

EXTERNAL SCIENTIFIC REPORT

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Assessment of the probability of entry of Rift Valley fever virus into the EU through active or passive movement of vectors

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Abstract

The overall aim of this scientific report is the assessment of the probability of entry of Rift Valley fever virus (RVFV) into the European Union (EU) through active or passive movement of vectors. Two different import pathways were considered in this report, i.e. import through flights and import via cargo on ships. The import through road transport, eggs or immature stages, and wind was not considered in this report as thought to be zero or negligible. In total 39 potential RVFV vectors were identified based on our review. Of the 39 identified potential vectors of RVFV, the five highest ranked based on their distribution in the African at-risk countries, their potential role as vector, and their behavioural and ecological traits influencing the risk of transportation were: *Anopheles pharoensis*, *Aedes aegypti*, *Mansonia uniformis*, *Aedes mcintoshi*, and *Culex quinquefasciatus*. Four of these species were also detected in airports or airplanes in the EU. The estimated probability of entry of RVFV infected mosquito vectors into the EU through the passive movement of mosquito vectors by flights is medium for the Netherlands, France, Germany and Italy. These countries are heavily connected through direct flights from the 14 at-risk countries in Africa. A low risk of RVFV import was estimated for Spain, Poland, Belgium and Austria and for 16 countries the risk was zero. Overall the risk of RVFV import through ship-cargo was zero for most of the EU Member States and low for the Netherlands, Spain, Germany and Belgium.

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Key words: Rift Valley fever virus, vector, Africa, Europe, import risk

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Summary

The overall aim of this scientific report is the assessment of the probability of entry of Rift Valley fever virus (RVFV) into the European Union (EU) through active or passive movement of vectors. Rift Valley fever (RVF) is a mosquito-borne viral disease affecting mainly ruminants. It causes abortion in pregnant susceptible ruminants and high mortality in new-born animals. The introduction of RVFV through the active or passive movement of vectors will depend on the stages of the vector that can be infected, the import pathways through which these stages can actively move or be imported, the infection rate found in vector species, the distribution of the vector species in countries where RVF outbreak occur, and the frequency of the import pathway commodities, such as number of flights or containers. Hence, this assessment reviewed the known vectors of RVFV in the endemic and epidemic countries, and their biology, ecology and distribution in order to assess the import pathways; reviewed the spatial and temporal occurrence of RVF outbreaks in animals reported to the World Organisation for Animal Health (OIE) between 2006 and 2019; and modelled the probability of entry of RVFV into the EU Member States through identified import pathways.

Two different import pathways were considered in this report, i.e. import through flights and import via cargo on ships. The import through road transport, eggs or immature stages, and wind was not considered in this report as thought to be zero or negligible.

In total 39 potential RVFV vectors were identified based on our review. Of the 39 identified potential vectors of RVFV, the five highest ranked based on their distribution in the African at-risk countries, their potential role as vector, and their behavioural and ecological traits influencing the risk of transportation were: *Anopheles pharoensis*, *Aedes aegypti*, *Mansonia uniformis*, *Aedes mcintoshi*, and *Culex quinquefasciatus*. Four of these species were also detected in airports or airplanes in the EU. The ten highest ranked potential RVFV mosquito vectors are all present in South Africa, Kenya, Mozambique, Nigeria, Sudan and Uganda. These countries are also heavily connected to the EU Member States and contributed for 72% of the direct flights from the at-risk countries to the EU Member States in 2018.

The probability of passing through the preventive or control measures before or at transport was set as unknown. Yet, the assessment was done on female mosquitoes found alive in airplanes or in containers at arrival. Hence, these mosquitoes escaped any potential control measure that could have been applied.

The probability of introduction of a RVFV infected mosquito through air transport in one year was around 0.5 for the Netherlands, France, Germany and Italy (from 0.579 to 0.452). These countries were followed by Spain, Poland, Belgium and Austria with a probability of 0.287, 0.204, 0.202, and 0.163, respectively. The number of direct flights from at-risk countries to the respective EU Member State was the driver of risk difference between the Member States. Overall the probability of introduction of an RVFV infected mosquito through sea transport was low with maximum value of 0.209 and 0.156 for the Netherlands and Spain, respectively.

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1. Introduction

1.1. Background and Terms of Reference as provided by the requestor

This contract/grant was awarded by EFSA to: VectorNet (VectorNext consortium)

Contractor/Beneficiary: VectorNet (VectorNext consortium)

Contract/Grant title: Assessment of the probability of entry of RVFV into the EU through movement (passive or active) of vectors

Contract/Grant number: SPECIFIC CONTRACT No 01/EFSA implementing framework contract NO ECDC/2019/020

1.2. Interpretation of the Terms of Reference

The overall aim of this scientific report is the assessment of the probability of entry of Rift Valley fever virus (RVFV) into the EU through active or passive movement of vectors.

Rift Valley fever (RVF) is a mosquito-borne viral disease affecting mainly ruminants. It causes abortion in pregnant susceptible ruminants and high mortality in new-borne animals. During epidemics, it can have a high impact on public health and the economy in the affected regions. The disease is caused by the RVFV, a virus of the family Bunyaviridae and genus *Phlebovirus*. The virus has been isolated from more than 30 mosquito species (Linthicum et al., 2016). Mosquitoes belonging to the *Aedes* and *Culex* genera are considered to be the main vectors. The disease is widespread in Africa and it spread to the Arabian Peninsula in 2000-2001.

The introduction of RVFV through the active or passive movement of vectors will depend on the stages of the vector that can be infected, the import pathways through which these stages can actively move or be imported, the infection rate found in vector species, the distribution of the vector species, and the frequency of the import pathway commodities, such as number of flights or containers.

This assessment addressed the following aspects:

1. Review the known vectors of RVFV in the endemic and epidemic areas, their biology and ecology in order to assess the import pathways. Special emphasis will be put on characteristics that might influence their introduction and their presence in the at-risk countries defined for this assessment (see below point 1.3);
2. Review the spatial and temporal occurrence of RVF outbreaks in animals reported to the OIE between 2006 and 2019;
3. Model the probability of entry of RVFV into the EU Member States through identified import pathways.

1.3. Additional information

EFSA informed that the following 14 countries needed to be included in the assessment: Central African Republic, Chad, The Gambia, Kenya, Mali, Mayotte, Mozambique, Niger, Nigeria, South Africa, South Sudan, Sudan, Uganda, Rwanda. These countries are subsequently called African at-risk countries.

Further, Table 1 lists the output for each EU Member State that has been requested to parameterise entomological aspects of import risk of RVF in Europe using MintRisk, a method for integral risk assessment of vector-borne livestock infections (de Vos et al., 2012).

Table 1: MintRisk questions for the risk of introduction.

| Pathways to be considered | MintRisk questions for risk of introduction | | |
|--|---|---|--|
| | What are the average numbers/volumes of animals/commodities moved along the pathway per year? | What is the probability of passing through the preventive/control measures before/at transport? | What is the probability that a viable VBD-agent is still present upon arrival in the area at risk? |
| Vectors shipped by flights | N (number) | P1 (probability) | P2 (probability) |
| Vectors shipped by container on cargo ship | N | P1 | P2 |
| Vector shipped by road transport | N | P1 | P2 |
| Vectors moved by winds | N | P1 | P2 |

2. Data and Methodologies

2.1. Data

2.1.1. Overview of the vectors, their biology and possible import pathways

Following data sources were consulted in order to review the potential vectors, their biology and possible import pathways, and their distribution in the African at-risk countries (Table 2). Journal articles were searched from Google Scholar for each of potential vector species for oviposition habits, breeding sites, host preference and flight capacity. Journal articles on biology of mosquito species were rare, the most valuable information was found in the textbooks describing African mosquitoes. These textbooks were also consulted to assess the presence of the mosquito species in at-risk countries in Africa. This information was validated by consulting the “A catalog of the mosquitoes of the world (Diptera: Culicidae)” (Knight and Stone, 1977) and a final check was done through the online WRBU Systematic Catalogue of Culicidae (Walter Reed Biosystematics Unit). Mosquito fauna of Mayotte was found in one journal article only (Le Goff et al., 2014).

