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Vector-borne diseases

EFSA Panel on Animal Health and Welfare,
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Abstract

After a request from the European Commission, EFSA's Panel on Animal Health and Welfare summarised the main characteristics of 36 vector-borne diseases (VBDs) in 36 web-based storymaps. The risk of introduction in the EU through movement of livestock or pets was assessed for each of the 36 VBDs individually, using a semiquantitative Method to INTegrate all relevant RISK aspects (MINTRISK model), which was further modified to a European scale into the EFSA-VBD-RISK-model. Only eight of the 36 VBD-agents had an overall rate of introduction in the EU (being the combination of the rate of entry, vector transmission and establishment) which was estimated to be above 0.001 introductions per year. These were Crimean-Congo haemorrhagic fever virus, bluetongue virus, West Nile virus, Schmallenberg virus, *Hepatozoon canis*, *Leishmania infantum*, Bunyamwera virus and Highlands J. virus. For these eight diseases, the annual extent of spread was assessed, assuming the implementation of available, authorised prevention and control measures in the EU. Further, the probability of overwintering was assessed, as well as the possible impact of the VBDs on public health, animal health and farm production. For the other 28 VBD-agents for which the rate of introduction was estimated to be very low, no further assessments were made. Due to the uncertainty related to some parameters used for the risk assessment or the instable or unpredictability disease situation in some of the source regions, it is recommended to update the assessment when new information becomes available. Since this risk assessment was carried out for large regions in the EU for many VBD-agents, it should be considered as a first screening. If a more detailed risk assessment for a specific VBD is wished for on a national or subnational level, the EFSA-VBD-RISK-model is freely available for this purpose.

Keywords: vector-borne diseases

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Summary

According to a request from the European Commission, EFSA's Panel on Animal Health and Welfare (AHAW) was asked to: identify, rank and briefly characterise the vector-borne diseases (VBDs) that present a risk for the European Union (EU) because of their introduction, re-introduction or further spread (Term of Reference 1 (TOR 1)); identify and rank possible pathways of introduction and further spread into the EU and Assess the potential speed of propagation in the EU for each disease identified in point 1 (TOR 2); detail the potential health consequences and other impacts to the EU (TOR 3); assess the risk of each disease becoming endemic in the animal population in the EU (TOR 4); briefly review the feasibility, availability and effectiveness of the main disease prevention and control measures (TOR 5).

The risk was assessed separately for four regions in the EU: northern EU (N-EU): Lithuania, Denmark, Latvia, Ireland, Finland, Estonia, Sweden, United Kingdom); southern EU (S-EU): Spain, Greece, Malta, Italy, Croatia, Slovenia, Portugal, Cyprus); W-EU (W-EU): Belgium, Netherlands, Luxembourg, France, Germany, Austria; and eastern EU (E-EU): Hungary, Poland, Czech Republic, Bulgaria, Slovakia, Romania).

To identify and characterise the VBDs (TOR 1), a set of selection criteria was agreed upon with the requestor of the mandate, to prioritise the vector-borne disease agents (VBD-agents) for which the risk assessment had to be carried out. First, the assessment was restricted to pathogens that are biologically transmitted by arthropod vectors, such as sandflies, mosquitoes, ticks or biting midges. Thus, pathogens that are transmitted by other vectors, such as rodent-borne pathogens or mechanically transmitted pathogens, were excluded from this risk assessment. Additionally, in the context of potentially fine-tuning or updating animal health legislation, it was suggested to focus the risk assessment on exotic pathogens (here defined as the individual pathogen being present in maximum one EU-region in the EU) affecting the most important livestock and pet species. Exceptions on this latter selection criterion were bluetongue virus, Schmallenberg virus, African swine fever virus, West Nile virus, and *Leishmania infantum* which were also included in the risk assessment on special request, although they are not considered exotic, as each individually occur in more than one region in the EU. Diseases that were transmitted by tsetse flies were also excluded as to date there is no evidence of the presence of these vectors in the EU. Applying these criteria resulted in the identification of 39 pathogens. During the data collection for the risk assessment, another three disease agents (Semliki forest disease virus, Cocal virus and Ibaraki virus) were removed from the list of selected diseases, as there was either no evidence found that the disease agents affect livestock or pet species (Semliki forest disease) or they were considered the same species of other disease agents already in the list (such as Cocal virus and Ibaraki virus, which were assessed together with vesicular stomatitis virus and epizootic haemorrhagic disease, respectively). The remaining 36 VBDs were characterised in 36 web-based storymaps and the risk of introduction was assessed for each individually.

For the risk assessment and ranking (TOR 2), a **M**ethod to **INT**egrate all relevant **RISK** aspects (**MINTRISK**) developed by de Vos et al. (2016) to assess the risk for VBDs in the Netherlands was further modified to a European scale into the EFSA-VBD_RISK model. The tool allowed for a systematic, semiquantitative risk assessment and was further used for the ranking of the VBDs. The probability of each step of the risk pathway was calculated choosing from a low, moderate or high uncertainty level. Data inputs from systematic literature review and expert opinions were used to obtain the required parameters according to the model. Therefore, the model sampled a value from different triangular distributions according to the chosen uncertainty levels.

First, the rates of entry, the level of transmission, and the probability of establishment were calculated separately, and then these three probabilities were combined into **an overall rate of introduction (TOR 2).**

According to the model there is a high to very high **rate of entry** (1 entry per 10 years to 1 entry per year) of *L. infantum*, *Hepatozoon canis*, bluetongue virus, West Nile virus, Bhanja virus Crimean Congo haemorrhagic fever virus, Schmallenberg virus, Thogoto virus, equine encephalosis virus Palyam virus and Venezuelan equine encephalitis virus in all four EU regions through movement of livestock or pets from infected regions in or outside the EU.

In contrast, the rate of entry of Aino virus, bovine ephemeral fever virus, Akabane virus, Kotonkon virus, Middelburg virus, Wesselbron virus, Nairobi sheep disease virus, epizootic haemorrhagic disease virus, African horse sickness virus, Getah virus, Japanese encephalitis virus and Rift Valley fever virus was estimated to be very low (less than 1 entry every 10,000 years).

The main parameters contributing to the probability of entry were the prevalence of infection in susceptible hosts in source areas, the numbers of animals moved into the EU and the probability that the pathogen is still present in the host upon arrival in the EU. Detection of the latter is determined mainly by the sensitivity of the tests (if testing is carried out) and the infectious period in the hosts. There was a high uncertainty around the prevalence of some of the VBDs in the source areas and the frequency of the outbreaks for not-reportable diseases. It should be noted that when the number of animals imported change due to different trade policies or the prevalences of the VBDs in the source areas changes, the rate of entry will subsequently change too. It should be noted that the entry through movement of vectors and free movement of wild animals were not considered in the model.

The expected level of **vector transmission** of epizootic haemorrhagic disease virus, Palyam virus, bluetongue virus and equine encephalosis virus was estimated to be high in the four regions of the EU, with basic reproduction ratio (R_0) values between 3 and 10.

Bunyamwera virus, Eastern equine encephalitis virus, Shuni virus, Venezuelan equine encephalitis virus, Western equine encephalitis virus, Getah virus, Highlands J. virus and Middelburg virus were estimated to have a low to very low level of transmission everywhere in the EU with R_0 values smaller than 0.3.

For all the other VBD-agents, the level of transmission was expected to be moderate everywhere in the EU (R_0 between 1 and 3), except in W-EU where the level of transmission of Alkhurma haemorrhagic fever virus, *Ehrlichia ruminantium*, Nairobi sheep disease virus, Thogoto virus and Yunnan orbivirus (YUOV) was estimated to be very low. Also, in E-EU, the level of transmission of Bhanja virus, *E. ruminantium*, Nairobi sheep disease virus was estimated to be very low, as well as in S-EU the level of transmission of Alkhurma haemorrhagic fever virus, in N-EU the level of transmission of *L. infantum*, Nairobi sheep disease virus and Yunnan orbivirus.

The R_0 values were generally associated with a moderate to high uncertainty, due to the high uncertainty related to one or more of the parameters needed to calculate the ratio, such as the biting rate, the vector competence or the extrinsic incubation period in the vectors. Additionally, for some of the VBD pathogens, the distribution of the potential competent vectors in the EU has never been investigated.

The **probability of establishment**, being the probability that the pathogen can spread from vector to host and vice versa given the conditions of introduction (pathway, time and place) of Akabane virus, bluetongue virus, Crimean-Congo haemorrhagic fever virus, Eastern equine encephalitis virus, epizootic haemorrhagic disease virus, Schmallenberg virus, West Nile virus, Getah virus and Japanese encephalitis virus was estimated to be high to very high (with a probability of 0.1 to 1 per introduction), depending on the region of the EU.

For most of the other diseases, however, the probability of establishment was estimated to be low to very low (with a probability of less than 0.0001 per introduction). In general, there is a much higher probability of establishment for animals which are imported for breeding, compared to animals which are imported for direct slaughter upon arrival.

The proportion of areas with a high vector density could not be calculated for Alkhurma haemorrhagic fever virus, African swine fever virus, *E. ruminantium*, *H. canis*, Palyam virus, Kotonkon virus, main drain virus, Middelburg virus, Nairobi sheep disease virus, Peruvian horse sickness virus, Thogoto virus and vesicular stomatitis virus as there is lack of spatial data on the distribution of the vectors. Therefore, the probability of establishment of these diseases was associated with a high uncertainty.

According to the model Crimean-Congo haemorrhagic fever virus, bluetongue virus, West Nile virus, Schmallenberg virus, *H. canis*, *L. infantum*, Bunyamwera virus and Highlands J. virus have an **overall rate of introduction** (being the combination of entry, vectorial transmission and establishment) in each of the four EU regions of more than 0.001 overall introductions per year, for the other diseases, the rate of introduction of VBD-agents was estimated to be lower.

Subsequently, if the combined overall rate of introduction exceeded 0.001 introductions per year **the annual extent of spread** (taking into account the existing **mitigation measures**) was calculated **(TOR 2 and TOR 5)**. First, studies on the accuracy of the diagnostic tools to be used to test animals before introduction, as described in the EU legislation, were reviewed. Also studies on the efficacy of vaccines, preventive and curative pharmaceutical treatments, as well as the mitigation effect of vector control procedures authorised for use in the EU were reviewed. Then, it was identified for which of the VBDs culling or movement restrictions are laid down in the EU regulations in case of an outbreak. Then, the potential reduction of the probability of spread of the VBD was evaluated when implementing the mitigation measures after an outbreak of a given VBD. The model estimated that the

annual extent of spread after introduction of bluetongue virus, West Nile virus and Schmallenberg virus in a previously free area would be moderate to very high, depending on the region. On contrary, the model estimated that the annual extent of spread after introduction of *H. canis*, Crimean-Congo haemorrhagic fever virus, *L. infantum*, Bunyamwera virus and Eastern equine encephalitis virus in a previously free area would be very low.

Next, **the probability of overwintering** and the **impact of disease were** assessed **(TOR 4)**. The model estimated the probability of overwintering of Crimean-Congo haemorrhagic fever virus and West Nile virus to be very high in the four regions of the EU. *H. canis* and *L. infantum* were estimated to overwinter with a high probability and Schmallenberg virus, Bunyamwera virus and bluetongue virus with a moderate probability.

Finally, for those VBDs for which the overall rate of introduction exceeded 0.001, the possible **impact of the VBD on public health, animal health and the economic impact on farm production** were also assessed **(TOR 3)**. A summary was provided on the biocidal products approved by European Environmental Agency (ECHA) and their specifications about hazard statements (including environmental ones) and Risk Characterisation Ratios are provided.

When combining the estimated size of the epidemic with the severity of the infections, Schmallenberg virus and bluetongue virus introductions were estimated by the model to cause a low **impact on animal health and welfare** in S-and W-EU and very low in the other regions. For *H. canis, L. infantum*, Eastern equine encephalitis virus, Crimean-Congo haemorrhagic fever virus, Bunyamwera virus and West Nile virus the impact on animal health and welfare was estimated to be very low everywhere in the EU.

The impact on **production losses** on infected farms with BTV was estimated to be very low to low depending on the region in the EU. The impact of SBV was estimated to be moderate in S-and W-EU, low in eastern EU and very low in N-EU. For all the other diseases there was either no impact on production in the infected farms (*L. infantum*, *H. canis,* Crimean-Congo haemorrhagic fever virus and West Nile virus) or there was no information available on the production losses in infected farms (Bunyamwera virus and Eastern equine encephalitis virus). Note that this assessment considered only potential losses due to the infection, and not due cost related to prevention and control measures.

The impact of the introduction of *L. infantum* in previously free areas on public health was estimated to be very low. For the other diseases (Crimean-Congo haemorrhagic fever virus, West Nile virus, Bunyamwera virus and Eastern equine encephalitis virus), there were not sufficient data available to assess the impact on public health.

To assess the potential **impact on the environment of chemical biocidal products** used to control potential outbreaks of VBDs, information was extracted from ECHA's website on approved active substances which may be used for controlling the relevant vector species. Any potential impact on the environment of the use of biocidal products beyond the intended uses, doses and target species as evaluated by ECHA is unknown.

Due to the uncertainty related to some parameters used for the risk assessment (e.g. the biting rate or vector competence of some vectors for certain uncommon VBD-agents, as well as the prevalence of VBDs in endemic areas) or the instable or unpredictability disease situation in the source regions, it is recommended to update the assessment as soon as new information becomes available.

Finally, as this risk assessment was carried out for large regions in the EU for a large number of diseases, this assessment should be considered as a first preliminary/rough screening. If a more detailed risk assessment on VBDs is wished for on a national or subnational level, the in EFSA-VBD_RISK model is freely available for this purpose.

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

1.1. Background

The European Union (EU) is constantly under the threat of introducing new animal diseases in its territory. The changing distribution of arthropod vectors can create the conditions for the vector-borne animal diseases to enter and spread across the EU, with a variable speed, depending on the epidemiology of each disease.

There are several vector-borne diseases and infections that entered, or re-entered, the EU in recent times (e.g. bluetongue, West Nile fever and Schmallenberg virus) and the introduction routes have not always been identified. The list of vector-borne diseases, including the most relevant zoonoses, which could enter the EU and become endemic could be rather long but the likely impact may vary in its significance. Therefore these hazards need to be identified and ranked in relation to the risk they represent for the EU.

This work should be done together with the identification and ranking of the most relevant routes of introduction for each pathogen. The work of the European Food Safety Authority (EFSA) should focus primarily on diseases listed by the World Organisation for Animal Health (OIE) as well as emerging diseases that are recognised as a serious threat for the EU.

There are several legislative acts in the EU that address vector-borne diseases from a horizontal perspective, of which the most relevant ones are:

- Council Directive 82/894/EEC of 21 December 1982 on the notification of animal diseases within the Community which sets an obligation for Member States to notify the Commission of the confirmation of any outbreak of diseases listed in Annex I.
- Council Directive 90/425/EEC of 26 June 1990 concerning veterinary and zootechnical checks applicable in intracommunity trade in certain live animals and products with a view to the completion of the internal market that recognises a series of vector-borne disease being subject to mandatory emergency action, including territorial restrictions.
- Council Directive 92/65/EEC of 13 July 1992 laying down animal health requirements governing trade in and imports into the Community of animals, semen, ova and embryos which identifies diseases listed in Annex A as notifiable and requires that trade in specific species of animals and their products be subject to specific health requirements.
- Council Directive 92/119/EEC of 17 December 1992 introducing general Community measures for the control of certain animal diseases that foresees control and eradication measures for certain vector-borne diseases, exotic to the EU, listed in Annex I.

