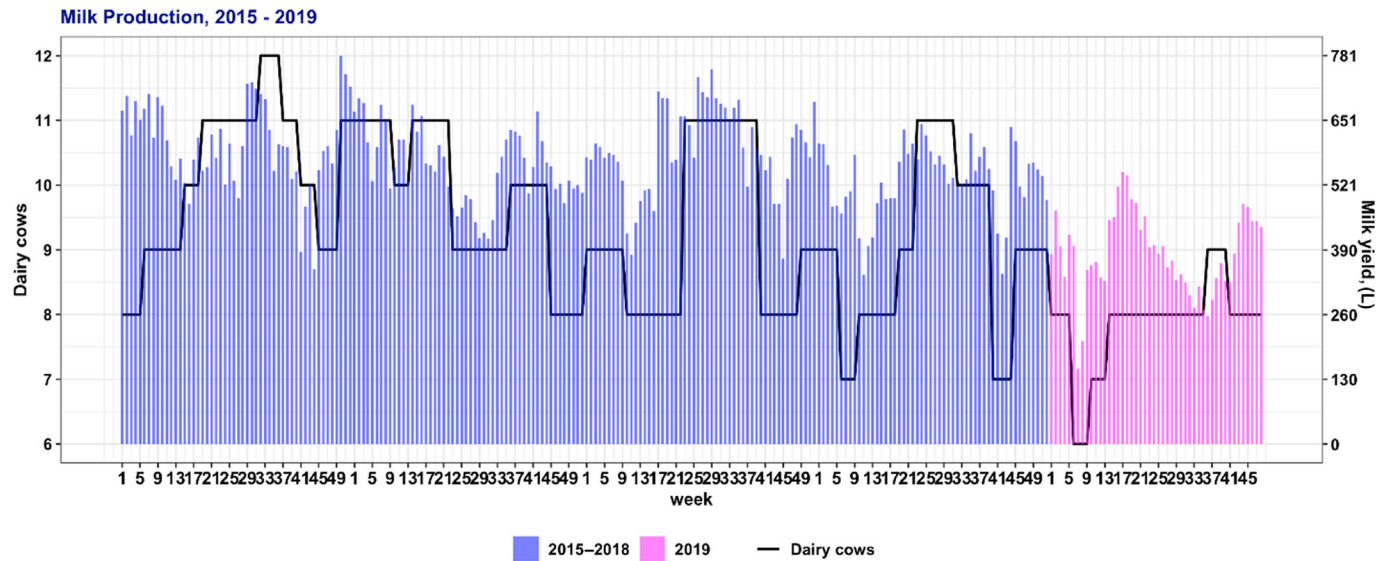


**Figure E.1:** Weekly milk production (total milk yield, right Y-axis) during period 2015–2018 and in 2019 in relation to number of dairy cows (left Y-axis) present in the study farm

In Figure E.2, the deviation of milk production in 2019 from expected production in the reference period (2015–2018) is shown per week expressed as milk production in 2019 minus the lowest bound of reference period 2015–2018 (low CI) divided by low CI. The cumulated milk loss in litres is also shown.
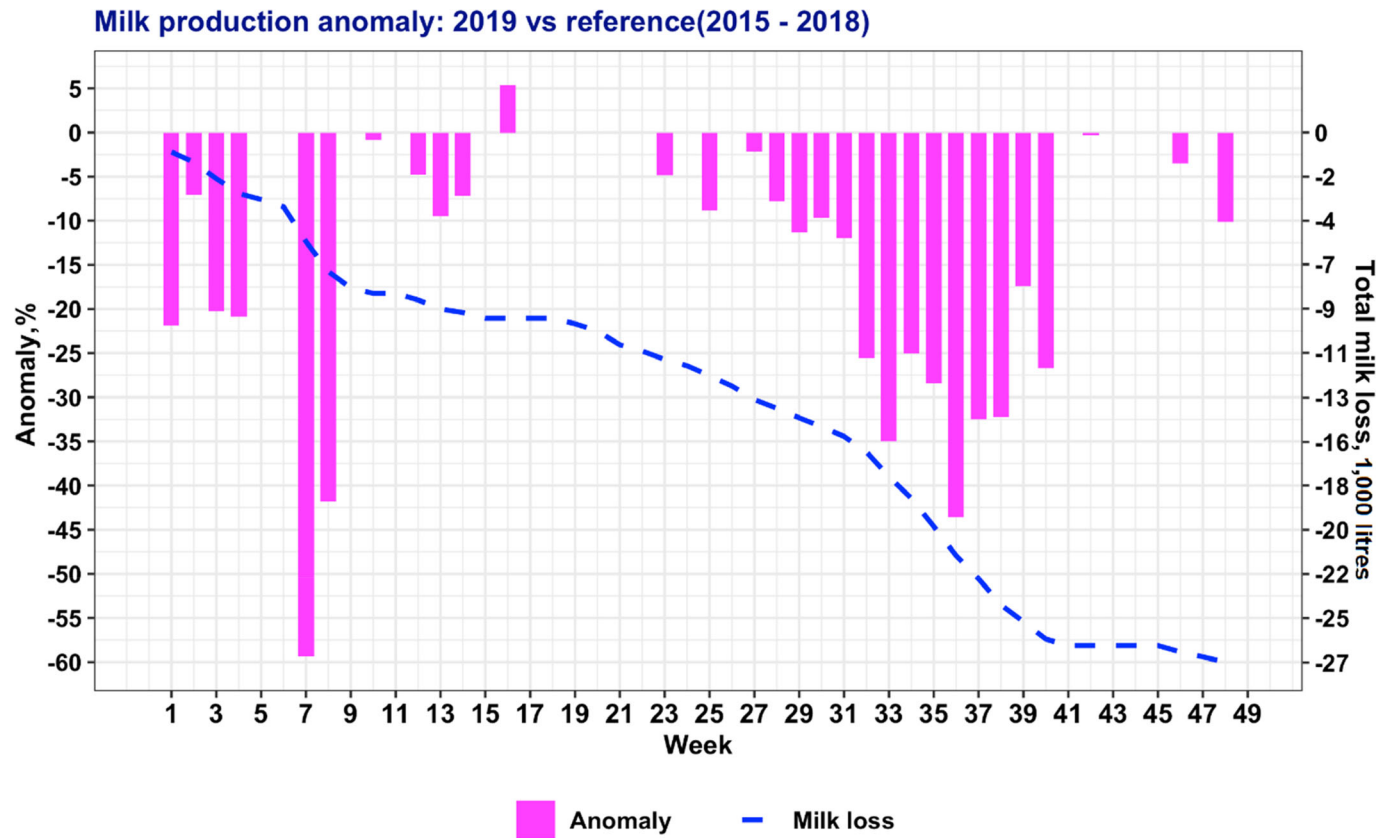
Left y-axis corresponds to the production anomaly (vertical bars, expressed as milk production in 2019 minus the lowest bound of reference period 2015–2018 (low CI) divided by low CI and the right y-axis to the total loss of milk (dashed line) in 1,000 L.

**Figure E.2:** Deviation of milk production in 2019 from expected production in the reference period (2015–2018)