Table 2: Overview of the consulted references for the vector assessment.

| Description | References |
|---|---|
| Overview of potential vector species | (EFSA Panel on Animal Health and Welfare (AHAW), 2013; Linthicum et al., 2016; Braks et al., 2017b) |
| Vector distribution in target countries | (Gaffigan et al.; Walter Reed Biosystematics Unit; Evans, 1938; Edwards, 1941; Gillies and DeMeillon, 1968; Knight and Stone, 1977; Linthicum et al., 1985; Fontenille and Jupp, 1989; Jupp, 1996; Becker et al., 2010; Le Goff et al., 2014; Ndiaye et al., 2016; Vorou, 2016; Makanda et al., 2019) |
| Vector biology and ecology | (Kerr, 1933; Evans, 1938; Edwards, 1941; Hopkins, 1952; McIntosh, 1973; Linthicum et al., 1985; Jupp and Harbach, 1990; Jupp, 1996; Khan et al., 1997; Becker et al., 2010; Ndiaye et al., 2016; Huestis et al., 2019) |
| Vector transport pathways | (Le Maitre and Chadee, 1983; Russell et al., 1984; Douglas et al., 2007; Haseyama et al., 2007; Scholte et al., 2010; Scholte et al., 2014; Ibanez-Justicia et al., 2017; Mier-y-Teran-Romero et al., 2017; Ammar et al., 2019; Schmidt et al., 2019) |

2.1.2. Assessment of the reported RVF outbreaks reported between 2006-2019 to the OIE

EFSA provided a database with the overview of the RVF outbreaks from 2006 to 2019 officially reported to the OIE as of 6 November 2019. This database contains outbreaks in animals and has following variables listed in Table 3.

Table 3: Overview of the variables in the OIE database on RVF outbreaks 2006-2019.

| Variable | Variable type | Description |
|--------------------|---------------|--|
| Disease | character | Rift Valley fever |
| Country | character | Country from where outbreak was reported |
| Code | character | Country code |
| Latitude | numeric | Latitude of the reported outbreak |
| Longitude | numeric | Longitude of the reported outbreak |
| Admin1 | character | Administrative unit level 1 |
| OBStartDate | date | Start data of the outbreak |
| OBEndDate | date | End date of the outbreak |
| Species | character | Host species affected |
| Susceptible | numeric | Number of susceptible |
| Cases | numeric | Number of cases |

2.1.3. Quantitative assessment of the risk of importation of RVFV into the EU through the active or passive movement of mosquito vectors

The following data sources were provided by EFSA (Table 4). In this report, the vector shipped by road transport was considered absent or negligible because the available international annual road freight transport was zero for all countries and over all reporting years. The number of flights reported in the database are the number of arriving flights from African at-risk countries to EU Member States.

Table 4: Overview of the database with information on flights, cargo and road transport.

| Database | Extracted on | Variables |
|---|--------------|---|
| International extra-EU air passenger transport by reporting country and partner world regions and countries | 18/11/2019 | sender country; receiver country; number of passengers 2016; number of passengers 2017; number of passengers 2018; number of flights 2016; number of flights 2017; number of flights 2018 |
| Volume of containers transported to/from main ports – quarterly data (2015-2016) | 18/11/2019 | PAR_MAR (sender country); REP_MAR (receiver country); number of containers per quarter 2015Q1, 2015Q2, 2015Q3, 2015Q4, 2016Q1, 2016Q2, 2016Q3, 2016Q4 |
| Volume of containers transported to/from main ports – quarterly data (2017-2018) | 18/11/2019 | PAR_MAR (sender country); REP_MAR (receiver country); number of containers per quarter 2017Q1, 2017Q2, 2017Q3, 2017Q4, 2018Q1, 2018Q2, 2018Q3, 2018Q4 |
| International annual road freight transport by country of loading and unloading with breakdown by reporting country | 18/11/2019 | C_LOAD (sender country); C_UNLOAD (receiver country); Units in Thousand tonnes for years 2016, 2017, 2018 |

2.2. Methodologies

2.2.1. Overview of the vectors, their biology and possible import pathways

The known vectors of RVFV in the endemic and epidemic areas were reviewed by combining three reviews (EFSA Panel on Animal Health and Welfare (AHAW), 2013; Linthicum et al., 2016; Braks et al., 2017b). These overviews contained data on mosquitoes, sand flies, flies and tick species indicating (i) whether the species was found infected with RVFV under experimental conditions or field conditions; (ii) whether the species was found capable of mechanical transmission of RVFV under experimental conditions (data provided by (Linthicum et al., 2016) only); and (iii) the country where the observations were made. This resulted in a compiled list including 134 taxa.

The following steps were taken to clean-up the list and to identify the important potential RVFV vector species:

1. The multiple species or groups were excluded from the compilation list because of duplication, species being absent from Africa, ambiguity, and synonymy (70 taxa excluded). For the classification of the Tribe Aedini, Wilkerson et al. (Wilkerson et al., 2015) was followed.
2. After the initial clean-up, the second selection criteria considered the vector potential of the species. A score from one (lowest vector potential) to six (highest vector potential) was assigned to each species based on the criteria available in the initial lists (EFSA Panel on Animal Health and Welfare (AHAW), 2013; Linthicum et al., 2016; Braks et al., 2017b) being: species from which RVFV has been isolated from field-collected specimens (field isolations, FI), species that

have been infected with RVFV under experimental conditions (lab infections, LI), species that have transmitted RVFV under experimental conditions (lab transmissions, LT), and species that are capable of mechanical transmission of RVFV under experimental conditions (mechanical transmission, MT). Vector potential parameters were ranked as following: 6 = FI+LT+MT, 5 = FI+LT, 4 = FI+MT and LI+LT+MT, 3 = LT, 2 = MT, and 1 = FI or LI, or both.

3. Seventeen taxa were excluded from the list because the vector potential was scored one or it was recorded before 1985.
4. RVFV can be biologically and mechanically transmitted by a broad range of arthropod vectors. Besides mosquitoes, they include biting midges, sand flies, flies and ticks. Supporting data for these taxa are either experimental or natural but never both. Therefore, arthropod vectors other than mosquitoes were excluded (eight taxa with scores from one to three).

Scoring of the ecological and biological characteristics of the potential mosquito vectors was applied in the next stage by grading the characteristics that can change the risk of transportation of mosquito vectors to Europe. The scoring range was the same as the one applied for the vector potential (six the highest score; one the lowest score). Ecological and biological traits chosen for this selection step were:

1. breeding site type: 6 = urban/semi urban, 3 = with rural preference but can breed in urban/semi urban, 1 = rural;
2. active flight range: 6 = active flight range 3-30 km, 3 = rarely fly over 3 km, 1 = 1-3 km; wind-borne flight range was not scored but used for modelling; and
3. host preference: 6 = human but can bite animals, 3 = animal but occasionally humans, 1 = animal.

Scoring of all the potential vector characteristics was performed according to the probability of mosquito vector to enter an airplane or container at cargo terminals, i.e. related to the risk of transportation. Therefore, the breeding site type scoring reflected the proximity to the transport point and was given the same weight as flight capacity (urban + weak flyer = rural + strong flier). Host preference was not rated to vectorial capacity but to the probability of entering the means of transportation. Anthropophilic mosquitoes were considered to have the highest chance to enter a cabin of an airplane or container at departure transport point. Oviposition habits were only indicated in the table for reference.

An alternative ranking of the ecological and biological characteristics was made. In the initial ranking, we assumed that anthropophilic species have a higher probability to be transported. Yet, these mosquitoes might not be very successful for transmitting the virus to the animal host after arriving in Europe. Therefore, we reversed the host presence scoring (6 = animal, 1 = human, 0.5 = rarely feeds on human). Reversion provided the highest weight for zoophilic mosquito species, assuming that the probability of transmitting RVFV after arrival to Europe should be higher for zoophilic mosquitoes.

Finally, to further rank the vector species, the presence/absence of 39 potential mosquito vectors in the 14 African at-risk countries was assessed.

2.2.2. Assessment of the RVF outbreaks reported between 2006-2019 to the OIE

The outbreaks reported from 2006-2019 to the OIE were reviewed in terms of the period of the year the outbreaks were reported to identify a possible at-risk period for introduction of vectors; the frequency of the outbreak occurrence; the minimum distance from the outbreaks to large airports and large and medium sized ports.

The outbreaks in the database were reported per geolocation and host species. For the analysis, data were pooled per year (considering the start date of the reported outbreak) and administrative unit level 1 (as reported in the database). The start date of the outbreak within an administrative unit and a

particular year was the earliest report date in that year and the end date the latest reported date. As reference for the subsequent analysis the smallest reported distance to airport or port was taken.