The following EU legislative acts provide specific prescriptions related to bluetongue and African horse sickness:

- Council Directive 2000/75/EC of 20 November 2000 laying down specific provisions for the control and eradication of bluetongue.
- Commission Regulation (EC) No 1266/2007 of 26 October 2007 on implementing rules for Council Directive 2000/75/EC as regards the control, monitoring, surveillance and restrictions on movements of certain animals of susceptible species in relation to bluetongue.
- Council Directive 92/35/EEC of 29 April 1992 laying down control rules and measures to combat African horse sickness which lays down animal health conditions for the movement between Member States and importation from third countries of live Equidae.
- Council Directive 2009/156/EC of 30 November 2009 on animal health conditions governing the movement and importation from third countries of Equidae, which also takes into account the situation on African horse sickness.

The risk manager is in need of updated scientific advice in order to assess the risk of introduction of new vector-borne diseases and to determine if further measures are needed. This is linked to the existence of a potentially devastating effect in case these diseases were to enter in the EU. The existence of the current control measures need to be considered when identifying and ranking the documented and likely entry routes into the EU. The outcome of this work will assist the Commission in prioritising the use of resources for preventive actions in the field of animal diseases.

1.2. Terms of Reference

1) Identify, rank and briefly **characterise** the vector-borne diseases that present a risk for the EU. This work should cover both animal diseases and relevant zoonoses that present a risk for the EU because of their introduction, re-introduction or further spread.
2) For each disease identified in point 1, **identify and rank possible pathways of introduction** (or re-introduction) and further **spread** into the EU and assess the potential **speed of propagation** in the EU.
3) For each disease identified in point 1, detail the potential **health consequences and other impacts** to the EU in relation to the existence of suitable vectors and their interaction with local animal populations.
4) Assess the **risk of each disease becoming endemic** in the animal population in the EU.
5) Briefly review the **feasibility, availability and effectiveness of the main disease prevention and control measures** (e.g. diagnostic tools, biosecurity measures, restrictions on the movement, culling, vaccination).

2. Introduction

2.1. Interpretation of the Terms of Reference

To answer ToR 1, a brief characterisation of each of the vector-borne diseases (VBDs) was provided. The characterisation of the diseases included: a description of the disease agent; basic facts about the most important vectors involved in the transmission and their possible occurrence in the EU; the geographic distribution of the disease agent; a brief description of the available prevention and control measures of the infection in animals; a short description of the possible impact on animal health and public health and a brief summary of the risk assessment.

Subsequently, the rate of entry (1), the level of transmission (2) and the probability of establishment (3) were assessed to address the second part of ToR 1. For those diseases where the overall expected rate of introduction (4), being the combination of the rate of entry, the level of transmission and the probability of establishment exceeded 0.001[1] (1 introduction in 1,000 years), also the annual extent of spread (5) was assessed.

To answer ToR 2, the rates of entry were ranked for each of the VBDs and the pathways for entry of the pathogens with the highest rates were ranked and discussed. Secondly, the level of transmission, the probability of establishment, as well as the extent of spread were ranked for all the VBDs.

To answer ToR 3, those VBDs for which the overall rate of introduction exceeded 0.001, the possible impact of the VBD on public health, animal health and the economic impact on farm production were also assessed (7). A summary was provided on the biocidal products approved by the European Chemicals Agency (ECHA) but an environmental impact assessment of their use was not within the scope of this mandate.

To answer ToR 4, for each VBD for which the overall rate of introduction exceeded 0.001, also the probability of overwintering (6) was assessed.

To answer ToR 5, first studies on the accuracy of the diagnostic tools to be used to test animals before introduction, as described in the EU legislation, were reviewed. Also, studies on the efficacy of vaccines and preventive and curative pharmaceutical treatments authorised for use in the EU were reviewed. Then, it was identified for which of the VBDs culling or movement restrictions are laid down in the EU regulations in case of a particular VBD outbreak. Then the potential reduction of the probability of spread of the VBD was evaluated when implementing the mitigation measures to be taken after an outbreak of a given VBD.

The following definitions are used in this opinion:

1) **Rate of entry**, i.e. the expected number of introductions of the pathogen per year.
2) **Level of transmission**, i.e. the extent at which the pathogen is able to be transmitted from vertebrate host to vector and to vertebrate host in at least one location of the area at risk during a specific time period in which climatic and environmental conditions are suitable

[1] This low threshold was chosen because of (a) the high number (36) of VBD considered and (b) the uncertainty in the assessment.

for replication and spread of the pathogen (thus the level of transmission is evaluated for the optimal situation).

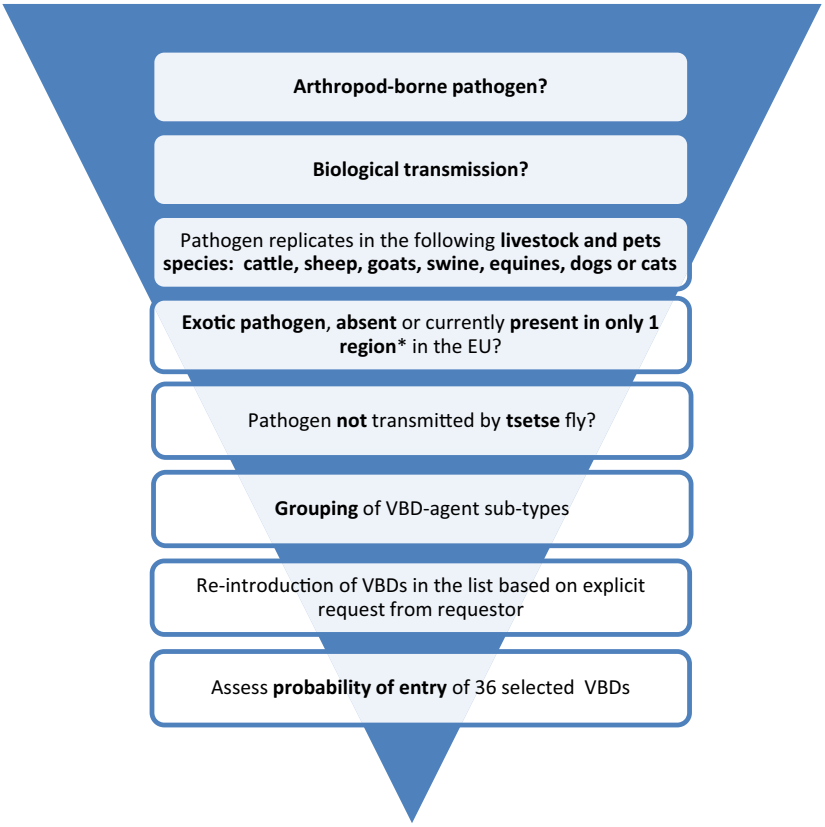
3) **Probability of establishment**, i.e. the probability that the pathogen can spread from vector to host and vice versa given the conditions of introduction (pathway, time and place).
4) **Overall rate of introduction**, i.e. the combination of the rate of entry, the level of transmission and the probability of establishment.

If the overall rate of introduction is > 0.001 per year, the framework proceeds to evaluate the:

5) **Annual extent of spread**, i.e. the extent to which the pathogen is able to spread in a year during the vector season, considering both local dispersal and long-distance spread, including spread through animal movements, accounting for the number of animals/herds infected and the geographic area affected.
6) **Probability of overwintering**, i.e. the likelihood that the pathogen will assert itself in the area at risk for a prolonged period (i.e. for more than 1 vector season), possibly resulting in endemicity.
7) **Impact of the disease being present in an area**, being the combination of the impact on animal health, the production losses on case farms; and the impact on public health (expressed as disability-adjusted-life-years in humans).

2.2. Selection of vector-borne pathogens to be included in the risk assessment

A set of selection criteria (Figure 1) was agreed upon with the requestor of the mandate, to prioritise the pathogens for which the risk assessment had to be carried out. First, the assessment was restricted to pathogens that are transported and biologically transmitted by arthropod vectors, such as sandflies, mosquitoes, ticks or midges. Thus, pathogens that are borne by other vectors, e.g. rodent-borne pathogens, or mechanically transmitted pathogens were excluded from this risk assessment. Additionally, in the context of potentially fine-tuning or updating animal health legislation, it was suggested to focus the risk assessment on exotic pathogens (here defined as a pathogen present in maximum one region in the EU (see Section 2.3) affecting the most important livestock and pet species. Exceptions on this latter selection criterion were bluetongue virus, Schmallenberg virus, African swine fever virus and West Nile virus, which were also included in the risk assessment on special request. Also, canine leishmaniosis was included, although it occurs in two EU regions, namely S- and W-EU. Although they are not considered exotic, as they occur in more than one region in the EU, it was considered important to evaluate the potential routes that may lead to introduction and spread in the EU, and the efficacy of the available control measures. Diseases that were transmitted solely by tsetse flies were also excluded as to date there is no evidence of the presence of these vectors in the EU. Applying these criteria resulted in the identification of 39 pathogens, of which 14 are notifiable to the OIE (Table 1). During the data collection for the risk assessment, another three disease agents (Semliki forest disease virus, Cocal virus and Ibaraki virus) were removed from the list of selected diseases, as there was either no evidence found that the disease agents affect livestock or pet species (Semliki forest disease) or they were considered the same species of other disease agents already in the list (such as Cocal virus and Ibaraki virus, which were assessed together with vesicular stomatitis virus and epizootic haemorrhagic disease, respectively). The remaining 36 VBDs were characterised and the risk of introduction was assessed for all of them (Table 1).



*UN-regions: see Section 2.3.

Figure 1: Selection criteria for including pathogens in the risk assessment

Table 1: Causative agents of vector-borne diseases selected using the criteria as shown in Figure 1

Nr	Family	Genus	Species	Acronym	OIE notifiable
1	Asfarviridae	*Asfivirus*	African swine fever virus	ASFV	Yes
2	Bunyaviridae	*Nairovirus*	Crimean-Congo haemorrhagic fever virus	CCHFV	Yes
3	Bunyaviridae	*Nairovirus*	Nairobi sheep disease virus	NSDV	Yes
4	Bunyaviridae	*Orthobunyavirus*	Aino virus	AINOV	No
5	Bunyaviridae	*Orthobunyavirus*	Akabane virus	AKAV	No
6	Bunyaviridae	*Orthobunyavirus*	Bunyamwera virus	CVV	No
7	Bunyaviridae	*Orthobunyavirus*	Main drain virus	MDV	No
8	Bunyaviridae	*Orthobunyavirus*	Schmallenberg virus	SBV	No
9	Bunyaviridae	*Orthobunyavirus*	Shuni virus	SHUV	No
10	Bunyaviridae	*Phlebovirus*	Rift Valley fever virus	RVFV	Yes
11	Bunyaviridae	Unassigned	Bhanja virus	BHAV	No
12	Flaviviridae	*Flavivirus*	Japanese encephalitis virus	JEV	Yes
13	Flaviviridae	*Flavivirus*	St. Louis encephalitis virus	SLEV	No
14	Flaviviridae	*Flavivirus*	Wesselsbron virus	WSLV	No
15	Flaviviridae	*Flavivirus*	West Nile virus	WNV	Yes
16	Flaviviridae	*Flavivirus*	Alkhurma haemorrhagic fever virus	AHFV	No
17	Hepatozoidae	*Hepatozoon*	*Hepatozoon canis*	Hepat	No
18	Orthomyxoviridae	*Thogotovirus*	Thogoto virus	THOV	No

Nr	Family	Genus	Species	Acronym	OIE notifiable
19	Reoviridae	*Orbivirus*	African horse sickness virus	AHSV	Yes
20	Reoviridae	*Orbivirus*	bluetongue virus	BTV	Yes
21	Reoviridae	*Orbivirus*	Epizootic haemorrhagic disease virus (epizootic haemorrhagic disease virus and Ibaraki virus)	EHDV	Yes
22	Reoviridae	Orbivirus	Equine encephalosis virus	EEV	No
23	Reoviridae	*Orbivirus*	Palyam virus	KASV	No
24	Reoviridae	*Orbivirus*	Peruvian horse sickness virus	PHSV	No
25	Reoviridae	*Orbivirus*	Yunnan orbivirus	YUOV	No
26	Rhabdoviridae	*Ephemerovirus*	Bovine ephemeral fever virus	BEFV	No
27	Rhabdoviridae	Unassigned	Kotonkon virus	KOTV	No
28	Rhabdoviridae	*Vesiculovirus*	Vesicular stomatitis virus (Indiana, Cocal, Alagoas and New Jersey)	VSV	No
29	Rickettsiaceae	*Ehrlichia*	*Ehrlichia ruminantium*	Cowdr	Yes
30	Togaviridae	*Alphavirus*	Eastern equine encephalitis virus	EEEV	Yes
31	Togaviridae	*Alphavirus*	Getah virus	GETV	No
32	Togaviridae	Alphavirus	Highlands J. virus	HJV	No
33	Togaviridae	*Alphavirus*	Middelburg virus	MIDV	No
34	Togaviridae	*Alphavirus*	Venezuelan equine encephalitis virus	VEE	Yes
35	Togaviridae	*Alphavirus*	Western equine encephalitis virus	WEEV	Yes
36	Trypanosomidae	*Leishmania*	*Leishmania infantum*	CanL	Yes

2.3. Selection of the regions potentially at risk and source areas of disease agents

It was agreed that separate risk assessments for the 28 individual EU Member States were not feasible for all pathogens identified in Table 1. This risk assessment was carried out for regions and -regions used by the United Nations.[2] This subdivision was chosen because data on trade and host populations are available for these administrative regions, whilst the proposed ecological divisions are not yet sufficiently linked with the diseases. The **potential source regions** (Figure 2) of disease agents are all UN regions in the world where the VBDs are endemic or epidemic at the risk assessment.

[2] Composition of macrogeographical (continental) regions, geographical sub-regions, and selected economic and other groupings, http://unstats.un.org/unsd/methods/m49/m49regin.htm#europe

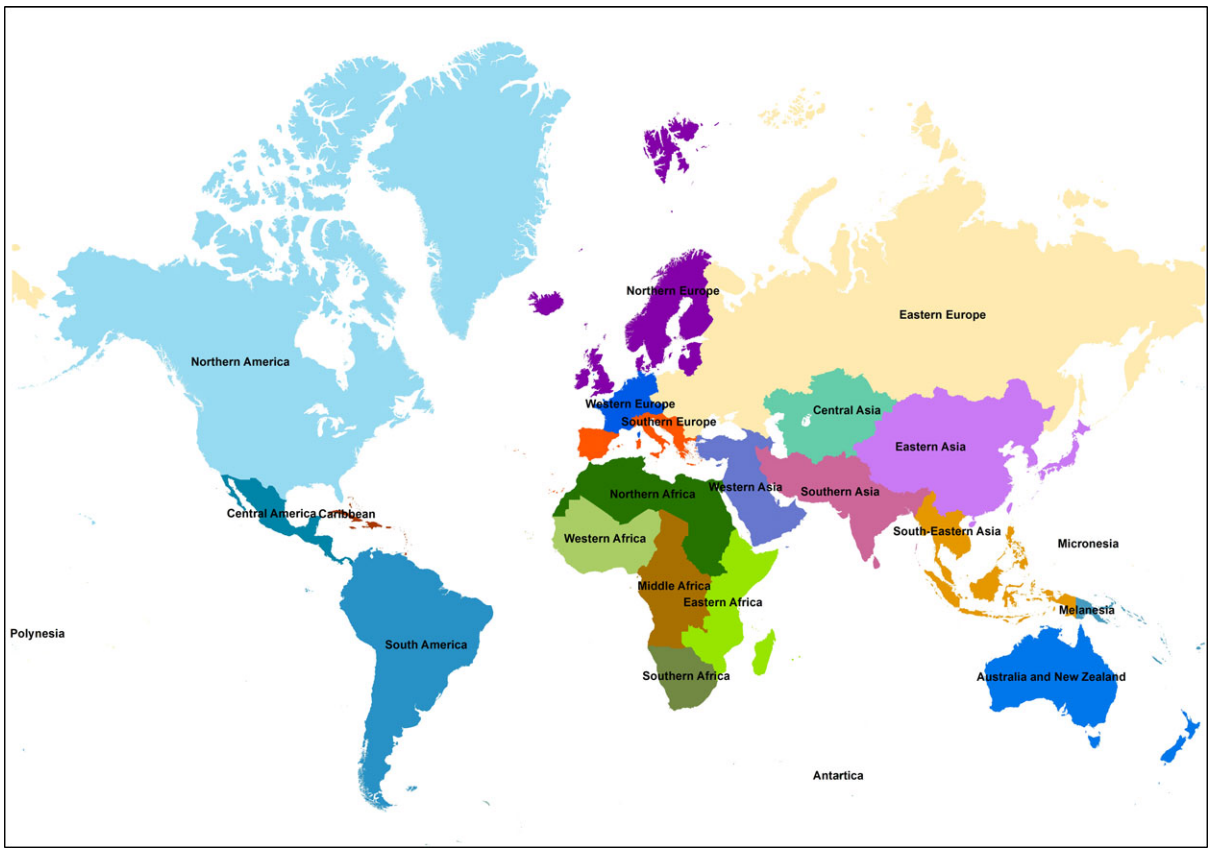


Figure 2: Potential source regions of vector-borne diseases: regions of the United Nations

From the countries in the UN regions of Europe, only the Member States of the European Union were considered. Thus, the **regions potentially at risk in the European Union** (Figure 3) for which the risk assessment was carried out were:

- **Northern EU (N-EU):** Lithuania, Denmark, Latvia, Ireland, Finland, Estonia, Sweden, United Kingdom;
- **Southern EU (S-EU):** Spain, Greece, Malta, Italy, Croatia, Slovenia, Portugal, Cyprus;
- **Western EU (W-EU):** Belgium, Netherlands, Luxembourg, France, Germany, Austria;
- **Eastern EU (E-EU):** Hungary, Poland, Czech Republic, Bulgaria, Slovakia, Romania.