2.2.3. Quantitative assessment of the risk of importation of RVFV into the EU through the active or passive movement of mosquito vectors

The quantitative assessment of the risk of importation of RVFV into the EU through the active or passive movement of mosquito vectors followed the steps mentioned here below (Figure 1, Table 5).

1. The number of potential RVF mosquito vectors per airplane (M_A) or cargo ship (M_C) from African at-risk countries was estimated based on the number of flights from African at-risk countries to a EU Member State (A), the number of containers transported by ship from at-risk countries to a EU Member State (C) and the number of mosquitoes per flight (M_A) or the number of mosquitoes per container (M_C). The number of mosquitoes per flight was taken from Scholte et al. (Scholte et al., 2014) based on a study at an European airport. In 2010 and 2011, cabins of 38 airplanes were inspected over the period August 2010-October 2011. Of the 38 inspected cabins, 21 flights had come from Africa. Living specimens were found in 10 of the 38 inspected cabins (26.3%). Fourteen specimens were found (13 collected, 1 escaped), all female, belonging to three species: *Culex quinquefasciatus* (n=9), *Culex antennatus* (n=2), and *Aedes mcintoshi* (n=1), and *Culex* spp. (n=1). All mosquitoes collected in this study were found in airplanes that came from Africa, and most of them were found in flights originating from Tanzania. All three collected mosquito species are known vectors of human and/or veterinary pathogens including RVFV. For mosquitoes per container we relied on the information used on the study of Oliveira et al. (Oliveira et al., 2018) assessing the introduction of the Japanese encephalitis virus in the United States via infected mosquitoes.
2. Not all mosquitoes found in flights or containers will come from an outbreak area during the time an outbreak happens. We used the number of outbreaks (n_A or n_C) in a distance <295 km to an airport/port and the outbreaks median duration (d_A or d_C) per year to estimate the total number of potential RVF mosquito vectors from an outbreak area during an outbreak entering a EU Members State in airplanes (Y) or cargo ships (Z). The number of RVF outbreaks and their median duration was estimated based on the outbreak reported from 2006-2019 to OIE (see points 2.1.2 and 2.2.2). The 295 km cut-off was used, as we assumed that a mosquito can potentially be present at the premises of an airport or port introduced by wind from an outbreak located at a maximum distance from the airport or port (Huestis et al., 2019). Beyond that distance it was assumed that this probability was very small. Within the MintRisk table (Table 1) these estimates refer to (N) "*what are the average numbers/volumes of animals/commodities moved along the pathway per year?*"
3. Subsequently we estimated the probability that one infected mosquito enters a EU Member State in one year. Within the MintRisk table (Table 1) these estimates refer to (P2 of Table 1) "*what is the probability that a viable VBD-agent is still present upon arrival in the area at risk?*". For the mosquito RVFV infection rate we used the values compiled by Braks et al. in the context of the EFSA mandate "*Identify, rank and briefly characterise the vector-borne diseases that present a risk for the EU*" (Braks et al., 2017a). The calculations are based on an iterative process (5000 iterations). From the "total number RVF mosquito vectors from outbreaks entering an EU Members state during one year" we estimated the number of infected mosquitoes entering a EU Members state during one year. For this, we used values of the infection rate drawn from a distribution (Pert distribution with median value of 0.47%). Based on this simulation, we obtained a distribution of number of infected mosquitoes for each iteration (can be zero), from which we calculated the risk, i.e. the probability of introduction of an infected RVFV mosquito in one year.

4. The (P1 of Table 1) of the MintRisk table (Table 1) "*what is the probability of passing through the preventive/control measures before/at transport?*" was set as unknown. The assessment was done on female mosquitoes found alive in airplanes upon arrival (Scholte et al., 2014). Hence, mosquitoes escaped any potential control measure that could have been applied on these flights. Also mosquitoes found in containers were found alive as well (Oliveira et al., 2018).

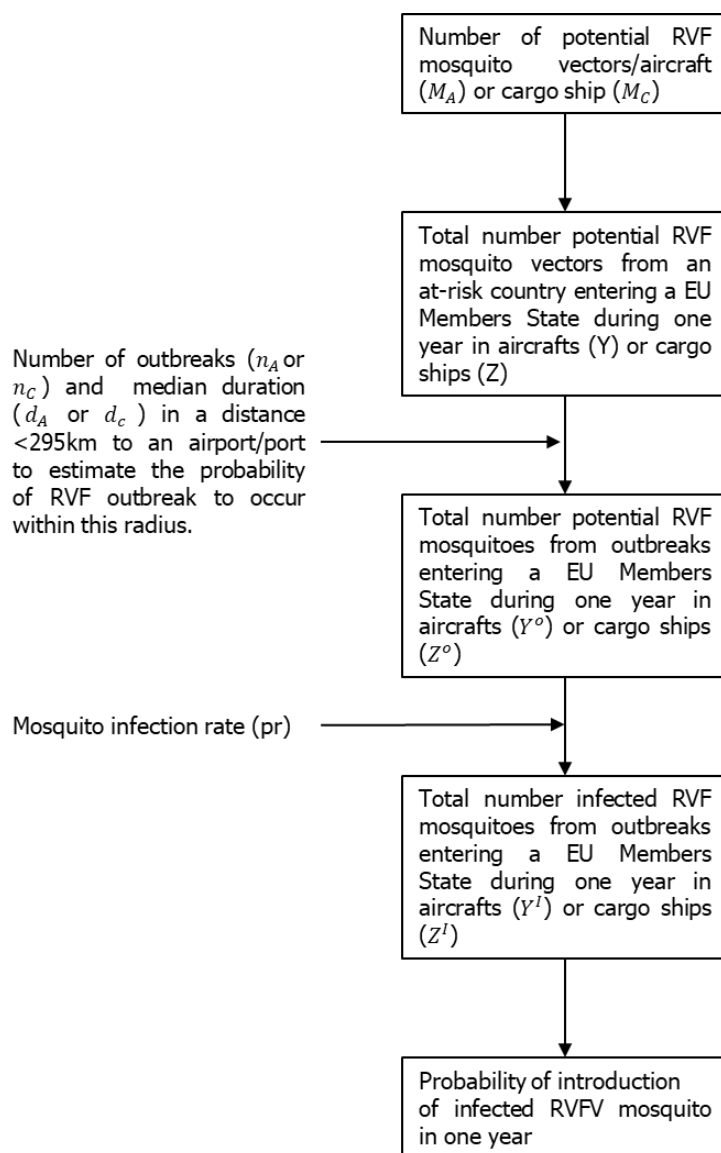


Figure 1: Overview of the model to assess the import risk of RVFV through active or passive movement of vectors.

Table 5: Overview of the parameters used in the model to assess the import risk of RVFV through active or passive movement of vectors.

| Parameter | Description | Formula | Value | Distribution | References |
|-----------|---|--------------------------------------|---|--------------|--|
| A | Number of flights from at-risk countries to an EU Member State | PERT(a,b,c) | EFSA database | PERT | EFSA database |
| C | Number of containers transported by ship from at-risk countries to an EU Member state | PERT(a,b,c) | EFSA database | PERT | EFSA database |
| M_A | Number of potential mosquito vectors per flight | $\text{Gamma}(12, \frac{1}{21})$ | | Gamma | (Scholte et al., 2014) |
| M_C | Number of mosquitoes per container | $\text{Gamma}(4, \frac{1}{11265})$ | | Gamma | Boarder Management group. Cited in (Oliveira et al., 2018) |
| Y | Number of mosquitoes from at-risk countries to an EU Member State (flights) | $M_A * A$ | | Poisson | |
| Z | Number of mosquitoes from at-risk countries to an EU Member State (containers) | $M_C * C$ | | Poisson | |
| p | Probability of an RVF outbreak in at-risk country to occur | Uniform | Sampled from the data from 2006 to 2018 | Uniform | Estimated from OIE database |
| d_A | Median duration of an RVF outbreak within a radius of 295 km from a large airport per at-risk countries (in days) | | | | Estimated from OIE database |
| n_A | Number of an RVF outbreak within a radius of 295 km from a large airport per a sampled year | | | | Estimated from OIE database |
| d_C | Median duration of an RVF outbreak within a radius of 295 km from a large or medium sized port (in days) | | | | Estimated from OIE database |
| n_C | Number of an RVF outbreak within a radius of 295 km from a large or medium sized port per a sampled year | | | | Estimated from OIE database |
| pr | Mosquito RVFV infection rate | PERT(a,b,c) | a = 0 b = 0.47% c = 25% | PERT | (Braks et al., 2017a) |
| Y^o | Number of mosquitoes from outbreak areas to an EU Member State (flights) | $Y * \min(1, \frac{n_A * d_A}{365})$ | | | |
| Z^o | Number of mosquitoes from outbreak areas to an EU Member State (containers) | $Z * \min(1, \frac{n_C * d_C}{365})$ | | | |
| Y^I | Number of infected mosquitoes from outbreak areas to an EU Member State (flights) | $\text{BINOM}(pr, Y^o)$ | | Binomial | |
| Z^I | Number of infected mosquitoes from outbreak areas to an EU Member State (containers) | $\text{BINOM}(pr, Z^o)$ | | Binomial | |

3. Assessment/Results

3.1.1. Overview of the mosquito vectors, their biology and possible import pathways

3.1.1.1. Mosquito vector species assessment

In total 39 potential RVFV mosquito vectors were identified based on the review of the three lists. Of the 39 identified potential vectors of RVFV, the five highest ranked based on their distribution in the African at-risk countries, their potential role as vector, and their behavioural and ecological traits influencing the risk of transportation were *Anopheles pharoensis*, *Aedes aegypti*, *Mansonia uniformis*, *Aedes mcintoshi*, and *Culex quinquefasciatus* (Appendix A, Table A-1). The first four species were also ranked first when giving more weight to the zoophilic behaviour of the species, i.e. assuming that the probability of transmitting RVFV after arrival to Europe should be higher for zoophilic mosquitoes (Appendix A, Table A-2).

Two out of the five top-ranked mosquito species (*Aedes mcintoshi* and *Culex quinquefasciatus*) were intercepted in the aircraft cabins in Schiphol, the Netherlands (Scholte et al., 2014). Several *Aedes aegypti* were also collected during surveillance inside the premises of the airport of Schiphol in 2016 (Ibanez-Justicia et al., 2017), 2017, 2018, and 2019 (Ibáñez-Justicia, personal communication). *Anopheles pharoensis* was collected in the cargo area of the airport of Liège, Belgium in 2018 (Van Bortel, personal communication). *Culex antennatus*, ranked 11th and 14th on the lists (Appendix A) was also intercepted in the aircraft cabins in Schiphol, the Netherlands (Scholte et al., 2014).

The ten highest listed potential RVFV mosquito vectors of either ranking (Appendix A) are all present in South Africa, Kenya, Mozambique, Nigeria, Sudan and Uganda (Appendix B). These countries are also heavily connected to the EU Member States and contributed for 72% of the direct flights from the at-risk countries to the EU Member States in 2018.

3.1.1.2. Import pathways

Transport of immature stages via airplanes or ships. The long-term maintenance of RVFV involves vertical transmission of virus to mosquito progeny, with the virus surviving long inter-epizootic periods within the egg. Lumley et al. (Lumley et al., 2017) comprehensively reviewed the evidence for and against the vertical transmission of RVFV, factors limiting its detection in natural and experimental data, and the vertical transmission of other arboviruses in the genera *Alphavirus*, *Flavivirus* and *Orthobunyavirus*. Within the context of RVFV, the authors concluded that "*Vertical transmission of RVFV is likely but that current data are insufficient to prove this hypothesis irrefutably.*" Vertical transmission was detected in *Aedes mcintoshi* and *Aedes vexans*. These mosquitoes are flood water mosquitoes and it is very unlikely that eggs of these mosquitoes are transported via goods and will arrive into Europe. No vertical transmission of RVFV was reported in container-breeding *Aedes* mosquitoes (which eggs are frequently transported). Hence, we assessed that the importation of RVFV through the transport of eggs is unlikely. The ecology and biology of eggs, larvae/pupae, as well as the likelihood for their transportation, were not further considered.

Wind dispersal. A recent paper showed that wind dispersal of mosquitoes is possible (Huestis et al., 2019). In this study a maximum wind dispersal of 295 km was observed. The African at-risk countries are beyond this wind-dispersal distance to Europe (e.g. more than 1000 km from the border of Sudan to Crete). Hence, we assumed that it is very unlikely that mosquitoes are transported alive from African at-risk countries to EU Member States and we did not further consider the risk of importation of RVFV through wind dispersal of mosquito vectors.

3.1.2. Assessment of the RVF outbreaks reported between 2006-2019 to the OIE

Most of the outbreaks reported to the OIE between 2006-2019 were located at a distance of more than 30 km from a large airport or port, which is beyond the active flight range of the RVF mosquito vectors (Figure 2, Figure 3, Appendix A). For the modelling of import through flights or ports we assumed that a mosquito can potentially be present at the premises of an airport or port introduced by wind from an outbreak located at a maximum distance of 295 km (Huestis et al., 2019) from the airport or port.

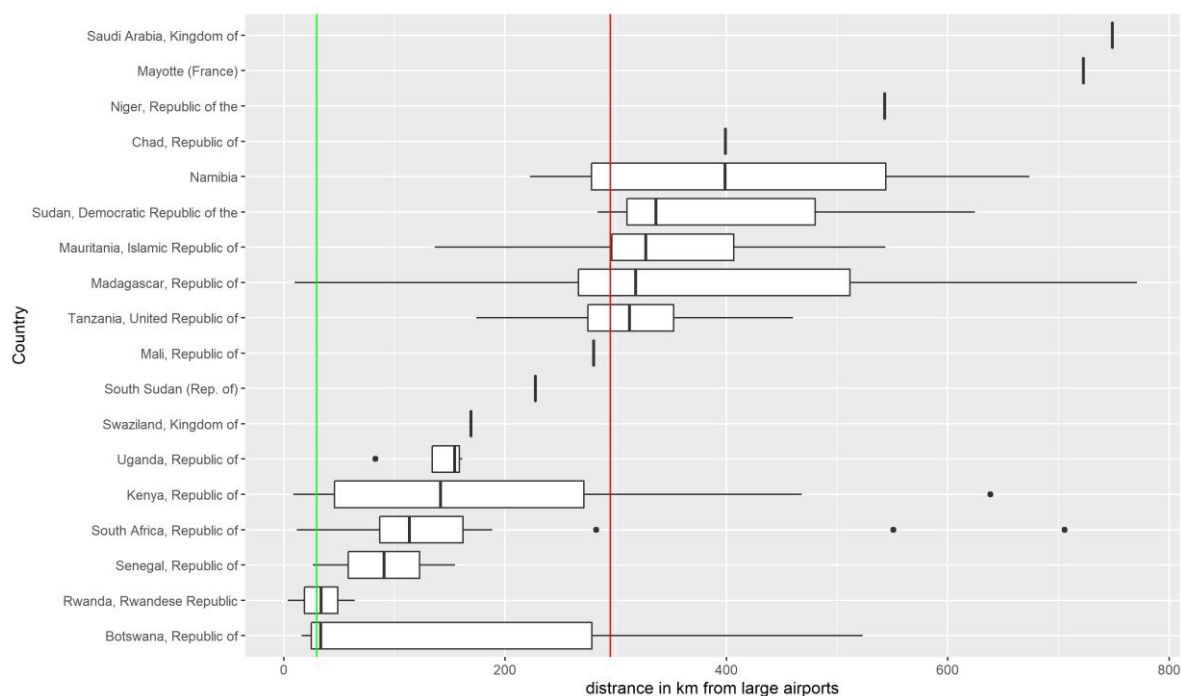


Figure 2: The distance of the RVF outbreaks reported between 2006-2019 from large airports. The green line indicates the maximum active flight range of the RVF mosquito vectors. The red line indicates the 295 km limit of wind dispersal observed in (Huestis et al., 2019).