The vector distribution, host density or transportation may be different within an EU region, leading to an uncertainty in the assessment.

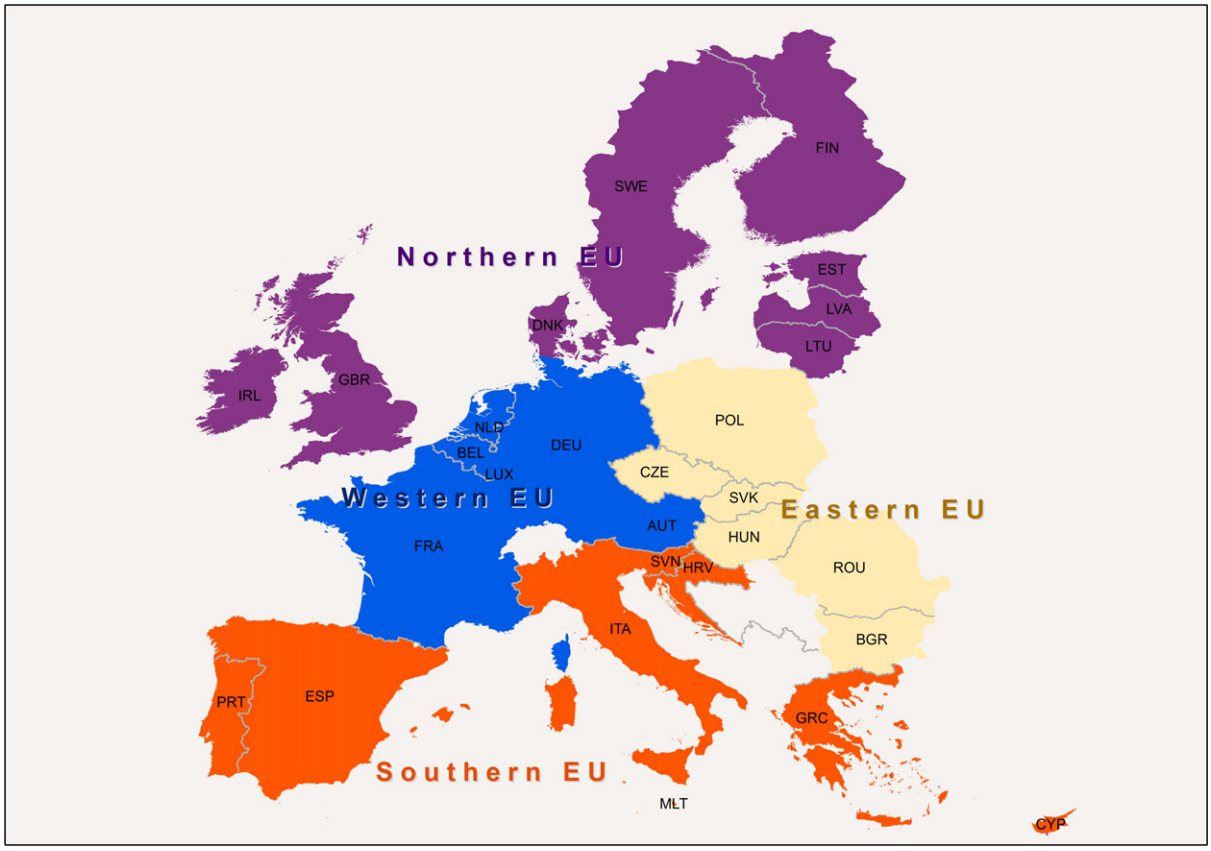


Figure 3: Regions potentially at risk

2.4. Period for which the risk assessment was carried out

This assessment was carried out in 2016 and was based on trade data, published scientific literature and the global disease occurrence available until 1 March 2016. In the future, this risk assessment will be updated on a regular basis in the light of new relevant information.

2.5. Risk assessment framework

Several frameworks or models exist to characterise a disease agent (e.g. Discontools, Phylum, DEFRA), to assess the risk of introduction (e.g. Discontools, Phylum, AHVLA), to assess the level of transmission and spread of VBD or their overwintering (e.g. Fischer et al., 2013). Additionally, several frameworks exist to deal with the impact of animals' disease after they have entered a previously free area (e.g. ANSES, EC 2007, OIE-Phylum, Discontools, ECDC). The **F**ramework developed to guide the risk assessment of possible **E**merging **VE**ctor-borne disease **R**isks (FEVER) (De Vos, 2011) uses a stepwise approach, helping the risk assessor to consider all relevant steps of the risk pathways. It was considered fit for the purpose of this mandate, as it covers most aspects of the terms of reference. The basic steps of the risk pathways distinguished in FEVER are displayed in Figure 4.

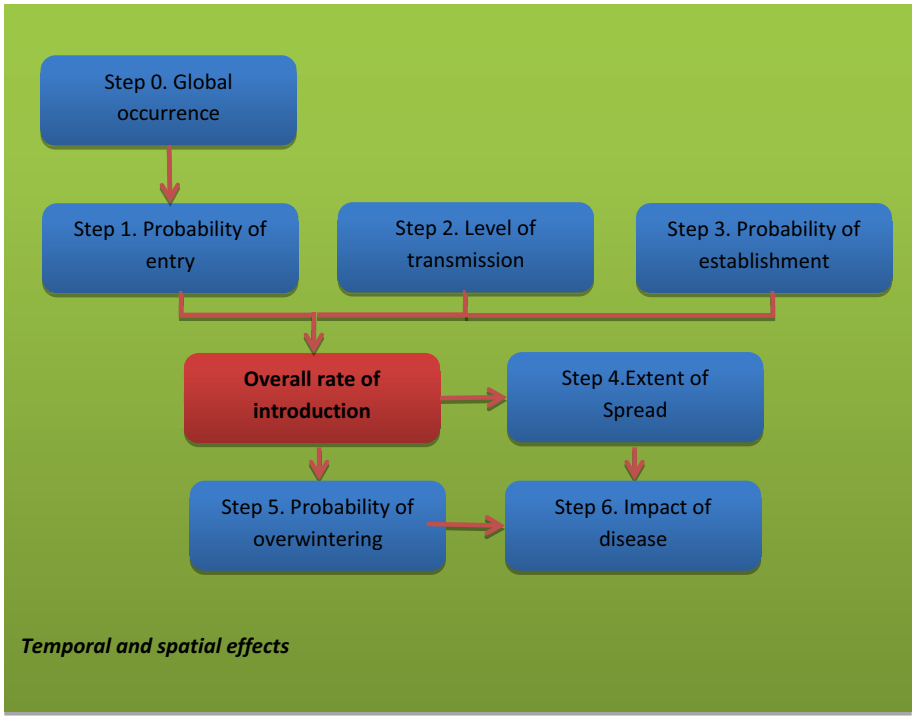


Figure 4: Framework used to assess the risk of 36 vector-borne diseases (amended from: De Vos et al., 2011)

2.6. The risk assessment model

Based on the above described risk assessment framework 'FEVER', a **M**ethod to **INT**egrate all relevant **RISK** aspects (**MINTRISK**) was developed in Excel and Visual Basic. A web based version with a central database and using Csharp for underlying calculations has been created for practical use and access. This tool is called the EFSA-VBD_RISK model. The 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 probability of each step of the risk pathway was calculated. First, the rates of entry, level of transmission, and probability of establishment were calculated separately, and then these three probabilities were combined into an overall rate of introduction. Subsequently, if the combined overall rate of introduction exceeded 0.001 introductions per year (which equals an entry score of 0.2 in the model), the annual extent of spread, the probability of overwintering and the impact of disease were assessed.

The questions to be addressed in EFSA-VBD_RISK model to assess the probability for each step mostly could be answered by choosing from qualitative categories (each with their own underlying quantitative explanation) associated with three options for the uncertainty about this estimate. 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. When using logarithmic scales for the answer categories, the contrast between the categories become higher, which makes it easier to choose amongst the most appropriate answer category. This results in more distinguishable outputs values and a higher impact of the choices.

However, to communicate the answer categories and results, these are translated back into EFSA-VBD_RISK qualitative terms, such as 'very high' or 'high'. In the methodology Sections, the quantitative meaning of the qualitative terms are described for each of the answer categories for those who are more interested in the quantitative estimates as such.

As described in Figure 4, there are six steps in the risk pathway developed in the FEVER framework: (1) rate of entry, (2) level of transmission, (3) probability of establishment, (4) annual extent of spread, (5) probability of overwintering and (6) the impact of the disease being present in an area. Before step 1, however, an assessment of the worldwide occurrence of the infection needs to be undertaken (step 0).

The VBDs were ranked for each horizontal step of the risk assessment according to their decreasing rate of entry, level of transmission and probability of establishment, the extent of spread and probability of overwintering and impact. Additionally, for those VBDs with a high risk, the most important factors leading to this high risk were discussed.

In the methodology sections, for each step of the risk assessment follows a detailed description of all the questions of the EFSA-VBD_RISK model that needed to be addressed for each of the steps of the risk pathways in the FEVER framework. To allow comparing or ranking of diseases for each step, a uniform approach was needed. Therefore, data were aggregated and assumptions made, often involving expert judgement. The level of uncertainty was estimated for each question/answer.

2.7. Assumptions and limitations

After the extensive literature reviews, as described in Section 4.3.2 and reported in (Braks et al., 2017a), it was decided to limit assessment of the rate of entry only for risk pathways which could be sufficiently quantified. Due to very scarce or inexistent knowledge on the numbers of potentially infected vectors and wildlife species moving into the EU regions, it was decided to assess the rate of entry only for potentially infected livestock species and pets (cats and dogs). For commodities, for which *a priori* it was known that there would be no further transmission of the disease agents after entry, either because exposure to susceptible hosts or vectors could be excluded (e.g. by importing fresh meat from infected animals with strictly VBDs), or because the hosts were considered to be dead end hosts, the rate of entry was not assessed.

For this last reason, the rate of entry through movement of infected humans with the zoonotic VBD-agents was not assessed because humans are not considered to play a role as amplifying hosts for any of the zoonotic disease agents amongst those listed in Table 1 based on current knowledge.

2.8. Uncertainty

Three uncertainty levels can be selected to describe the certainty when answering the questions in the EFSA-VBD_RISK model, low, moderate and high. The model will sample a value from triangular distributions with different ranges around the answer category according to the chosen uncertainty level as visualised in Figure 5 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. Values around the 'moderate' category are most likely to be drawn when a low uncertainty is selected; however, if high uncertainty is selected, values far from the moderate category are also quite likely to be drawn due to the two 'fat tails' of the distribution.

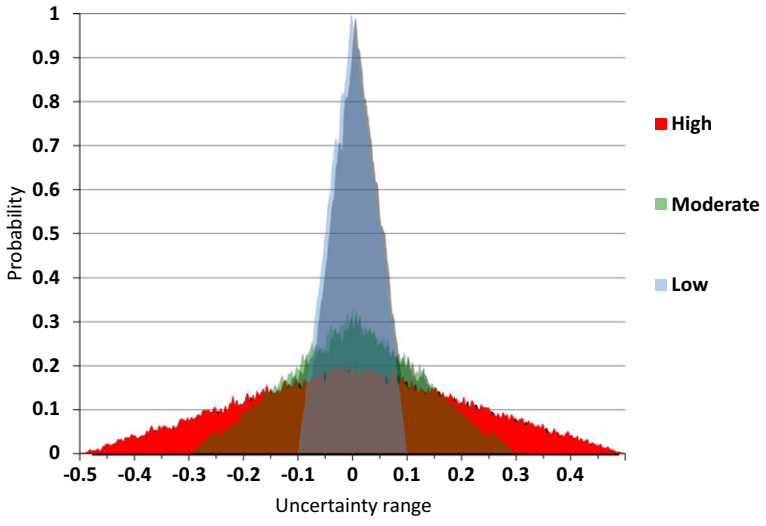


Figure 5: Triangular distributions from which the EFSA-VBD_RISK model will sample according to different levels of uncertainty

To answer each question in the EFSA-VBD_RISK model, data were collected as described in Section 2.1. For those questions where no data were found in peer-reviewed research studies and no data were provided from official institutions, the answer category 'unknown' was chosen. This answer

was always paired with a high uncertainty. The uncertainly of an answer to a question in the model was moderate, when there was very scarce information or it involved expert opinion of few experts only. For all the other answers where data from official institutions or published scientific journals were available, the uncertainty of the answers was considered to be low.

Given an example, when for Question 11 (see Section 4.3.1): 'What is the estimated value of the basic reproduction ratio?' There was no information available about the reproduction number (R_0) in the literature based on passed outbreaks elsewhere or no data were found to calculate the reproduction number, then 'Unknown' was chosen as answer, together with a high uncertainty. When the R_0 was already found, based on passed outbreaks in the same region for which the risk was to be assessed, the appropriate answer range was chosen in which the published R_0 was situated, together with a low uncertainty. When, however the R_0 needed to be calculated based on extrapolations of R_0 from other regions, or based on parameters that were extrapolated from other regions, a moderate uncertainty was chosen.

3. Characterisation of selected vector-borne diseases (ToR 1 and ToR 5)

A short characterisation of each of the diseases is given via the links in Table 2, including a summary of the characteristics of the disease agent, the transmission, the geographic distribution, the potential vectors involved, the impact of the disease on animal health and welfare and a summary of the available prevention and control measures. Additionally, the results of the risk assessment are summarised per disease.

Table 2: Characterisation of the selected vector-borne diseases

No	Links to online characterisation of VBDs (Storymaps)	Acronym
1	Characterisation of African horse sickness	AHS
2	Characterisation of African swine fever	ASFV
3	Characterisation of Aino virus infection	AINOV
4	Characterisation of Akabane virus infection	AKAV
5	Characterisation of Alkhurma haemorrhagic fever virus infection	AHFV
6	Characterisation of Bhanja virus infection	BHAV
7	Characterisation of bluetongue	BTV
8	Characterisation of bovine ephemeral fever	BEFV
9	Characterisation of Bunyamwera virus infection	CVV
10	Characterisation of Crimean-Congo haemorrhagic fever	CCHF
11	Characterisation of eastern equine encephalitis	EEE
12	Characterisation of epizootic haemorrhagic disease	EHDV
13	Characterisation of equine encephalosis	EEV
14	Characterisation of Getah virus infection	GETV
15	Characterisation of heartwater	Cowdr
16	Characterisation of hepatozoonosis (*H. canis*)	Hepat
17	Characterisation of Highlands J. virus infection	HJV
18	Characterisation of Japanese encephalitis	JEV
19	Characterisation of Kotonkan virus infection	KOTV
20	Characterisation of leishmaniosis (*L. infantum)*	CanL
21	Characterisation of main drain virus infection	MDV
22	Characterisation of Middelburg virus infection	MIDV
23	Characterisation of Nairobi sheep disease	NSDV
24	Characterisation of Palyam virus (Chuzan disease)	KASV
25	Characterisation of Peruvian horse sickness	PHSV
26	Characterisation of Rift Valley fever	RVF
27	Characterisation of Saint Louis encephalitis	SLEV
28	Characterisation of Schmallenberg virus infection	SBV
29	Characterisation of Shuni virus infection	SHUV
30	Characterisation of Thogoto virus infection	THOV

No	Links to online characterisation of VBDs (Storymaps)	Acronym
31	Characterisation of Venezuelan equine encephalitis	VEE
32	Characterisation of vesicular stomatitis	VSV
33	Characterisation of Wesselsbron virus infection	WSLV
34	Characterisation of West Nile fever	WNV
35	Characterisation of Western equine encephalitis	WEEV
36	Characterisation of Yunnan orbivirus infection	YUOV

4. Overall rate of introduction (ToR 2)

4.1. Worldwide occurrence of selected vector-borne diseases

4.1.1. Methodology to assess the worldwide occurrence of the VBD

Figure 6 displays six questions that needed to be answered in the EFSA-VBD_RISK model to assess the occurrence of the 36 VBDs across the world (step 0 of the risk assessment framework, see Figure 4).

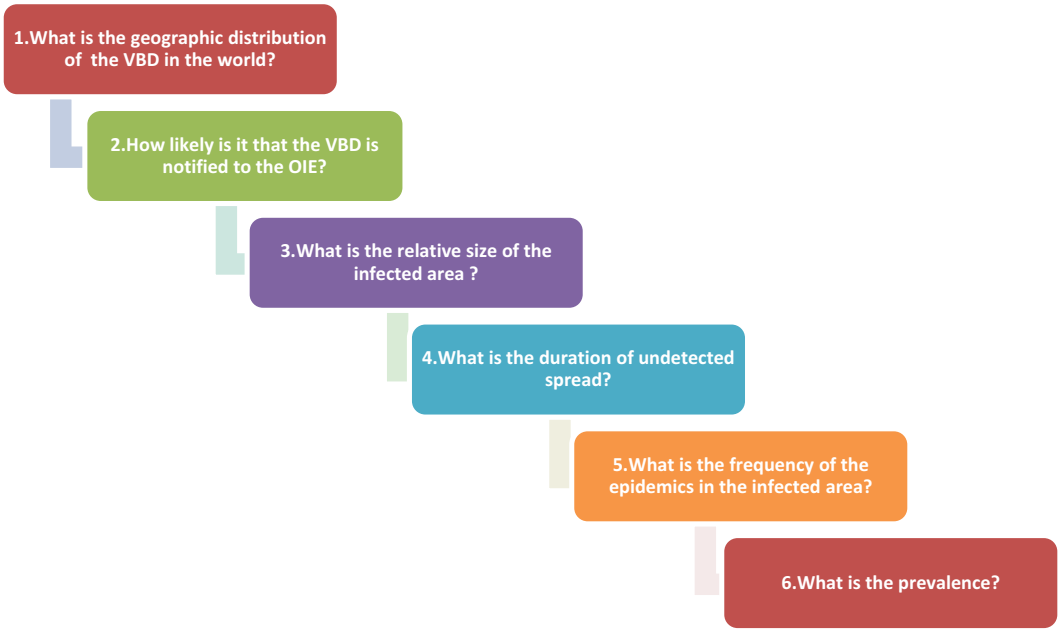


Figure 6: Steps to describe the worldwide disease occurrence of each of the VBD in the EFSA-VBD_RISK model

Below follows a brief interpretation of each and a short guidance for the scoring. The data needed to answer these questions are described in Section 4.1.2.

4.1.1.1. Methodology to assess the geographic distribution of the VBD in the world

The geographic distribution of each VBD has been grouped by UN region (see Section 2.3). Therefore, if a disease occurred (either reported to the OIE, or published in scientific literature) in at least one country within a UN region, then the entire UN region was marked as positive.

4.1.1.2. Methodology to assess the probability that a new epidemic of a VBD would NOT be notified to the OIE

The probability that a new epidemic of a VBD would NOT be notified to the OIE equals to one for a non-OIE-notifiable disease. For the notifiable diseases, it will depend on several factors such as the effect on animal and/or public health and/or the economic impact or political willingness. A matrix was developed (Table 3) to harmonise the judgements on the probability of not reporting and to choose

one of the probability ranges as they appear in the EFSA-VBD_RISK model. The items that are influential for reporting were assumed to be hierarchical, i.e. the effect on public health was considered the most important trigger for reporting the disease. Quantitative probabilities were assigned using the logarithmic scale to express this hierarchy.

Table 3: Matrix to assess the likelihood that an OIE notifiable VBD epidemic is not notified to the OIE

	Effect on public health	Effect on trade	Effect on farm production	Effect on animal health and welfare	No effect
Effect on public health	< 0.2[(a)]	< 0.2	< 0.2	< 0.2	< 0.2
Effect on trade	< 0.2	0.2–0.9	0.2–0.9	0.2–0.9	0.2–0.9
Effect on farm production	< 0.2	0.2–0.9	0.9–0.99	0.9–0.99	0.9–0.99
Effect on animal health and welfare	< 0.2	0.2–0.9	0.9–0.99	0.99–0.999	0.99–0.999
No effect	< 0.2	0.2–0.9	0.9–0.99	0.99–0.999	> 0.999

(a): Probabilities as they appear in EFSA-VBD_RISK model, using a logarithmic scale to assign the probability to the categories.

4.1.1.3. Methodology to assess the relative size of the infected areas

To evaluate the size of the infected areas (i.e. the size of the areas where outbreaks have occurred between 2005 and 2016 relative to the total size of the positive UN regions) all of the OIE outbreak/event notification locations, have been linked to NUTS1, NUTS2, GAUL 1 or GAUL 2 geographical layers using ArcGIS and considered as infected areas. In order to calculate the size of the infected areas relative to the positive UN regions, the following fraction was used:

Infected areas (km2)/Total areas of positive UN regions (km2)

Based on the outcomes of the equation the appropriate classes of the EFSA-VBD_RISK model were chosen (which were derived from square root of 10 log steps): Very small (< 0.01), Small (0.01–0.03), Moderate (0.03–0.10), Large (0.1–0.3) and Very Large (> 0.3). For non-notifiable diseases, for which the occurrence is only known from scientific publications, studying, e.g. the prevalence of the disease, the relative size of the infected area was unknown.

4.1.1.4. Methodology to assess the duration of the period of undetected spread

The duration will depend on many factors, such as the length of the incubation period in individual animals, the severity of the clinical signs, the capability of the farmers and the veterinarians to recognise the clinical signs, the transmissibility of the disease agent, the functioning of the veterinary services and laboratories, and some political and economic interests. Assuming the awareness of the farmers, the capacity of the veterinary services and the laboratories, the political and economic environment to be constant for all the diseases in a given country, the duration of the period of undetected spread was considered a function of the probability of notifying (P_notified), the length of the incubation period (both the extrinsic incubation period in the vector (EIP), and the intrinsic incubation period in the host (IIP). The decision tree (Figure 7) was followed and the most appropriate range for the undetected spread was chosen. When the disease is not notifiable, 'very long' was chosen as an answer. When the disease is notifiable, the duration of undetected spread is dependent on the length of the incubation periods (Intrinsic and extrinsic) and the probability of notifying the disease. Depending on their relation, the most appropriate of the five classes was chosen.

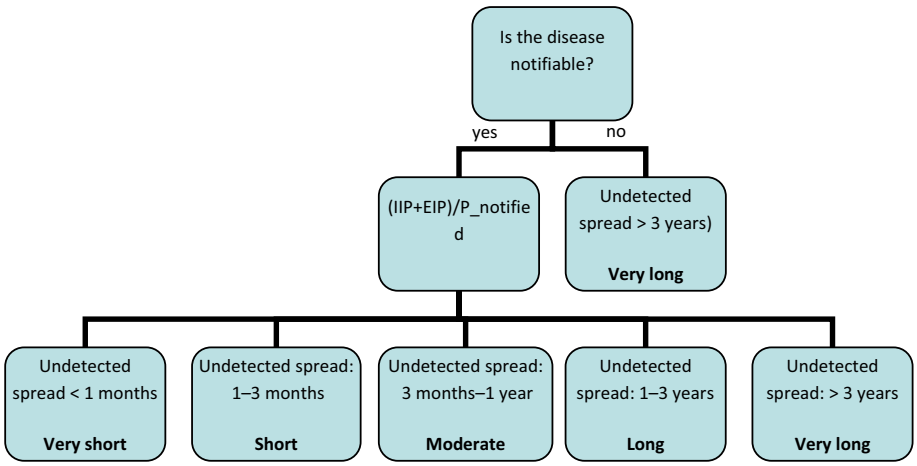


Figure 7: Decision tree to choose the ranges for the duration of undetected spread

4.1.1.5. Methodology to assess the frequency of the epidemics

The OIE's summary of immediate notifications and follow-ups on the WAHID interface was used to gather information on the frequency of epidemics. Each new 'event notification' has been counted as an epidemic, regardless of how many outbreaks occurred within each notification. Each event reports the country and the resolution date (if resolved) and these variables have been used to distinguish one epidemic from another. The result of the frequency calculation was evaluated against the frequency classes which were derived from a square root of 10 log steps: Very low (< 1 per 10 years), Low (1–3 per 10 years), Moderate (3–10 per 10 years), High (1–3 per year), Very high (Very high) and unknown. For non-notifiable diseases, the answer was chosen to be 'unknown'. The estimate for frequency of epidemics caused by the VBDs was accompanied with a moderate uncertainty for the OIE notifiable diseases, and with a high uncertainty for the not-notifiable diseases.

4.1.1.6. Methodology to assess the prevalence

The ranges of the prevalence values reported in the cross-sectional prevalence surveys carried out in the different regions found by the scientific literature were aggregated for each VBD per animal family and evaluated against the available prevalence classes in the EFSA-VBD_RISK model were used to estimate the numbers of animals imported: Very low (< 1E-4), Low (1E-4 to 0.001), Moderate (0.001–0.01), High (0.01–0.1), Very high (> 0.1) and unknown. Before doing so, seroprevalences were transformed into prevalences of infectious animals in a population, by using the following equation[3]:

$$\text{Prevalence of infectious animals} = \frac{\text{Median Infectious Period} \times \text{Seroprevalence}}{\text{Median duration of Immunity}}.$$

The median duration of immunity was assumed to be equal to the average lifespan of the animals: cattle (breeding: 60 months; slaughter 12 months), camels (390 months), horses (breeding 330 months, slaughter 20 months), swine (breeding 24 months, slaughter 10 month), sheep and goats (breeding 24 months, slaughter 4 months), dogs (138 months) and poultry (layer 70 weeks, broiler 6 weeks).

4.1.2. Data to assess the worldwide disease occurrence

To answer the six questions in the EFSA-VBD_RISK model to assess the occurrence of the different VBDs across the world (Figure 6), the data items described below were collected. A summary of the data that was used as input for the model is provided in the supporting material.

4.1.2.1. Data used to assess the geographic distribution of the VBD in the world

Information on disease distribution was collected from two source types:

[3] Assuming an endemic equilibrium and constant risk over the year. Seasonality was taken into account during the calculation of the probability of establishment (Section 4.4.1).

1) For diseases notifiable to the World Organisation for Animal Health (OIE) (Table 1), the OIE's WAHID Interface[4] was used to gather information on disease distribution. Data were recorded between 1 January 2005 and 1 March 2016.
   The WAHID database contains information on the location and the duration of the outbreaks, and whether the situation has been resolved or not. Each new 'event notification' lists all geographic areas where outbreaks occurred or are occurring.
   Additionally data of outbreaks that were reported to the OIE monthly or every semester were collected to assess the occurrence of the VBDs. In general, the OIE notification reports the first or second subdivision of a country i.e. the region or province. In Europe this corresponds to either the NUTS1 or NUTS2 statistical subdivisions or for the rest of the world, the GAUL 1 or GAUL 2 subdivisions.[5] Point references were recorded whenever reported, or otherwise the smallest administrative unit reported was recorded.
2) Data on the distribution of diseases that are not notifiable to the OIE were extracted from websites and reports of international authorities (e.g. http://www.oie.int/, http://ecdc.europa.eu/en/Pages/home.aspx and http://www.cdc.gov/) and through an extensive literature search that was performed to identify and extract information on disease prevalence (see section below). Case studies were also included in the disease distribution database.

4.1.2.2. Below follows a brief interpretation of each question that needed to be answered to assess the worldwide occurrence of the 36 VBDs and a short guidance for the scoring. The data needed to answer these questions are described in Sections 4.1.2 and 4.1.2.2. Data used to assess the likelihood of the VBD being notified to the OIE

The list of OIE notifiable diseases was consulted (see also Table 1). Additionally, a narrative literature review was carried out to evaluate if the disease is zoonotic (see disease characterisation and Section 7.3.1) and what effect an epidemic would have on trade (see Section 4.2.2.3 for measures influencing trade)) and farm production (see Section 7.1.4 for production losses). To evaluate the effect on animal health and welfare, a systematic review (Dórea et al., 2017) was carried out to evaluate the clinical signs (see also Section 4.2.2.3 for description on data collected about the clinical signs).

4.1.2.3. Data used to assess the relative size of the infected area

ESRI's World Albers Equal Area Conic projection coordinates[6] was used to calculate world land surface areas.

4.1.2.4. Data used to assess the duration of undetected spread

To assess the duration of the undetected spread, the list of OIE notifiable diseases was consulted, together with the probability of notifying the disease (Section 4.1.2.2). Additionally, data on the intrinsic incubation period were collected through a systematic review (Dórea et al., 2017; see also Section 4.2.2.1). Data on the extrinsic incubation period were collected by Braks et al. (2017b) (see also Appendix A for a short summary).

4.1.2.5. Data used to assess the frequency of the epidemics in the infected area

The OIE's WAHID Interface was consulted to gather information on outbreak frequency. Data were recorded between 1 January 2005 and 1 March 2016.

4.1.2.6. Data used to assess the prevalence

An extensive literature search was performed using the Web of Knowledge database (ISI Thomson-Reuters) using the following search string:

((''pathogen full name'') and (*prevalence OR incidence OR infection OR epidemiol* OR outbreak OR surveillance OR monitoring OR basic reproduction number OR basic reproduction ratio)) from 1 January 2005 to 31 January 2016.

[4] http://www.oie.int/wahis_2/public/wahid.php/Wahidhome/Home
[5] The Global Administrative Unit Layers (GAUL) is an initiative implemented by FAO within the EC-FAO Food Security Programme funded by the European Commission. The NUTS classification (Nomenclature of territorial units for statistics) is a hierarchical syshGem for dividing up the economic territory of the EU.
[6] Albers Equal Area Conic: http://webhelp.esri.com/arcgisdesktop/9.3/index.cfm?TopicName=Albers_Equal_Area_Conic

At first, titles and abstracts were screened to see if the study had the objective to study the prevalence, incidence or occurrence of the pathogen or a previous exposure to the pathogen in an area. In a second step, also the full texts were screened. Prevalence data were used if they were obtained from prevalence surveys implementing a cross-sectional study design. The following information was extracted from the included papers: number of animals sampled, number of animals positive, host animal species; diagnostic test/assay types; sampling strategy; study type; reference type and the geographic location of study. If studies did not report the diagnostic test, or the location where the survey took place, they were excluded.