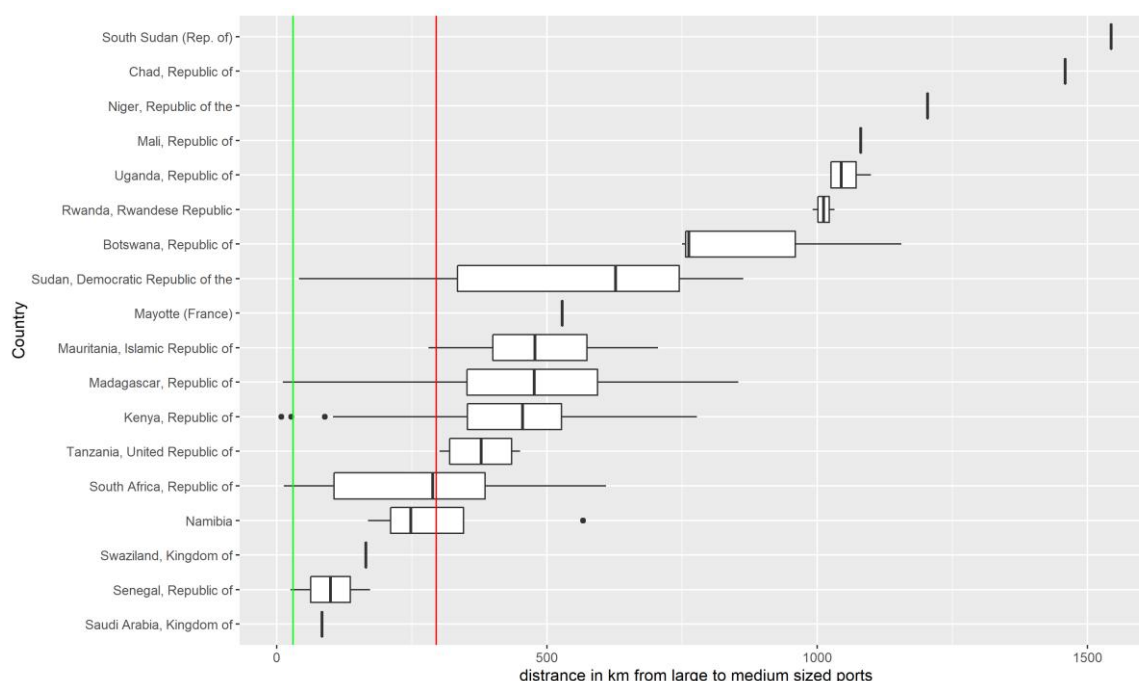


Figure 3: The distance of the RVFV outbreaks reported between 2006-2019 from ports. The green line indicates the maximum active flight range of the RVFV mosquito vectors. The red line indicates the 295 km limit of wind dispersal observed in (Huestis et al., 2019).

3.1.3. Quantitative risk assessment of the risk of importation of Rift Valley fever virus into the EU through the active or passive movement of mosquito vectors

The probability of introduction of a RVFV infected mosquito through air and sea transport in one year is reported in Appendix C. This probability was around 0.5 (from 0.579 to 0.452) for the Netherlands, France, Germany and Italy. These countries were followed by Spain, Poland, Belgium and Austria with a probability of 0.287, 0.204, 0.202, and 0.163, respectively. The number of direct flights from at-risk countries to the respective EU Member State was the driver of risk difference between the Member States. The fact that potential RVFV mosquito vectors were detected in 10 of the 21 inspected cabins (12 specimens of potential RVFV mosquito vectors) in the study of Scholte et al. (Scholte et al., 2014) determined the overall risk level. This study was done on one of the busiest airports of the EU, Schiphol, which is ranked second in number of air transport movements in Europe (Schiphol_nl, 2019). Hence our estimates of the import risk might be on the high side.

Overall the probability of introduction of a RVFV infected mosquito through sea transport was low with a maximum value of 0.209 and 0.156 for the Netherlands and Spain, respectively.

In this report, the vectors shipped by road transport were considered absent or negligible because, based on the available data, the international annual road freight transport was zero for all countries and over all reporting years.

In a recent study a maximum wind dispersal of 295 km was observed for a number of mosquito species. Since the at-risk countries are beyond this wind-dispersal distance (e.g. more than 1000 km from the

border of Sudan to Crete) we assumed that it is very unlikely that mosquitoes are transported alive from African at-risk countries to EU Member States through wind.

4. Conclusions

The estimated probability of entry of RVFV infected mosquito vectors into the EU through the passive movement of mosquito vectors by flights is medium for the Netherlands, France, Germany and Italy. These countries are heavily connected through direct flights from the 14 at-risk countries in Africa. A low risk of RVFV import was estimated for Spain, Poland, Belgium and Austria and for 16 countries the risk was zero. Overall the risk of RVFV import through ship-cargo was zero for most of the EU Member States and low for the Netherlands, Spain, Germany and Belgium.

The probability of passing through the preventive/control measures before or at transport was set as unknown. Yet, the assessment was done on female mosquitoes found alive in airplanes (Scholte et al., 2010) or in containers at arrival. Hence, these mosquitoes escaped any potential control measure that could have been applied.

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Appendix A – RVFV mosquito vector species ranking according to their potential role as vector, their behavioural and ecological traits influencing the risk of transportation and their distribution in the at-risk countries

Table A-1: Scoring of all the potential vector characteristics was performed according to the probability of mosquito vector to enter the airplane or container at cargo terminals, i.e. related to the risk of transportation.