4.1.3. Assessment of the worldwide occurrence of the VBD

A summary of the data collected which was used as input for the EFSA-VBD_RISK model to answer is provided in the Supporting Material. Maps of the geographic distribution of each of the 36 VBDs can be found in the characterisation of the diseases (Section 3).

4.2. Rate of entry of selected vector-borne diseases

4.2.1. Methodology to assess the rate of entry

There are three questions that needed to be answered to assess the rate of entry (Step 1 of the risk assessment framework, see Figure 4) of the 36 VBD-agents in the EFSA-VBD_RISK model (Figure 8).

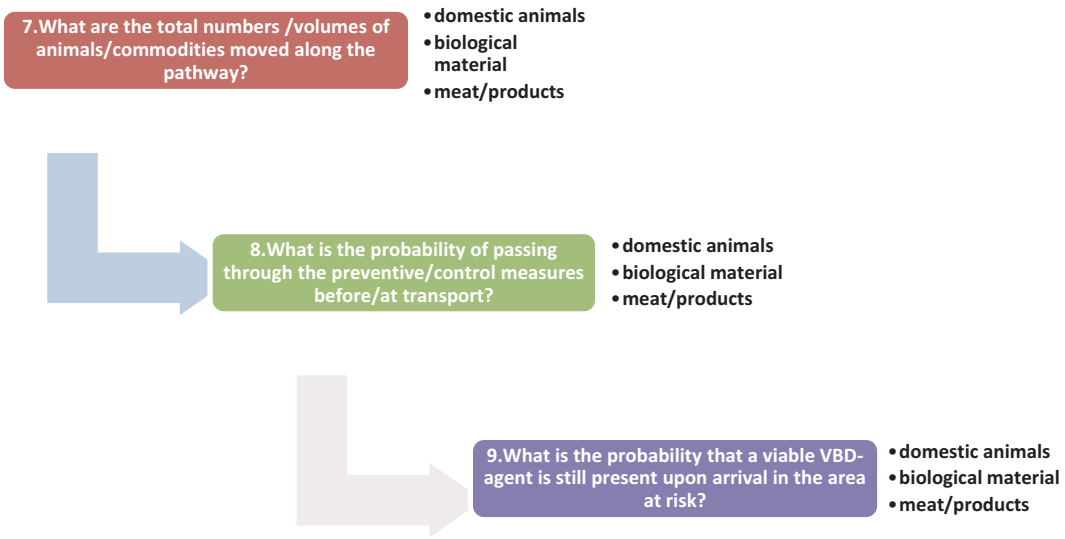


Figure 8: Steps to describe the rate of entry each of the VBD in the EFSA-VBD_RISK model

4.2.1.1. Methodology to assess the total numbers of animals moved along the pathways

The numbers of animals that moved into each of the four EU regions were grouped per family for the mammals and per class for the birds (Equidae, Bovidae, Suidae, Canidae and Camelidae, and aves). Animal species belonging to other families were not taken into account for this assessment. As only the weights of the animals were reported per 100 kg, average weights of cattle (500 kg), camels (500 kg), horses (400 kg), swine (350 kg), sheep (45 kg), goats (40 kg), dogs (20 kg) and cats (4 kg), and poultry (2 kg) were used to estimate the numbers of animals imported.

Animals imported for slaughter and breeding purposes were considered separately as this may have an impact on the probability of agent establishment (see Section 4.4.1).

The quantities extracted from EUROSTAT were then evaluated against the ranges provided in the EFSA-VBD_RISK model: Minimal (< 100), Minor (100–1,000), Moderate (1,000–10,000), Major (10,000–100,000), Massive (> 100,000). It should be noted that even when there was no trade reported to EUROSTAT or TRACES, the minimum category includes a movement up to 100 animals, assuming that a certain amount of unregistered movements of animals would always take place.

4.2.1.2. Methodology to assess the probability of passing through the preventive/control measures before or during transport

To assess the rate of entry of a VBD-agent, first the question whether the VBD-agent would persist/survive despite the applied preventive/control measures before or during transport was dealt with. More specifically, information was extracted from the EU legislation about which diseases must be tested for at the export country, as well as information about the quarantine details and the veterinary checks. Hence, the probability that a viable disease agent would be still present upon arrival of an infected live animal in the EU equals approximately: (1 – Sensitivity of the diagnostic test) × (Probability of surviving the quarantine) (Figure 9). The probability of surviving the quarantine would be approximately = $\mathbf{exp}^{-[\text{duration of the quarantine period}/(\text{latent period} + \text{infectious period})]}$. The outcomes were evaluated against the classes provided by the EFSA-VBD_RISK model: Very low (< 0.001), Low (0.001–0.01), Moderate (0.01–0.1), High (0.1–0.8) and Very high (> 0.8).

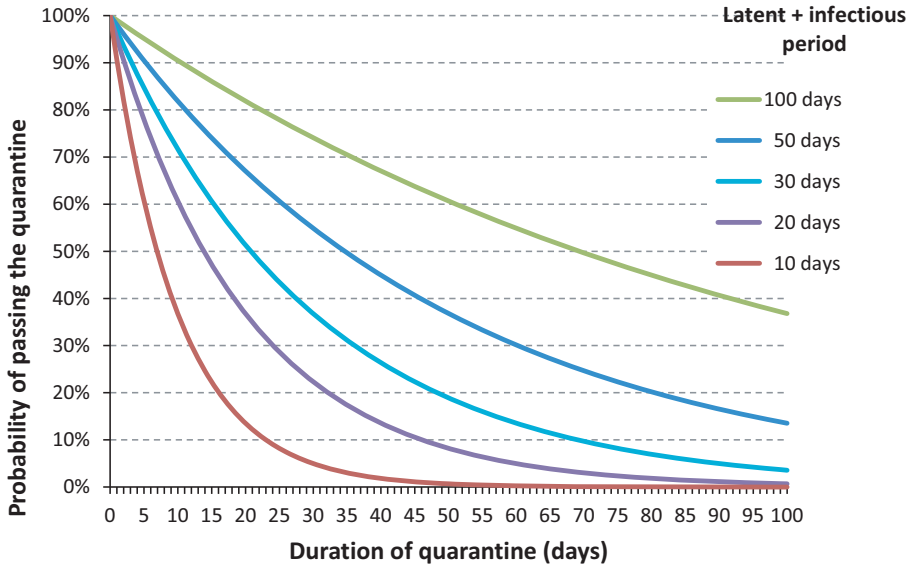


Figure 9: Probability to pass quarantine for alternative latent and infectious periods

4.2.1.3. Methodology to assess the probability that a viable VBD-agent is still present upon arrival in the area at risk

Secondly, the probability was assessed that a viable VBD-agent is still present upon arrival in the area at risk. For live animals, this probability will depend on the duration of the journey, the duration of the latent period and the duration of the infectious period of infected animals and it was approximated by the following equation: equation: $\mathbf{exp}^{-[\text{duration journey}/(\text{latent period} + \text{infectious period})]}$ (Figure 10).

For commodities, the probability that a viable disease agent would still be present upon arrival in the EU equals approximately = $\mathbf{exp}^{-[\text{duration of the journey}/(\text{maximum duration of survival in particular matrix at given temperature})]}$.

The calculated probabilities were then evaluated against the ranges provided in the EFSA-VBD_RISK model: Very low (< 0.001), Low (0.001–0.01), Moderate (0.01–0.1), High (0.1–0.8) and Very high (> 0.8).

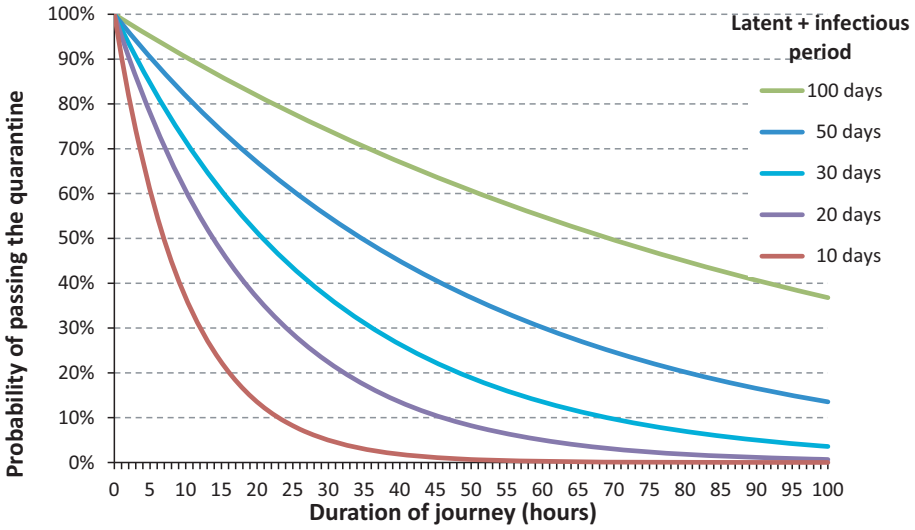


Figure 10: Probability that the VBD is still present upon arrival in the area at risk

4.2.2. Data to assess the rate of entry

To answer the three questions in the EFSA-VBD_RISK model to assess the rate of entry of 36 VBDs, the data items described below were collected. A summary of the data that was used as input for the model is provided in the supporting material.

4.2.2.1. Data used to assess the total numbers of animals moved along the pathway

- Data on the number of livestock moved from 2011 to 2016 was extracted from EUROSTAT's COMEXT database that contains the official European Foreign Trade Statistics. All trade of live animals is tied to specific health certificates that specify the purpose of a live animal being imported (e.g. breeding and slaughter). Each certificate specifies various preventive and control measures that importers/exporters must meet in order to ship live animals.
- Data on the movement of dogs were extracted from TRACES.

4.2.2.2. Data used to assess the probability of passing through the preventive/control measures before or during transport

An extensive literature review was carried out (Dórea et al., 2017 and Table A.1 in Appendix A) to investigate experimental infection of susceptible hosts with each of the 36 VBD-agents and collect data on their outcomes

- **Incubation period**: The median of the number of days between inoculation and first reports of clinical signs in the different studies, for each of the VBD subtypes in a host species. The animals that showed no clinical signs were excluded.
- **Median duration of latent period**: The median of the number of days between inoculation and first isolation of virus in the different studies for each of the VBD subtypes in a host species. Animals that were infected through transmission by direct contact with infected animals were excluded from this calculation, because the exact moment of infection was unknown.
- **Median duration of the infectious period**: Median of the number of days when virus was isolated for the last time in the different studies, for each of the VBD subtypes in a host species, minus the median duration of the latent period. Only those studies that were not terminated prematurely (i.e. the last observation was at least 3 days before the end of the experiment) were included.
- Evidence of **direct host-to-host transmission** through experiments including contact animals and excluding vectorial transmission.
- Evidence on **transplacental transmission** through detection of the virus in the fetus or in the neonate, excluding experimental infection *in utero* and vectorial infection of neonates.

- **Clinical signs**[7]: Data about clinical signs were retrieved from the papers at the animal group level. More in particular, when one or more animals in the group showed a particular sign, than the group was counted as having this clinical sign.

4.2.2.3. Data used to assess the probability that a viable VBD-agent is still present upon arrival in the area at risk

Survival time of the disease agents in different matrices

An extensive literature review and data collection relating to the survival time of each of the disease agents was carried out (see Dórea et al., 2017 for review protocol). Data on maximum duration of pathogen survival in several matrices were collected. The median was taken of the maximum numbers of days reported in the different studies at which a particular VBD-agent was isolated in a particular matrix.

Measures to prevent entry of disease agent in the EU

- Measures imposed on imports of animals and products from third countries

Information was recorded about specific requirements, e.g. which diseases must be tested for in the export country, quarantine details, veterinary checks and commodity treatments such as heating and freezing etc. Furthermore, information about the test types and methods prescribed to detect specific pathogens were recorded in the database. (http://ec.europa.eu/food/animals/index_en.htm).

Other types of information regarding border inspection controls and transport requirements, such as cleaning and spraying insecticides in shipping containers and aircrafts, were also recorded from the EU legislation.

- Specificity and sensitivity of diagnostic tools

An extensive literature search and data extraction on the performance of diagnostic tools intended to either demonstrate the presence or absence of infection (e.g. PCR, isolation of the pathogen), or to detect evidence of a previous infection (e.g. antibodies) was performed for each of the VBDs listed in Table 1 (Dórea et al., 2017). The lowest sensitivity of the obliged tests to detect a particular VBD-agent before importing it into the EU, or before exporting it to another country in the EU were taken for the risk assessment.

4.2.3. Assessment of the rate of entry

In Figure 11A–D, the entry scores of the VBDs through moving potentially infected livestock or pets into each of the four EU regions are ranked from high to a low. A distinction was made if the animals were moved for the purpose of breeding or slaughter into each of the regions in the EU. Further, it was distinguished if the origin of the animals was outside (extra-EU), or inside the EU (intra-EU), taking into account the different regulations applying for each of these pathways.

Only bars in the histogram in Figure 11A–D are visible for those VBDs with a rate of entry that was not zero for the different pathways. Given an example, the model estimated that RVFV had a rate of entry through livestock or pets either moved from inside and outside the EU, for breeding or slaughter, of zero.

The model estimated that there is a high to very high rate of entry (1 entry per 10 years to 1 entry per year) of CanL, Hepat, BTV, WNV, BHAV, CCHFV, SBV, THOV, EEV and VEE in all four EU regions through movement of livestock or pets from infected regions in or outside the EU. Main parameters contributing to the probability of entry are the prevalence of infection in susceptible hosts, the numbers of animals moved into the EU and the probability that the pathogen is still present upon arrival in the EU. The latter is determined mainly by the sensitivity of the tests (if testing is carried out) and the infectious period in the hosts. There is a high uncertainty around the prevalence of some of the VBDs in the source areas and the frequency of the outbreaks for not-reportable diseases.

Issues to take into account when interpreting the results of the assessment:

It should be noted that a high entry rate does not necessarily result in a high rate of introduction, because the agent may not be transmitted or become established. Additionally, it should be taken into account that for all VBDs an arbitrary default minimum of 100 susceptible animals were always

[7] Clinical signs of infected animals in experimental studies are not reported in a uniform way. Often the number of animals with a certain clinical sign is not mentioned. Also, in many cases, the first or last day of individual animals showing particular clinical sings are not mentioned in the papers.