| Number | Vector species | Subgenus | Oviposition habits | | | Breeding site type | | | Flight range | | | Wind-borne: average/maximum distance in km | | Host preference | | Role as vector | Species presence index in African at-risk countries ^d | Overall score |
|--------|--------------------------------------|------------------------|--------------------|----------------|----------------|--------------------|-------|---------|--------------|-------------------------|--|--|--|-----------------|--------|----------------|--|---------------|
| | | | container | water surface | ground | urban/semi-urban | rural | 3-30 km | 1-3 km | recorded distance in km | | | | human | animal | | | |
| 1 | <i>Anopheles pharoensis</i> | <i>Cellia</i> | | x | | 3 | 1 | 6 | | 29 to 45 | | 31.1/260 | | 6 | 1 | 5 | 5.14 | 27.14 |
| 2 | <i>Aedes aegypti</i> | <i>Stegomyia</i> | x | | | 6 | 1 | | | eo | | | | 6 | 1 | 6 | 6.00 | 27.00 |
| 3 | <i>Mansonia uniformis</i> | <i>Mansonioides</i> | | x ^a | | 6 | 1 | 6 | | 3 to 6 | | | | 6 | 1 | 1 | 5.14 | 26.14 |
| 4 | <i>Aedes mcintoshi</i> | <i>Neomelaniconion</i> | | | x | 3 | 1 | 6 | | eo | | | | 6 | 1 | 5 | 3.43 | 25.43 |
| 5 | <i>Culex quinquefasciatus</i> | <i>Culex</i> | | x | | 6 | 1 | | | eo | | | | 6 | 1 | 5 | 5.14 | 25.14 |
| 6 | <i>Anopheles gambiae</i> | <i>Cellia</i> | | x | | 6 | 1 | 6 | | 1 to 4.8 | | 33.5/- | | 6 | | 1 | 5.14 | 25.14 |
| 7 | <i>Aedes cumminsii</i> | <i>Aedimorphus</i> | | | x | 3 | 1 | 6 | | eo | | | | 6 | 1 | 5 | 3.00 | 25.00 |
| 8 | <i>Culex pipiens</i> | <i>Culex</i> | | x | | 6 | 1 | | | eo | | | | 6 | 1 | 6 | 3.86 | 24.86 |
| 9 | <i>Mansonia africana</i> | <i>Mansonioides</i> | | x ^a | | 6 | 1 | 6 | | eo | | | | 6 | 1 | 1 | 3.86 | 24.86 |
| 10 | <i>Aedes circumluteolus</i> | <i>Neomelaniconion</i> | | | x | | 1 | 6 | | eo | | | | 6 | 1 | 5 | 5.57 | 24.57 |
| 11 | <i>Culex antennatus</i> | <i>Culex</i> | | x | | 6 | 1 | | | eo | | | | 6 | 1 | 5 | 3.86 | 23.86 |
| 12 | <i>Aedes dalzieli</i> | <i>Aedimorphus</i> | | | x | 3 | 1 | 6 | | eo | | | | 6 | 1 | 5 | 1.71 | 23.71 |
| 13 | <i>Eretmapodites quinquevittatus</i> | n/a | x | x | | 6 | 1 | 3 | | rarely over 3 | | | | 3 | 1 | 5 | 3.86 | 22.86 |
| 14 | <i>Aedes tarsalis</i> | <i>Catageomyia</i> | | | x ^b | | 1 | 6 | | eo | | | | 6 | 1 | 5 | 3.00 | 22.00 |
| 15 | <i>Aedes palpalis</i> | <i>Neomelaniconion</i> | | | x | | 1 | 6 | | eo | | | | 6 | 1 | 5 | 3.00 | 22.00 |
| 16 | <i>Eretmapodites chrysogaster</i> | n/a | x | x | | 6 | 1 | 3 | | rarely over 3 | | | | 3 | 1 | 5 | 3.00 | 22.00 |
| 17 | <i>Culex theileri</i> | <i>Culex</i> | | x | | 6 | 1 | | | eo | | | | 6 | 1 | 5 | 1.71 | 21.71 |
| 18 | <i>Culex univittatus</i> | <i>Culex</i> | | x | | 6 | 1 | | | eo | | | | 3 | 1 | 5 | 4.71 | 21.71 |
| 19 | <i>Anopheles squamosus</i> | <i>Cellia</i> | | x | | | 1 | 6 | | | | 27.7/265 | | 3 | 1 | 5 | 5.57 | 21.57 |
| 20 | <i>Aedes fowleri</i> | <i>Aedimorphus</i> | | | x | | 1 | 6 | | eo | | | | 6 | 1 | 3 | 4.29 | 21.29 |
| 21 | <i>Aedes vexans</i> | <i>Aedimorphus</i> | | | x | | 1 | 6 | | eo | | | | 6 | 1 | 5 | 2.14 | 21.14 |
| 22 | <i>Anopheles coustani</i> | <i>Anopheles</i> | | x | | 3 | 1 | 6 | | | | 28.5/295 | | 3 | 1 | 1 | 6.00 | 21.00 |
| 23 | <i>Culex neavei</i> | <i>Culex</i> | | x | | 3 | 1 | | | eo | | | | 6 | 1 | 5 | 3.86 | 20.86 |
| 24 | <i>Aedes ochraceus</i> | <i>Aedimorphus</i> | | | x | | 1 | 6 | | eo | | | | 6 | 1 | 5 | 1.71 | 20.71 |
| 25 | <i>Aedes caballus</i> | <i>Ochlerotatus</i> | | | x | | 1 | 6 | | eo | | | | 6 | 1 | 5 | 1.71 | 20.71 |
| 26 | <i>Anopheles multicolor</i> | <i>Cellia</i> | | x | | 3 | 1 | 6 | | 13 | | | | 6 | 1 | 3 | 0.43 | 20.43 |
| 27 | <i>Anopheles arabiensis</i> | <i>Cellia</i> | | x | | 6 | 1 | | | eo | | | | 6 | 1 | 1 | 4.29 | 20.29 |
| 28 | <i>Aedes albopictus</i> | <i>Stegomyia</i> | x | | | 6 | 1 | | | eo | | | | 6 | 1 | 3 | 2.14 | 20.14 |
| 29 | <i>Aedes durbanensis</i> | <i>Aedimorphus</i> | | | x | | 1 | 6 | | eo | | | | 6 | 1 | 5 | 0.86 | 19.86 |
| 30 | <i>Aedes juppi</i> | <i>Ochlerotatus</i> | | | x | | 1 | 6 | | eo | | | | 6 | 1 | 5 | 0.43 | 19.43 |
| 31 | <i>Coquillettia fuscipennata</i> | <i>Coquillettia</i> | | x | | | 1 | 6 | | eo | | | | 3 | 1 | 5 | 2.14 | 18.14 |
| 32 | <i>Culex poicilipes</i> | <i>Oculeomyia</i> | | x | | | 1 | | | eo | | | | 6 | 1 | 5 | 3.43 | 17.43 |
| 33 | <i>Aedes caspius</i> | uncertain | | | x | | 1 | 6 | | eo | | | | 6 | 1 | 3 | 0.00 | 17.00 |
| 34 | <i>Culex zombaensis</i> | <i>Culex</i> | | x | | | 1 | | | eo | | | | 6 | 1 | 5 | 3.00 | 17.00 |
| 35 | <i>Culex bitaeniorhynchus</i> | <i>Oculeomyia</i> | | x | | 3 | 1 | | | eo | | | | 6 | 1 | 1 | 3.86 | 16.86 |
| 36 | <i>Eretmapodites intermedius</i> | n/a | x | x | | | 1 | 3 | | rarely over 3 | | | | 3 | 1 | 5 | 1.71 | 14.71 |
| 37 | <i>Culex perexiguus</i> | <i>Culex</i> | | x | | 3 | 1 | | | eo | | | | 3 | 1 | 3 | 1.71 | 13.71 |
| 38 | <i>Aedes pemaensis</i> | <i>Skusea</i> | | | x ^c | | 1 | 6 | | eo | | | | 3 | 1 | 1 | 0.86 | 12.86 |
| 39 | <i>Culex tritaeniorhynchus</i> | <i>Culex</i> | | x | | | 1 | | | eo | | | | 3 | 1 | 1 | 3.00 | 10.00 |

n/a: not applicable, there are no subgenera in the genus *Eretmapodites*; ^a: female glues the eggs underneath the floating leaves; ^b: oviposition habit doubtful; ^c: female glues the eggs on the crab front legs, larvae develop in crab burrows; eo: expert opinion; ^d: see Appendix B.

RVFV import through vectors

Table A-2: An alternative ranking of the ecological and biological characteristics was made. In the initial ranking, we assumed that anthropophilic species have a higher probability to be transported. Yet, these mosquitoes might not be very successful for transmitting the virus to the animal host after arriving in Europe. Therefore, we reversed the host presence scoring (6 = animal, 1 = human, 0.5 = rarely feeds on humans). Reversion provided the highest weight for zoophilic mosquito species, assuming that the probability of transmitting RVFV after arrival to Europe should be higher for zoophilic mosquitoes.