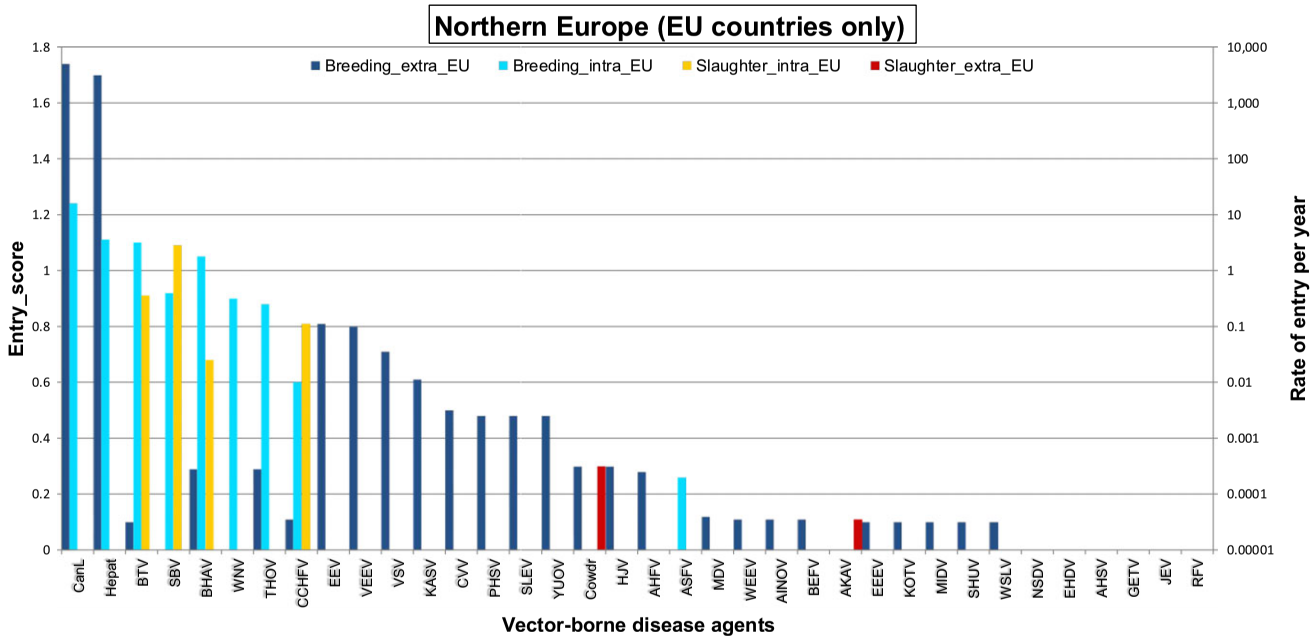
assumed to move into the EU regions in the model, when the import data had zero values. This should allow for illegal movements of livestock, movement of wildlife and underreporting but may lead to a slight overestimation of the rate of entry for some diseases especially for those with a single host represented by large animal species. Whenever more than 100 animals were reported imported, these reported data were used in the model.

At the same time, entry through the movement of vectors was not included in the assessment. The probability of the entry of pathogens via the vector route is mainly determined by the life history of the vector rather than the pathogen (Braks et al., 2017a). Considering available evidence, the highest rate of entry of VBD-agents through the vector route is considered to be caused by attached tick species. However, this route was assumed to be accounted for already through the movement of infected animals on which they would be attached. The rate of entry of VBD-agents through other routes (e.g. windborne movement of *Culicoides* or mosquitoes in containers) could not be assessed due to the absence of quantitative evidence on their numbers moving into the EU, and their infection rate (Braks et al., 2017a).

Finally, considering that entry of VBD-agents through the movement of wildlife species was not included in the assessment due to the lack of quantitative data, the true rates of entry could be higher, especially for those diseases affecting wild birds and connected migratory flyways for wild birds (e.g. WNV). Also, the rates of entry of disease agents present in regions neighbouring the EU, which are connected through wildlife corridors, could have been underestimated (e.g. ASFV entry into E-EU).

The confidence intervals around the outputs values visualised in Figure 11A–D can be found in Table D.1 in Appendix D.

A



(a): Entry_scores: very low rate of entry: 0–0.2; low rate of entry: 0.2–0.4; moderate rate of entry: 0.4–0.6; high rate of entry: 0.6–0.8; very high rate of entry > 0.8. (b): The entry score (sc) translates into rate of entry (Entry) using the following formula Rate of entry = 10^[5 × (sc − 1.0)]. Thus, an entry score of 1 translates to once per year and 0.8 translates to once per 10 years, 0.6 means once in 100 years, etc. (c): AHSV: African horse sickness virus; ASFV: African swine fever virus; AINOV: Aino virus; AKAV: Akabane virus; AHFV: Alkhurma haemorrhagic fever virus; BHAV: Bhanja virus; BTV: Bluetongue virus; BEFV: Bovine ephemeral fever virus; CVV: Bunyamwera virus; CCHF: Crimean-Congo haemorrhagic fever virus; EEE: Eastern equine encephalitis virus; EHDV: Epizootic haemorrhagic disease virus; EEV: Equine encephalosis virus; GETV: Getah virus; Cowdr: Heartwater (Cowdriosis); Hepat: Hepatozoonis; (*H. canis*); HJV: Highlands J. virus; JEV: Japanese encephalitis virus; KOTV: Kotonkan virus; CanL: Leishmaniosis (*L. infantum*); MDV: Main Drain virus; MIDV: Middelburg virus; NSDV: Nairobi sheep disease virus; KASV: Palyam virus; PHSV: Peruvian horse sickness virus; RVF: Rift Valley fever virus; SLEV: Saint Louis encephalitis virus; SBV: Schmallenberg virus; SHUV: Shuni virus; THOV: Thogoto virus; VEE: Venezuelan equine encephalitis virus; VSV: Vesicular stomatitis virus; WSLV: Wesselsbron virus; WNV: West Nile fever virus; WEEV: Western equine encephalitis virus; YUOV: Yunnan orbivirus virus.

Figure 11: (A, B, C and D) Ranking of the rate of entry of vector-borne diseases in the four regions in the EU

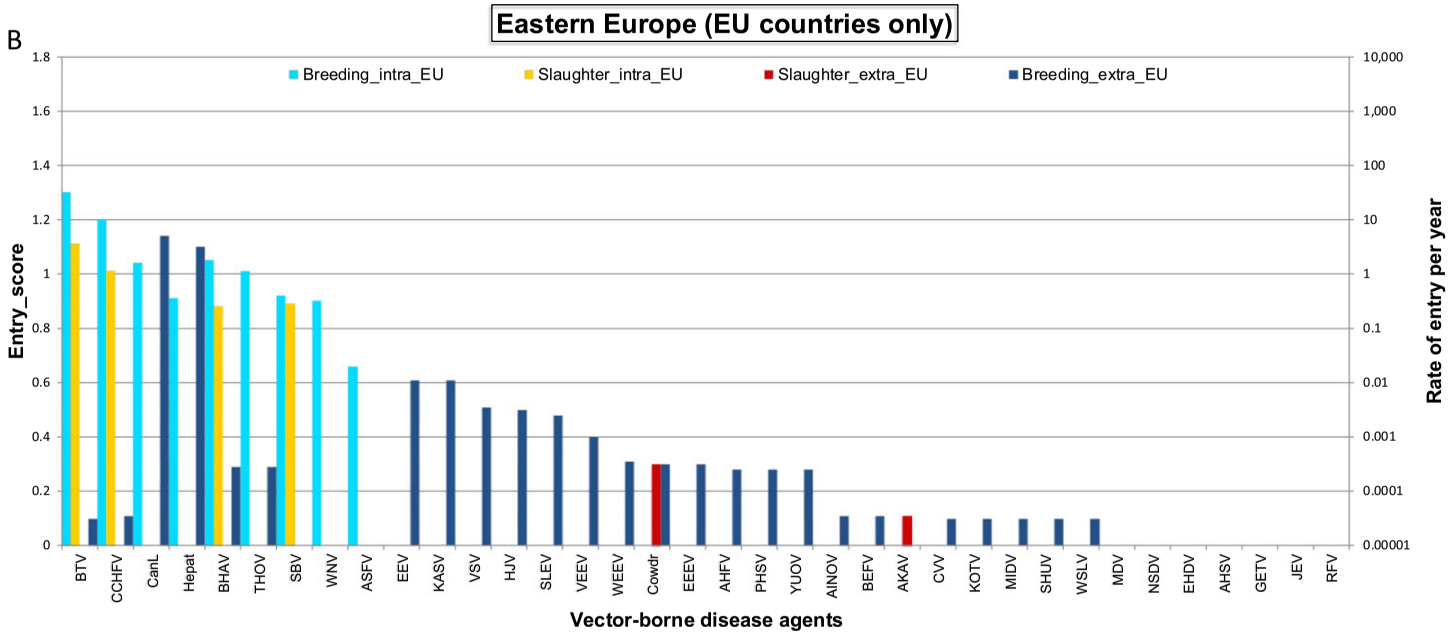


Figure 11: Continued

C

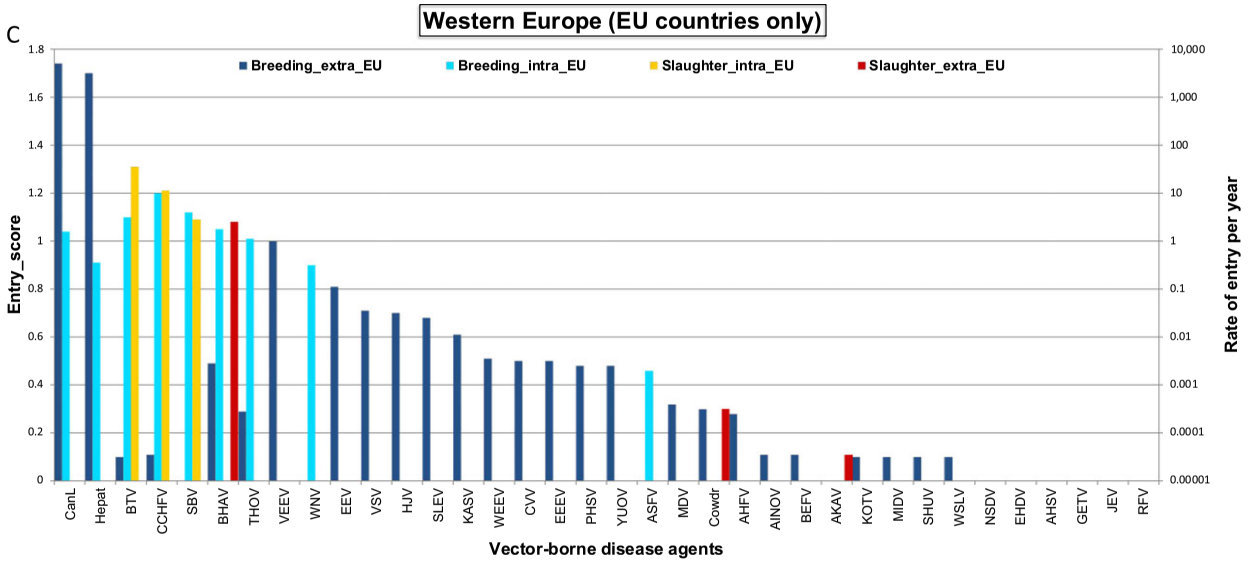


Figure 11: Continued

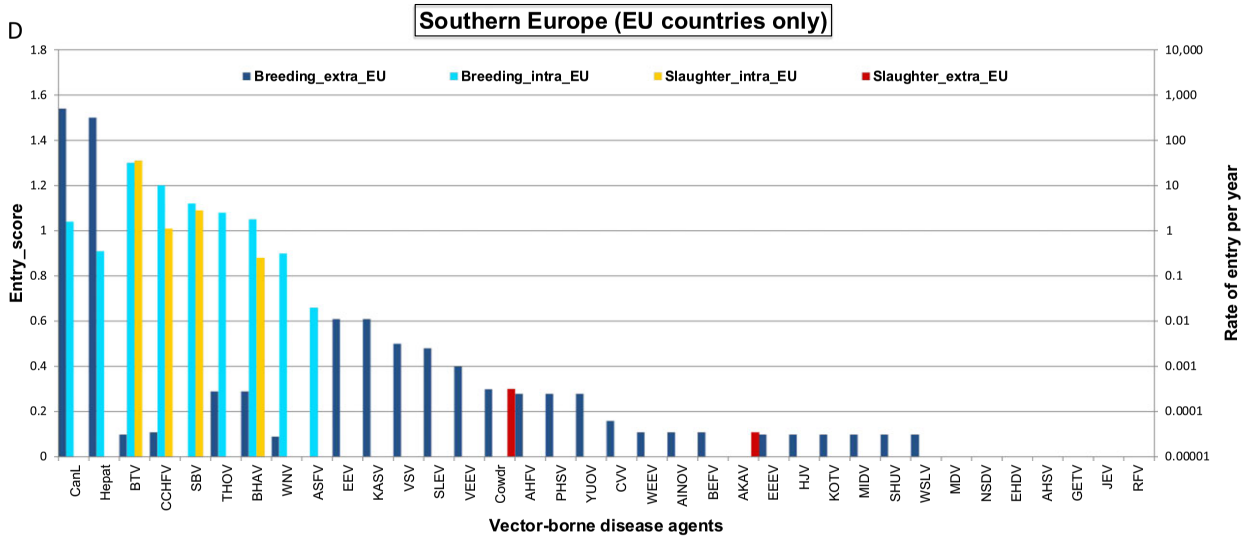


Figure 11: Continued

4.2.4. Conclusions

- According to the model, there is a moderate/high to very high rate of entry (1 entry per 10 years to 1 entry per year) of CanL, Hepat, BTV, BHAV, WNV, SBV, THOV, CCHFV, EEV and KASV in all four EU regions through movement of livestock or pets from infected regions inside or outside the EU.
- A moderate rate of entry was estimated for CVV, PHSV, SLEV and YUOV in N-EU; for VSV, HJV and SLEV in E-EU, for WEEV, CVV, EEEV, PHSV, YUOV and ASFV in W-EU; and for VSV, SLEV and VEE in S-EU
- According to the model, there is low to very low rate of entry (less than 1 entry every 10,000 years) of AINOV, BEFV, AKAV, KOTV, MIDV, SHUV, WSLV, NSDV, EHDV, AHSV, GETV, JEV and RVF.

4.3. Level of transmission of selected vector-borne diseases

4.3.1. Methodology to assess the level of vectorial transmission

There are three questions that needed to be answered to assess the level of transmission (Step 2 of the risk assessment framework, see Figure 4) of the 36 VBD-agents in the EFSA-VBD_RISK model (Figure 12).

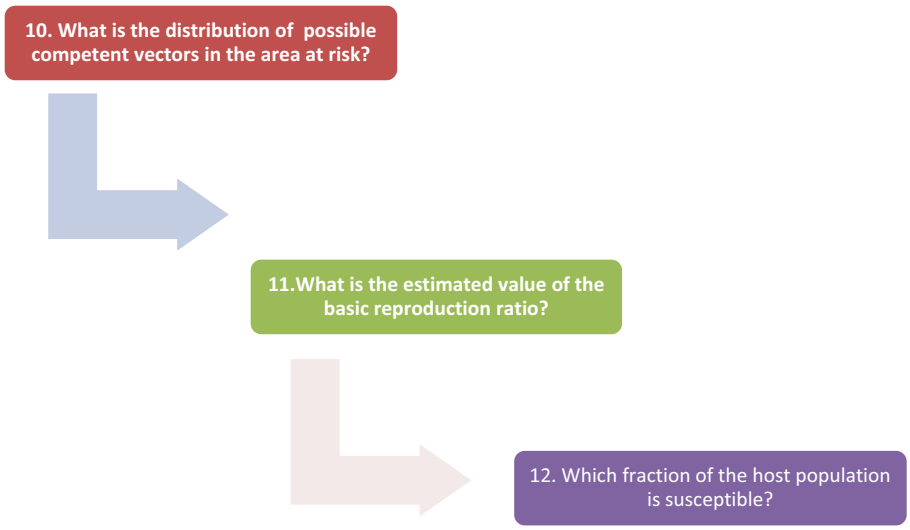


Figure 12: Questions to assess the level of transmission of a VBD-agent

4.3.1.1. Methodology to assess the distribution of competent vectors in the area at risk

The distribution of the possible vectors for each of the VBD-agents was evaluated against the classes of Table 4. Data for all the possible vector species were aggregated for each of the four EU regions. Whenever one possible competent vector species was reported to occur in one of the countries a given UN region, vectors were chosen to be 'present' in the UN region. When entomological surveillance activities have been carried out to detect a given vector species, but this could not be detected, than this vector species was recorded as absent. Whenever no entomological surveillance was carried out to detect a vector species, then this species distribution was unknown (Table 4). Finally, a fourth option was added, being the combination of vectors which were absent with vectors for which the distribution was unknown.

Table 4: EFSA-VBD_RISK model classes for the distribution of possible vectors of the VBD-agents in the EU regions

Absent	Unknown	Absent/unknown	Present
The vector species in which the VBD-agent was identified in laboratory or in field conditions elsewhere in the world have not been reported to occur in the EU region, despite surveillance efforts carried out to detect the particular vector species	The vector species in which the VBD-agent was identified in laboratory or in field conditions elsewhere in the world have not been surveyed in the EU region	The combination of either vector species that are absent, or vectors that have not been surveyed in the EU	At least one vector species in which the VBD-agent was identified in laboratory or in field conditions elsewhere in the world has been reported to occur in the EU region

4.3.1.2. Methodology to assess the value of the Basic Reproduction Ratio

The R_0 values delivered by the systematic review carried out by Braks et al., (2017b) are summarised in Appendix A. The median values of the R_0 were chosen to estimate the range of the R_0 in the EU sub-region. When the review did not identify any published values of R_0 for any of the infected regions worldwide for a given VBD, then a proxy of the R_0 was calculated. Therefore, the parameters defined below (A–E) had to be estimated and a proxy of R_0 was calculated with the following equation:

$$\mathbf{R_{0,proxy} = Vectors\ per\ host \times Biting\ rate\hat{}2 \times vector\ competence \times EXP(-EIP/expected\ lifespan) \times expected\ lifespan \times Infectious\ period\ host}$$

a) **Vectors per host:** estimates the expected ratio of vectors per host animals in the relevant habitat and vector season. Since this exact ratio is generally unknown, the attack rate was used as a proxy for this ratio. The latter is the number of vectors attacking a host at a given moment of time. The following values of attack rates were used: 20 specimens for hard ticks per host, five specimens for sandflies, 20 specimens for biting midges and five for mosquitoes (Braks et al., 2017a).

b) **Biting rate:** estimates the expected number of bites of a vector per day. For this assessment, the average number of bites per lifetime over the duration over the expected lifespan of the vector was used as proxy of the biting rate. This resulted in an average biting rate of 3/100 = 0.03 for hard ticks, 10/21 = 0.48 for sandflies, 10/14 = 0.71 for biting midges and 10/21 = 0.48 for mosquitoes.

c) **Vector competence:** estimates the level of transmission from infectious host to vector × level of transmission from infectious vector to host given that the vector bites the host. The first probability was estimated by taking the maximum of the numbers of infected vectors over the numbers of exposed vectors to a disease agent from studies that were reviewed by VectorNet. This information was provided in the External Scientific Report provided to EFSA by VectorNet (Braks et al., 2017b) or in Appendix B.

d) **Expected lifespan:** estimates the average days a vector lives in the vector season. For this assessment, the following values were used: 100 days for hard ticks, 21 days for sandflies, 14 days for biting midges and 21 days for mosquitoes. These values were based on Expert opinion, and provided by VectorNet (Braks et al., 2017a).

e) **Probability that the vector survives the extrinsic incubation period (EIP)** in the vector season, is estimated by the following formula:

$$\text{Surv (EIP)} = \text{EXP}(-\text{EIP/expected lifespan})$$

As a proxy for the EIP, the mean values per disease, forthcoming from the systematic review carried out by VectorNet were used (table 4a in Braks et al., 2017b) or when there were no data per disease, then the average of all the EIP per vector group were taken for this assessment (table 4b in Braks et al., 2017b).

f) **Infectious period in the host:**

See Section 4.2.2.2.

The ranges of the obtained R_0 from literature, or the calculated R_0 were evaluated against the ranges provided in the EFSA-VBD_RISK model: Very low (< 0.3), Low (0.3–1), Moderate (1–3), High (3–10) and Very high (> 10).

4.3.1.3. Methodology to assess the which fraction of the host population is susceptible

The fraction of susceptible hosts in a population depends on whether there has been a previous infection with the same VBD-agent or with a similar pathogen that might cause some cross-protection.

Additionally, vaccination campaigns will reduce the number of susceptible hosts in the population. Therefore, assuming a perfect vaccine the fraction of susceptible hosts in the population is an approximation of 1 – (the fraction of immunised hosts by natural infection or vaccination).

The fraction of immunised hosts in the population will depend on the time that has passed since the immunisation, the duration of the immunity, the efficacy of the vaccines and the lifespan of the immunised hosts (replacement). For populations where the VBD-agent has not entered before, or where no vaccination takes place, this fraction will approach 0. For immunised populations, this will approximate the seroprevalence.

The calculated probabilities were then evaluated against the ranges provided in the EFSA-VBD_RISK model: Very low (< 0.03), Low (0.03–0.1), Moderate (0.1–0.3), High (0.3–0.8), Very high (> 0.8).

4.3.2. Data to assess the level of vectorial transmission

To answer the three questions in the EFSA-VBD_RISK model to assess the level of transmission of the 36 VBDs, the data items described below were collected. A summary of the data that was used as input for the model is provided in the supporting material.

4.3.2.1. Data used to assess the distribution of competent vectors in the area at risk

To generate data on the distribution of possible competent vector species of the 36 VBD-agents in the four EU regions, an extensive literature review was carried out, identifying all possible vector species in which at least one of the VBD-agents were identified in laboratory or in field conditions. Then, based on the identified literature, 21 experts judged if these species occur in the four regions in the EU. Details for the review protocol and expert knowledge elicitation can be found here (Braks et al., 2017a).

4.3.2.2. Data used to assess the value of the Basic Reproduction Ratio

An extensive literature review was carried out to identify studies with the objective to calculate the basic reproduction ratio (see Braks et al., 2017b for search string). For studies using outbreak data, R_0 during the peak of the vector season was used. For those studies that estimated the R_0 based on estimated transmission parameters, the R_0 that represented the most ideal conditions for transmission were used for the risk assessment.

When no published values of R_0 were found for a given VBD-agent in any infected region in the world, its value was estimated according to Koeijer et al. (2014). Therefore, an extensive literature review was carried out to obtain information on the **average numbers of vectors per host**; the **average number of bites per lifetime**; the **duration over the expected lifespan**; the median **vector competence** and the **extrinsic incubation period** (see Braks et al., 2017a for the review protocol, and Appendix A for a short summary of the results).

4.3.2.3. Data used to assess which fraction of the host population is susceptible

To evaluate which fraction of the population that could be susceptible to a particular VBD, data were collected on the worldwide disease occurrence and seroprevalence (see Section 4.1.2.1).

4.3.3. Assessment of the level of vectorial transmission

Based on expert opinion (Vectornet 2016a), potential vectors of VBDs were considered to be absent in the following EU regions and transmission would be impossible:

- E-EU: Cowdr, MIDV, NSDV, THOV and WSLV;
- N- EU: CanL, MIDV, NSDV, SHUV, VEE, WSLV and YUOV;
- S-EU: MIDV and WSLV;
- W-EU: AHFV, Cowdr, MIDV, NSDV, WSLV, YUOV.

On the other hand, the occurrence of potential vectors was unknown for the following VBDs in each of the four EU regions:

- E-EU: AHFV, ASFV, BEFV, EEV, KASV, KOTV, PHSV, VSV, YUOV;
- N- EU: AHFV, ASFV, BEFV, Cowdr, EEV, KASV, KOTV, MDV, PHSV, THOV, VSV

- S-EU: AHFV, Cowdr, KASV, KOTV, PHSV, VSV,
- W-EU: KASV, KOTV, PHSV, THOV, VSV

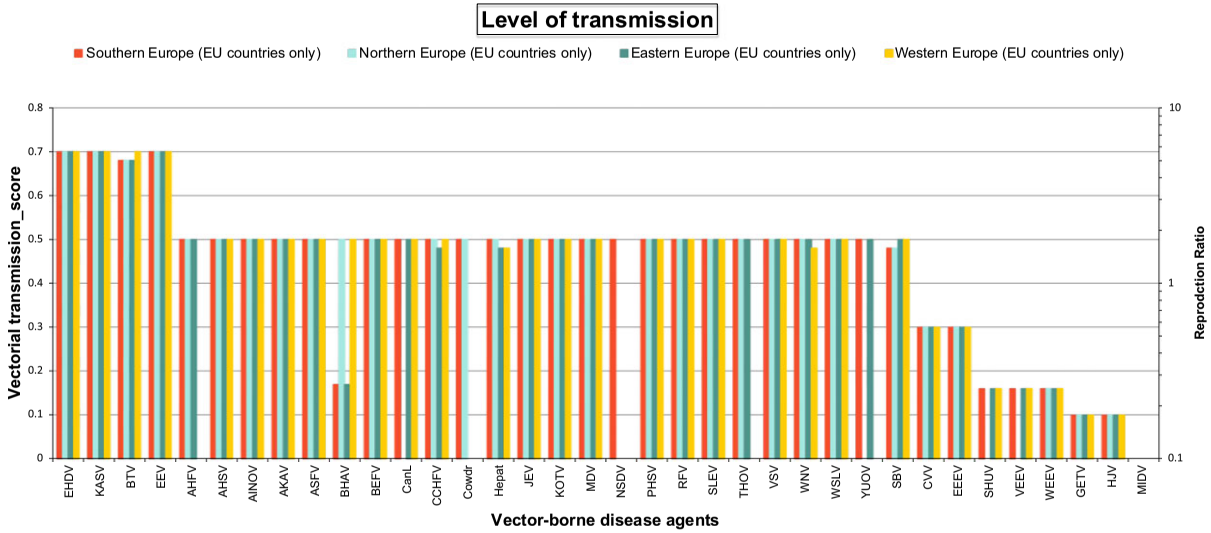
Figure 13 illustrates the estimated level of vectorial transmission of VBDs in each of the four EU regions, ranking the diseases from a high to a low level of vectorial transmission.

The figure illustrates that the expected level of vector transmission of EHDV, KASV, BTV and EEV is high in the four regions of the EU, with R_0 values between 3 and 10. Several factors are contributing to these high R_0 values, such as the long infectious periods in the host reported in experimental infections (e.g. medians of 17.5, 16.5, 21.3 and 16.5 dpi for EHDV, KASV, BTV and EEV, respectively). Further, the high numbers of the vectors per hosts estimated (average of 20 vectors per host), the high biting rate (0.51 on average) contributed to the high R_0 values.

The level of vector transmission was estimated to be low to very low for CVV, EEEV, SHUV, VEE, WEEV, GETV, HJV and MIDV everywhere in the EU with R_0 values smaller than 0.3. For these VBDs the estimated values of the numbers of vectors per host were much smaller (up to 5 vectors per host) and the infectious period in the hosts reported in experimental infections was much shorter (e.g. medians between 1 and 4 dpi).

For all the other VBD-agents, the level of transmission was expected to be moderate everywhere in the EU (R_0 between 1 and 3), except in W-EU where the level of transmission of AHFV, Cowdr, NSDV, THOV and YUOV was estimated to be very low; in E-EU, it was estimated to be very low for BHAV, Cowdr, NSDV; in S-EU, it was estimated to be very low for AHFV, and in N-EU, it was very low for CanL, NSDV and YUOV.

It should be noted that the model only takes into account vector transmission.



Scores: very low level of transmission: 0–0.2; low level of transmission: 0.2–0.4; moderate level of transmission: 0.4–0.6, high level of transmission: 0.6–0.8, very high level of transmission > 0.8. The transmission score is a measure representing a logarithmically adjusted reproduction ratio, where 0.4 represents a reproduction ratio around 1 (i.e. no epidemic development expected below 0.4. whereas 0.8 represents a reproduction ratio around 10). The transmission score (sc) translates into reproduction ratio (R_0) using the following formula: $R_0 = 10^{[2.5 \times (sc - 0.4)]}$. AHSV: African horse sickness virus; ASFV: African swine fever virus; AINOV: Aino virus; AKAV: Akabane virus; AHFV: Alkhurma haemorrhagic fever virus; BHAV: Bhanja virus; BTV: Bluetongue virus; BEFV: Bovine ephemeral fever virus; CVV: Bunyamwera virus; CCHFV: Crimean-Congo haemorrhagic fever virus; EEE: Eastern equine encephalitis virus; EHDV: Epizootic haemorrhagic disease virus; EEV: Equine encephalosis virus; GETV: Getah virus; Cowdr: Heartwater (Cowdriosis); Hepat: Hepatozoonis; *(H. canis*); HJV: Highlands J. virus; JEV: Japanese encephalitis virus; KOTV: Kotonkan virus; CanL: Leishmaniosis (*L. infantum*); MDV: Main Drain virus; MIDV: Middelburg virus; NSDV: Nairobi sheep disease virus; KASV: Palyam virus; PHSV: Peruvian horse sickness virus; RVF: Rift Valley fever virus; SLEV: Saint Louis encephalitis virus; SBV: Schmallenberg virus; SHUV: Shuni virus; THOV: Thogoto virus; VEE: Venezuelan equine encephalitis virus; VSV: Vesicular stomatitis virus; WSLV: Wesselsbron virus; WNV: West Nile fever virus; WEEV: Western equine encephalitis virus; YUOV: Yunnan orbivirus virus.

Figure 13: Ranking of the level of transmission of vector-borne diseases in the four regions in the EU

Issues to take into account when interpreting the results of the assessment:

With some exceptions for which good estimates of R_0 have been published (e.g. BTV in northern, W- and S-EU), the R_0 values were associated with a moderate to high uncertainty, due to the lack of documented data related to one or more of the parameters needed to calculate the ratio (such as the biting rate, the vector competence or the extrinsic incubation period in the vectors). In fact, due to the lack of data for some parameters, expert opinion was used to estimate the values at a general level needed for each of the group of vectors (ticks, sandflies, biting midges and mosquitoes). Additionally, for some of the VBD pathogens, the distribution of the potential competent vectors in the EU has never been investigated. The confidence intervals around the outputs values visualised in Figure 13 can be found in Table D.1 in Appendix D.

4.3.4. Conclusions

- The expected level of vector transmission of epizootic haemorrhagic disease virus, Palyam virus, bluetongue virus and equine encephalosis virus was estimated to be high in the four regions of the EU, with R_0 values between 3 and 10.
- The level of vector transmission was estimated to be low to very low for Bunyamwera virus, Eastern equine encephalitis virus, Shuni virus, Venezuelan equine encephalitis virus, Western equine encephalitis virus, Getah virus, Highlands J. virus and Middelburg virus everywhere in the EU with R_0 values smaller than 0.3.
- For all the other VBD-agents, the level of transmission was expected to be moderate everywhere in the EU (R_0 between 1 and 3), except in W-EU where the level of transmission of Alkhurma haemorrhagic fever virus, *Ehrlichia ruminantium*, Nairobi sheep disease virus, Thogoto virus and YUOV was estimated to be very low; in E-EU (very low level of Bhanja virus, *Ehrlichia ruminantium*, Nairobi sheep disease virus); S-EU (very low level of transmission of Alkhurma haemorrhagic fever virus,) and N-EU (very low level of transmission of *Leishmania infantum*, Nairobi sheep disease virus and Yunnan orbivirus).

4.4. Probability of establishment of selected vector-borne diseases

4.4.1. Methodology to assess the probability of establishment

There are two questions that needed to be answered to assess the probability of establishment (Step 3 of the risk assessment framework, see Figure 4) of the 36 VBD-agents in the EFSA-VBD_RISK model (Figure 14).

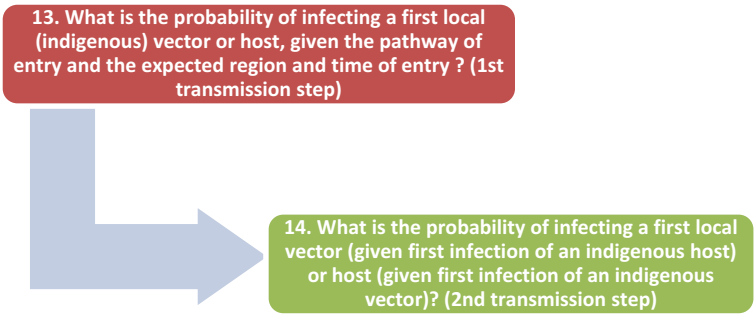


Figure 14: Questions to assess the level of transmission of a VBD-agent

4.4.1.1. Methodology to assess the probability of infecting a first local vector (1st transmission step)

This probability can be interpreted as the probability of contact of the infectious animal or commodity with a competent local vector or susceptible host respectively, hereby considering the season, the location and purpose of movement/importation. The following considerations have been used to guide this process:

For strictly vector-borne diseases, only the probability of contact of the imported host with local vectors should be considered for the first transmission step. The probability that the imported host will get in contact with a local vector was therefore judged to be approximately equal to: (the proportion

of the vector season over the whole year) × (the proportion of imported hosts that are not for immediate slaughter over all the imported hosts in the UN-region[8]) × (the proportion of the UN-region with the vector presence).