| Number | Vector species | Subgenus | Oviposition habits | | | Breeding site type | | Flight range | | | wind borne (average/maximum distance in km) | Host preference | | Role as vector | Species presence index in African at- risk countries ^d | Overall score |
|--------|--------------------------------------|------------------------|--------------------|----------------------|----------------|---------------------|-------|--------------|--------|-------------------------------|---|-----------------|--------|----------------------|--|------------------|
| | | | conta iner | water surfa ce | groun d | urban/ semiurban | rural | 3-30 km | 1-3 km | recorded distance in km | | human | animal | | | |
| 1 | <i>Anopheles pharoensis</i> | <i>Cellia</i> | | x | | 3 | 1 | 6 | | 29 to 45 | 31.1/260 | 1 | 6 | 5 | 5.14 | 27.14 |
| 2 | <i>Aedes aegypti</i> | <i>Stegomyia</i> | x | | | 6 | 1 | | 1 | eo | | 1 | 6 | 6 | 6.00 | 27.00 |
| 3 | <i>Mansonia uniformis</i> | <i>Mansonioides</i> | | x ^a | | 6 | 1 | 6 | | 3 to 6 | | 1 | 6 | 1 | 5.14 | 26.14 |
| 4 | <i>Aedes mcintoshi</i> | <i>Neomelaniconion</i> | | | x | 3 | 1 | 6 | | eo | | 1 | 6 | 5 | 3.43 | 25.43 |
| 5 | <i>Eretmapodites quinquevittatus</i> | n/a | x | x | | 6 | 1 | 3 | | rarely over 3 | | 0.5 | 6 | 5 | 3.86 | 25.36 |
| 6 | <i>Culex quinquefasciatus</i> | <i>Culex</i> | | x | | 6 | 1 | | 1 | eo | | 1 | 6 | 5 | 5.14 | 25.14 |
| 7 | <i>Anopheles squamosus</i> | <i>Cellia</i> | | x | | 6 | 1 | | 1 | eo | | 0.5 | 6 | 5 | 5.57 | 25.07 |
| 8 | <i>Aedes cumminsii</i> | <i>Aedimorphus</i> | | | x | 3 | 1 | 6 | | eo | | 1 | 6 | 5 | 3.00 | 25.00 |
| 9 | <i>Culex pipiens</i> | <i>Culex</i> | | x | | 6 | 1 | | 1 | eo | | 1 | 6 | 6 | 3.86 | 24.86 |
| 10 | <i>Mansonia africana</i> | <i>Mansonioides</i> | | x ^a | | 6 | 1 | 6 | | eo | | 1 | 6 | 1 | 3.86 | 24.86 |
| 11 | <i>Aedes circumluteolus</i> | <i>Neomelaniconion</i> | | | x | 1 | 1 | 6 | | eo | | 1 | 6 | 5 | 5.57 | 24.57 |
| 12 | <i>Eretmapodites chrysogaster</i> | n/a | x | x | | 6 | 1 | 3 | | rarely over 3 | | 0.5 | 6 | 5 | 3.00 | 24.50 |
| 13 | <i>Culex univittatus</i> | <i>Culex</i> | | x | | 6 | 1 | | 1 | eo | | 0.5 | 6 | 5 | 4.71 | 24.21 |
| 14 | <i>Culex antennatus</i> | <i>Culex</i> | | x | | 6 | 1 | | 1 | | | 1 | 6 | 5 | 3.86 | 23.86 |
| 15 | <i>Aedes dalzieli</i> | <i>Aedimorphus</i> | | | x | 3 | 1 | 6 | | eo | | 1 | 6 | 5 | 1.71 | 23.71 |
| 16 | <i>Anopheles coustani</i> | <i>Anopheles</i> | | x | | 3 | 1 | 6 | | | 28.5/295 | 0.5 | 6 | 1 | 6.00 | 23.50 |
| 17 | <i>Aedes tarsalis</i> | <i>Catagomyia</i> | | | x ^b | 1 | 1 | 6 | | eo | | 1 | 6 | 5 | 3.00 | 22.00 |
| 18 | <i>Aedes palpalis</i> | <i>Neomelaniconion</i> | | | x | 1 | 1 | 6 | | eo | | 1 | 6 | 5 | 3.00 | 22.00 |
| 19 | <i>Culex theileri</i> | <i>Culex</i> | | x | | 6 | 1 | | 1 | eo | | 1 | 6 | 5 | 1.71 | 21.71 |
| 20 | <i>Aedes fowleri</i> | <i>Aedimorphus</i> | | | x | 1 | 1 | 6 | | eo | | 1 | 6 | 3 | 4.29 | 21.29 |
| 21 | <i>Aedes vexans</i> | <i>Aedimorphus</i> | | | x | 1 | 1 | 6 | | eo | | 1 | 6 | 5 | 2.14 | 21.14 |
| 22 | <i>Culex neavei</i> | <i>Culex</i> | | x | | 3 | 1 | | 1 | eo | | 1 | 6 | 5 | 3.86 | 20.86 |
| 23 | <i>Aedes ochraceus</i> | <i>Aedimorphus</i> | | | x | 1 | 1 | 6 | | eo | | 1 | 6 | 5 | 1.71 | 20.71 |
| 24 | <i>Aedes caballus</i> | <i>Ochlerotatus</i> | | | x | 1 | 1 | 6 | | eo | | 1 | 6 | 5 | 1.71 | 20.71 |
| 25 | <i>Coquillettidia fuscopennata</i> | <i>Coquillettidia</i> | | x | | 1 | 1 | 6 | | eo | | 0.5 | 6 | 5 | 2.14 | 20.64 |
| 26 | <i>Anopheles multicolor</i> | <i>Cellia</i> | | x | | 3 | 1 | 6 | | 13 | | 1 | 6 | 3 | 0.43 | 20.43 |
| 27 | <i>Anopheles arabiensis</i> | <i>Cellia</i> | | x | | 6 | 1 | | 1 | eo | | 1 | 6 | 1 | 4.29 | 20.29 |
| 28 | <i>Aedes albopictus</i> | <i>Stegomyia</i> | x | | | 6 | 1 | | 1 | eo | | 1 | 6 | 3 | 2.14 | 20.14 |
| 29 | <i>Anopheles gambiae</i> | <i>Cellia</i> | | x | | 6 | 1 | | | 1 to 4.8 | 33.5/- | 1 | 1 | 1 | 5.14 | 20.14 |
| 30 | <i>Aedes durbanensis</i> | <i>Aedimorphus</i> | | | x | 1 | 1 | 6 | | eo | | 1 | 6 | 5 | 0.86 | 19.86 |
| 31 | <i>Aedes juppi</i> | <i>Ochlerotatus</i> | | | x | 1 | 1 | 6 | | eo | | 1 | 6 | 5 | 0.43 | 19.43 |
| 32 | <i>Culex poicilipes</i> | <i>Oculeomyia</i> | | x | | 1 | 1 | | 1 | eo | | 1 | 6 | 5 | 3.43 | 17.43 |
| 33 | <i>Eretmapodites intermedius</i> | n/a | x | x | | 1 | 1 | 3 | | rarely over 3 | | 0.5 | 6 | 5 | 1.71 | 17.21 |
| 34 | <i>Aedes caspius</i> | uncertain | | | x | 1 | 1 | 6 | | eo | | 1 | 6 | 3 | 0.00 | 17.00 |
| 35 | <i>Culex zombaensis</i> | <i>Culex</i> | | x | | 1 | 1 | | 1 | eo | | 1 | 6 | 5 | 3.00 | 17.00 |
| 36 | <i>Culex bitaeniorhynchus</i> | <i>Oculeomyia</i> | | x | | 3 | 1 | | 1 | eo | | 1 | 6 | 1 | 3.86 | 16.86 |
| 37 | <i>Culex perexiguus</i> | <i>Culex</i> | | x | | 3 | 1 | | 1 | eo | | 0.5 | 6 | 3 | 1.71 | 16.21 |
| 38 | <i>Aedes pambiaensis</i> | <i>Skusea</i> | | | x ^c | 1 | 1 | 6 | | eo | | 0.5 | 6 | 1 | 0.86 | 15.36 |
| 39 | <i>Culex tritaeniorhynchus</i> | <i>Culex</i> | | x | | 1 | 1 | | 1 | eo | | 0.5 | 6 | 1 | 3.00 | 12.50 |

n/a: not applicable, there are no subgenera in the genus *Eretmapodites*; ^a: female glues the eggs underneath the floating leaves; ^b: oviposition habit doubtful; ^c: female glues the eggs on the crab front legs, larvae develop in crab burrows; eo: expert opinion; ^d: see Appendix B.

Appendix B – RVFV mosquito vector species distribution in the African at-risk countries

| Number | Vector species | Subgenus | South Africa | Kenya | Mozambique | Nigeria | Sudan | Uganda | South Sudan | Central African Republic | The Gambia | Mali | Mayotte | Niger | Chad | Rwanda | Overall presence | Species presence index |
|--|--------------------------------------|------------------------|--------------|-----------|------------|-----------|-----------|-----------|-------------|--------------------------|------------|-----------|-----------|-----------|----------|----------|------------------|------------------------|
| 1 | <i>Anopheles coustani</i> | <i>Anopheles</i> | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 14 | 6.00 |
| 2 ^a | <i>Aedes aegypti</i> | <i>Stegomyia</i> | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 14 | 6.00 |
| 3 | <i>Anopheles squamosus</i> | <i>Cellia</i> | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 13 | 5.57 |
| 4 | <i>Aedes circumluteolus</i> | <i>Neomelanicolion</i> | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 13 | 5.57 |
| 5 | <i>Anopheles gambiae</i> | <i>Cellia</i> | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 0 | 12 | 5.14 |
| 6 ^a | <i>Anopheles pharoensis</i> | <i>Cellia</i> | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 12 | 5.14 |
| 7 ^a | <i>Culex quinquefasciatus</i> | <i>Culex</i> | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 0 | 12 | 5.14 |
| 8 | <i>Mansonia uniformis</i> | <i>Mansonioides</i> | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 0 | 12 | 5.14 |
| 9 | <i>Culex univittatus</i> | <i>Culex</i> | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 0 | 0 | 11 | 4.71 |
| 10 | <i>Anopheles arabiensis</i> | <i>Cellia</i> | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 0 | 1 | 1 | 0 | 1 | 1 | 0 | 10 | 4.29 |
| 11 | <i>Aedes fowleri</i> | <i>Aedimorphus</i> | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 0 | 0 | 0 | 10 | 4.29 |
| 12 | <i>Eretmapodites quinquevittatus</i> | n/a | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 0 | 0 | 0 | 9 | 3.86 |
| 13 ^a | <i>Culex antennatus</i> | <i>Culex</i> | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 0 | 1 | 1 | 0 | 0 | 0 | 9 | 3.86 |
| 14 | <i>Culex neavei</i> | <i>Culex</i> | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 9 | 3.86 |
| 15 | <i>Culex pipiens</i> | <i>Culex</i> | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 9 | 3.86 |
| 16 | <i>Culex bitaeniorhynchus</i> | <i>Oculeomyia</i> | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 9 | 3.86 |
| 17 | <i>Mansonia africana</i> | <i>Mansonioides</i> | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 9 | 3.86 |
| 18 ^a | <i>Aedes mcintoshi</i> | <i>Neomelanicolion</i> | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 8 | 3.43 |
| 19 | <i>Culex poicilipes</i> | <i>Oculeomyia</i> | 1 | 1 | 1 | 1 | 0 | 1 | 0 | 1 | 1 | 1 | 0 | 0 | 0 | 0 | 8 | 3.43 |
| 20 | <i>Aedes cumminsii</i> | <i>Aedimorphus</i> | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 7 | 3.00 |
| 21 | <i>Aedes tarsalis</i> | <i>Catagelomyia</i> | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 7 | 3.00 |
| 22 | <i>Aedes palpalis</i> | <i>Neomelanicolion</i> | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 7 | 3.00 |
| 23 | <i>Eretmapodites chrysogaster</i> | n/a | 1 | 1 | 0 | 1 | 0 | 1 | 0 | 1 | 1 | 1 | 0 | 0 | 0 | 0 | 7 | 3.00 |
| 24 | <i>Culex tritaeniorhynchus</i> | <i>Culex</i> | 1 | 1 | 1 | 1 | 0 | 0 | 0 | 1 | 1 | 1 | 1 | 0 | 0 | 0 | 7 | 3.00 |
| 25 | <i>Culex zombaensis</i> | <i>Culex</i> | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 7 | 3.00 |
| 26 | <i>Aedes vexans</i> | <i>Aedimorphus</i> | 1 | 0 | 0 | 1 | 1 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 5 | 2.14 |
| 27 | <i>Aedes albopictus</i> | <i>Stegomyia</i> | 1 | 0 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 5 | 2.14 |
| 28 | <i>Coquilletidia fuscopennata</i> | <i>Coquilletidia</i> | 1 | 1 | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 5 | 2.14 |
| 29 | <i>Aedes dalzieli</i> | <i>Aedimorphus</i> | 0 | 0 | 1 | 1 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 4 | 1.71 |
| 30 | <i>Aedes ochraceus</i> | <i>Aedimorphus</i> | 1 | 1 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 4 | 1.71 |
| 31 | <i>Aedes caballus</i> | <i>Ochlerotatus</i> | 1 | 1 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 4 | 1.71 |
| 32 | <i>Eretmapodites intermedius</i> | n/a | 0 | 1 | 0 | 0 | 1 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 4 | 1.71 |
| 33 | <i>Culex perexiguus</i> | <i>Culex</i> | 0 | 1 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 4 | 1.71 |
| 34 | <i>Culex theileri</i> | <i>Culex</i> | 1 | 1 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 4 | 1.71 |
| 35 | <i>Aedes durbanensis</i> | <i>Aedimorphus</i> | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 2 | 0.86 |
| 36 | <i>Aedes pembaensis</i> | <i>Skusea</i> | 0 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 2 | 0.86 |
| 37 | <i>Anopheles multicolor</i> | <i>Cellia</i> | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0.43 |
| 38 | <i>Aedes juppi</i> | <i>Ochlerotatus</i> | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0.43 |
| 39 | <i>Aedes caspius</i> | uncertain | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0.00 |
| Total potential vector species present in a country | | | 33 | 31 | 30 | 30 | 28 | 26 | 24 | 17 | 17 | 15 | 12 | 12 | 8 | 7 | | |

n/a: not applicable, there are no subgenera in the genus *Eretmapodites*; ^a: female mosquito transported alive from Africa to Europe.

Appendix C – Quantitative risk assessment of the risk of importation of RVFV into the EU through vectors introduced by flights and by container on cargo ships

Table C-0: Variable description.

| Variable | Description |
|---------------------|--|
| Country | Receiver EU Member State |
| Transport | air: assessment through flight; mar: assessment through container on cargo ships |
| MosqOutb | Total number RVF mosquitoes from outbreaks entering an EU Member state during one year |
| MosqOutbLCI | Lower CI nbr of Total number RVF mosquitoes from outbreaks entering an EU Member state during one year |
| MosqOutbUpCI | Upper CI nbr of total number RVF mosquitoes from outbreaks entering an EU Member state during one year |
| Risk | Probability of introduction of an infected RVFV mosquito in one year |
| RiskLCI | Lower CI of probability of introduction of an infected RVFV mosquito in one year |
| RiskUpCI | Upper CI probability of introduction of an infected RVFV mosquito in one year |

Table C-1: Risk of importation of RVFV into the EU through vectors introduced by flights.

| Country | Transport | MosqOutb | MosqOutbLCI | MosqOutbUpCI | Risk | RiskLCI | RiskUpCI |
|-------------|-----------|----------|-------------|--------------|-------|---------|----------|
| Austria | air | 7.619 | 6.814 | 8.411 | 0.163 | 0.141 | 0.186 |
| Belgium | air | 12.479 | 10.982 | 14.037 | 0.202 | 0.178 | 0.226 |
| Bulgaria | air | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 |
| Croatia | air | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 |
| Cyprus | air | 0.012 | 0.006 | 0.020 | 0.000 | 0.000 | 0.002 |
| Czechia | air | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 |
| Denmark | air | 0.012 | 0.006 | 0.020 | 0.000 | 0.000 | 0.002 |
| Estonia | air | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 |
| Finland | air | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 |
| France | air | 601.379 | 555.043 | 647.849 | 0.530 | 0.502 | 0.558 |
| Germany | air | 858.709 | 782.014 | 938.435 | 0.501 | 0.472 | 0.529 |
| Greece | air | 0.171 | 0.141 | 0.204 | 0.007 | 0.003 | 0.013 |
| Hungary | air | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 |
| Ireland | air | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 |
| Italy | air | 98.736 | 90.738 | 106.836 | 0.452 | 0.423 | 0.481 |
| Latvia | air | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 |
| Lithuania | air | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 |
| Luxembourg | air | 0.028 | 0.018 | 0.040 | 0.001 | 0.000 | 0.004 |
| Malta | air | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 |
| Netherlands | air | 770.358 | 711.589 | 831.024 | 0.579 | 0.552 | 0.605 |
| Poland | air | 18.446 | 16.233 | 20.773 | 0.204 | 0.179 | 0.228 |
| Portugal | air | 0.028 | 0.018 | 0.039 | 0.001 | 0.000 | 0.004 |
| Romania | air | 0.000 | 0.000 | 0.001 | 0.000 | 0.000 | 0.000 |
| Slovakia | air | 0.000 | 0.000 | 0.002 | 0.000 | 0.000 | 0.000 |
| Slovenia | air | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 |
| Spain | air | 65.534 | 58.665 | 72.516 | 0.287 | 0.260 | 0.317 |
| Sweden | air | 0.272 | 0.210 | 0.341 | 0.011 | 0.005 | 0.018 |
| UK | air | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 |

Table C-2: Risk of importation of RVFV into the EU though vectors introduced by container on cargo ships.

| Country | transport | MosqOutb | MosqOutbLCI | MosqOutbUpCI | Risk | RiskLCI | RiskUpCI |
|-------------|-----------|----------|-------------|--------------|-------|---------|----------|
| Austria | mar | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 |
| Belgium | mar | 4.434 | 3.934 | 4.945 | 0.122 | 0.102 | 0.143 |
| Bulgaria | mar | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 |
| Croatia | mar | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 |
| Cyprus | mar | 0.017 | 0.010 | 0.026 | 0.001 | 0.000 | 0.003 |
| Czechia | mar | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 |
| Denmark | mar | 0.002 | 0.000 | 0.005 | 0.000 | 0.000 | 0.001 |
| Estonia | mar | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 |
| Finland | mar | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 |
| France | mar | 0.885 | 0.783 | 0.993 | 0.036 | 0.025 | 0.048 |
| Germany | mar | 5.327 | 4.727 | 5.965 | 0.132 | 0.111 | 0.153 |
| Greece | mar | 0.052 | 0.038 | 0.067 | 0.002 | 0.000 | 0.006 |
| Hungary | mar | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 |
| Ireland | mar | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 |
| Italy | mar | 1.115 | 0.973 | 1.262 | 0.043 | 0.031 | 0.056 |
| Latvia | mar | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 |
| Lithuania | mar | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 |
| Luxembourg | mar | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 |
| Malta | mar | 0.017 | 0.010 | 0.026 | 0.001 | 0.000 | 0.003 |
| Netherlands | mar | 15.504 | 13.791 | 17.281 | 0.209 | 0.184 | 0.234 |
| Poland | mar | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 |
| Portugal | mar | 0.170 | 0.141 | 0.202 | 0.007 | 0.003 | 0.013 |
| Romania | mar | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 |
| Slovakia | mar | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 |
| Slovenia | mar | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 |
| Spain | mar | 6.954 | 6.180 | 7.761 | 0.156 | 0.134 | 0.180 |
| Sweden | mar | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 |
| UK | mar | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 |