The estimation of the proportion of animals that are not for immediate slaughter (within 5 days) was also based on expert opinion. For animals imported for slaughter, it was assumed that only a very small proportion would not be slaughtered. This proportion was estimated to be 0.1–0.5% of the animals. On the other hand, for animals that are imported for breeding or production (it was assumed that a high proportion would not be slaughtered within 5 days (between 90% and 95% of the animals).

High vector presence was assigned when the summed maximum abundance of competent midge vectors exceeded either 100 for *Culicoides imicola* or 1,000 for all other midge species Data were collected through VectorNet, and modelled according to Versteirt et al. (2017). For those species where no abundance data were available (sandflies, mosquitoes and ticks), high vector presence was assigned to a location if the probability of presence of all competent vectors exceeded 80%. The calculated probabilities were then evaluated against the ranges provided in the EFSA-VBD_RISK model: Very low (< 0.0001), Low (0.0001–0.001), Moderate (0.001–0.01), High (0.01–0.1), Very high (> 0.1).

4.4.1.2. Methodology to assess the probability of infecting a first indigenous host (given first transmission to an indigenous vector)? (2nd transmission step)

For strictly vector-borne diseases, assuming that the first transmission step took place and a local vector was infected, the probability that the infected local vector would get in contact with a local susceptible host would depend on the proportion of the total UN region with the vector presence and host presence. This proportion was calculated by overlaying the areas with the vector presence (see previous step), and a high host density (more than 25 horses per km^2 or more than 50 animals per km^2 for the other hosts). For these calculations, only host density data of horses, cattle, sheep, goats, swine and deer were available. The calculated probabilities were then evaluated against the ranges provided in the EFSA-VBD_RISK model: Very low (< 0.001), Low (0.001–0.01), Moderate (0.01–0.1), High (0.1–0.8), Very high (> 0.8).

4.4.2. Data to assess the probability of establishment

To answer the two questions in the EFSA-VBD_RISK model to assess the probability of establishment of 36 VBDs, the data items described below were collected. A summary of the data that was used as input for the model is provided in the supporting material.

4.4.2.1. Data used to assess the probability of infecting a first local vector (1st transmission step)

- **Vector season**: The length of the duration of the vector season (Table 5) was obtained by expert opinion. Twenty-one entomologist of VectorNet estimated the numbers of months when adult vector activity can be expected at the southern and northern edges of each of the UN regions.

Table 5: Numbers of months when adult vector activity can be expected (based on expert opinion)

	N-EU	E-EU	S-EU	W-EU
Mosquitoes	3–4*	3–9	8–12	4–8
Ticks	9–12	9–12	9–12	9–12
Sandflies	0–0	0–4	4–6	0–5
Biting midges	3–4	6–7	10–11	7–10

*: The numbers represent the number of months when adult vector activity can be expected at the northern and southern edges, respectively.

- **Purpose of imported animals:**
  - Animals imported for slaughter: trade of live animal reported to EUROSTAT
  - Animals imported for breeding or production: trade of live animal reported to EUROSTAT CN8 codes ending on 0 or 9.

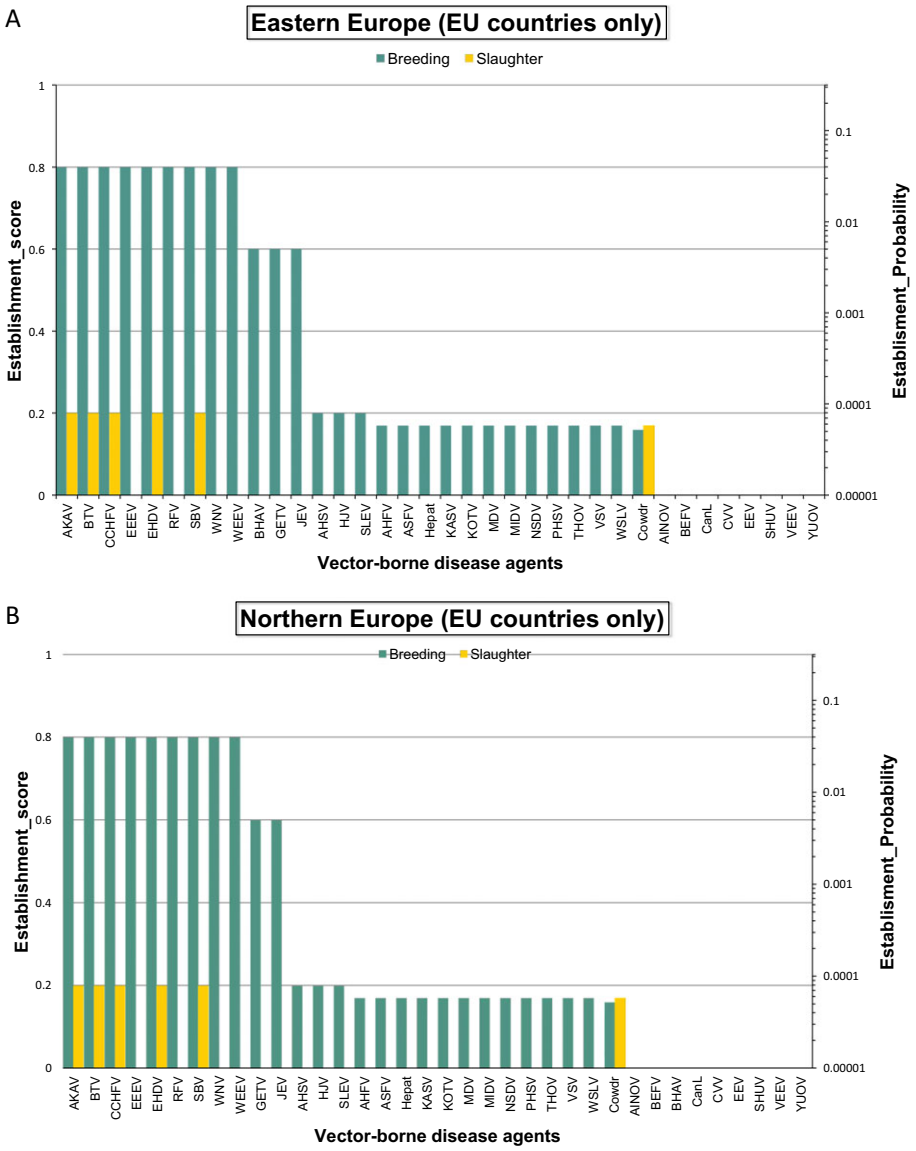
[8] The proportion of the vector season of the year was based on expert opinion (VectorNet knowledge matrix experts, 2016).

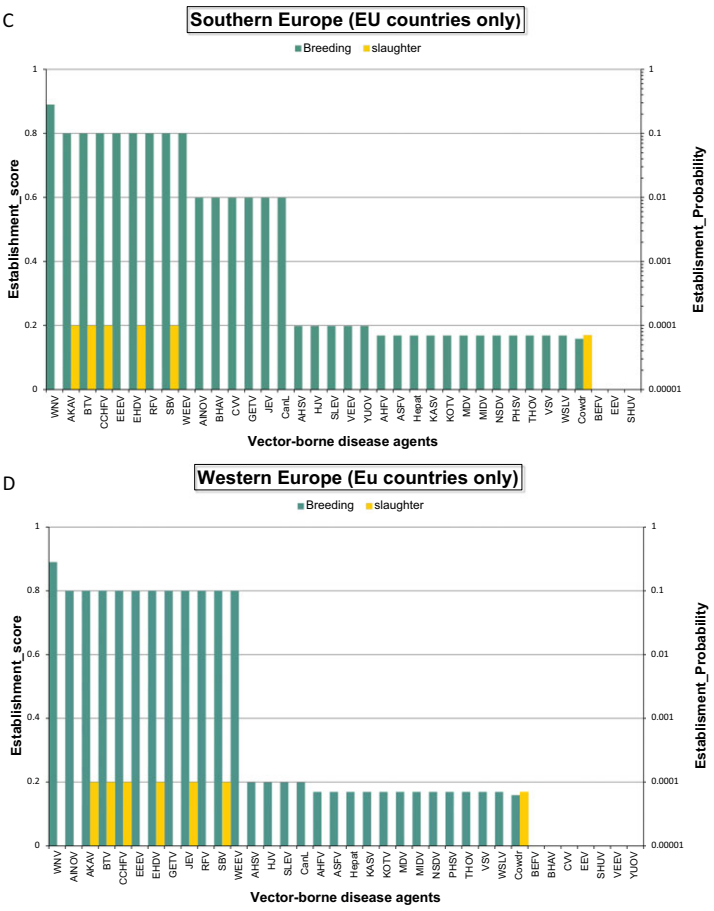
- **Data on the predicted vector presence** (sandflies, ticks and mosquitoes) and abundance (biting midges) was obtained from Braks et al. (2017a).

4.4.2.2. Data used to assess the probability of infecting a first indigenous host (given first transmission to an indigenous vector) (second transmission step)

- Data on the host distribution were extracted from EUROSTAT.

4.4.3. Assessment of the probability of establishment





(a): Establishment scores: very low probability of establishment: 0–0.19; low probability of establishment: 0.2–0.39; moderate probability of establishment: 0.4–0.59, high probability of establishment: 0.6–0.79, very high probability of establishment: ≥ 0.8. (b): The establishment score represents the log transformed probability of establishment, where 1 represents certain establishment, 0.8 translates to a probability of 10%, 0.6 translates to a probability of 1%, etc. The establishment score (sc) translates into establishment probability using the following formula: Establishment_Probability = 10^[5 × (sc − 1)]. (c): AHSV: African horse sickness virus; ASFV: African swine fever virus; AINOV: Aino virus; AKAV: Akabane virus; AHFV: Alkhurma haemorrhagic fever virus; BHAV: Bhanja virus; BTV: Bluetongue virus; BEFV: Bovine ephemeral fever virus; CVV: Bunyamwera virus; CCHF: Crimean-Congo haemorrhagic fever virus; EEE: Eastern equine encephalitis virus; EHDV: Epizootic haemorrhagic disease virus; EEV: Equine encephalosis virus; GETV: Getah virus; Cowdr: Heartwater (Cowdriosis); Hepat: Hepatozoonis; (*H. canis*); HJV: Highlands J. virus; JEV: Japanese encephalitis virus; KOTV: Kotonkan virus; CanL: Leishmaniosis (*L. infantum*); MDV: Main Drain virus; MIDV: Middelburg virus; NSDV: Nairobi sheep disease virus; KASV: Palyam virus; PHSV: Peruvian horse sickness virus; RVF: Rift Valley fever virus; SLEV: Saint Louis encephalitis virus; SBV: Schmallenberg virus; SHUV: Shuni virus; THOV: Thogoto virus; VEE: Venezuelan equine encephalitis virus; VSV: Vesicular stomatitis virus; WSLV: Wesselsbron virus; WNV: West Nile fever virus; WEEV: Western equine encephalitis virus; YUOV: Yunnan orbivirus virus.

Figure 15: ABCD Probability of establishment of vector-borne diseases in the four regions in the EU

Figure 15 illustrates the probability of establishment of VBDs in each of the four EU regions, ranking the diseases from a high to a low probability of establishment. The figure illustrates the high to very high probability of establishment of AKAV, BTV CCHFV, EEEV, EHDV, RVFV, SBV, WNV, WEEV in all EU regions. Further the probability of establishment is only **very high** for WNV in W-EU and S-EU and for AINOV only high in W-EU. GETV and JEV are moderate in N-EU, E-EU, and S-EU, while BHAV is moderate only in E-EU and S-EU and AINOV, BEFV and CVV high to very high only in S-EU (with a probability of 0.1–1 per introduction), depending on the region of the EU. For most of the other diseases, the probability of establishment is estimated to be low to very low (with a probability of less than 0.0001 per introduction).

Issues to take into account when interpreting the results of the assessment:

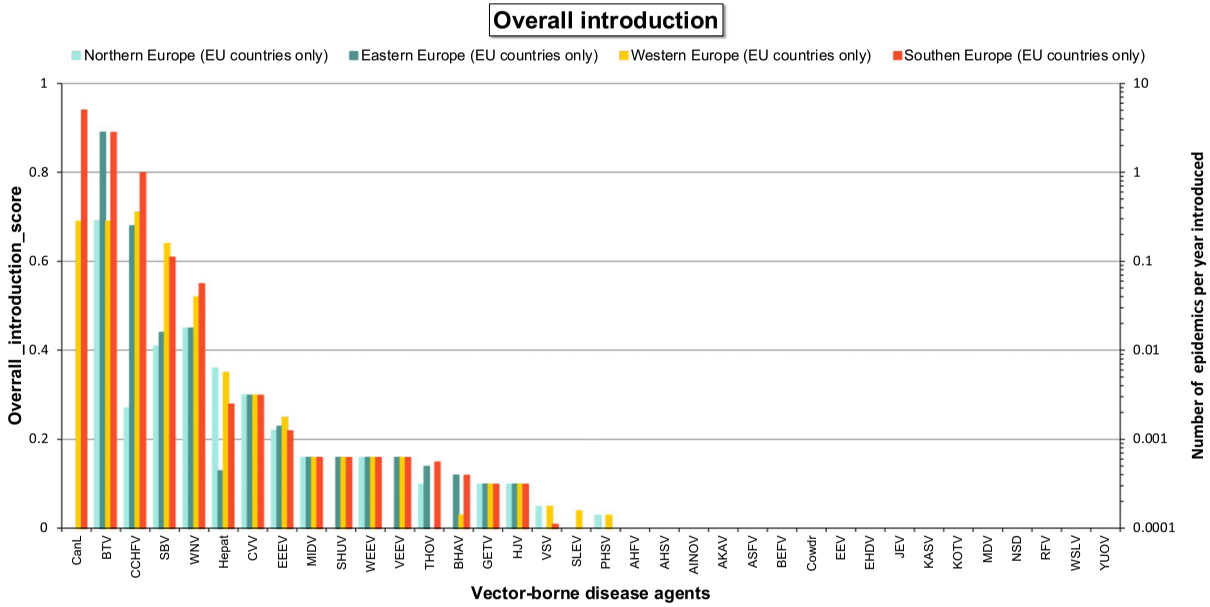
In general, there is a much higher probability of establishment for animals which are imported for breeding, compared to animals which are imported for direct slaughter upon arrival. Note also that this assessment is only based on vector transmission (i.e. the establishment being the probability that the pathogen can spread from vector to host and vice versa given the conditions of introduction (pathway, time and place). The proportion of areas with a high vectors density could not be calculated for AHFV, ASFV, Cowdr, Hepat, KASV, KOTV, MDV, MIDV, NSDV, PHSV, THOV, VSV as there is lack of spatial data on the distribution of the vectors. Therefore, the probability of establishment of these diseases was paired with a high uncertainty.

The confidence intervals around the outputs values visualised in Figure 15 can be found in Table D.1 in Appendix D.

4.4.4. Conclusions

- The model estimated the probability of establishment of Akabane virus, bluetongue virus, Crimean-Congo haemorrhagic fever virus, Eastern equine encephalitis virus, epizootic haemorrhagic disease virus, Schmallenberg virus, West Nile virus, Getah virus and Japanese encephalitis virus to be high to very high (with a probability of 0.1–1 per introduction), depending on the region of the EU.
- For most of the other diseases, the probability of establishment is estimated to be low to very low.
- In general, there is a much higher probability of establishment after introduction by animals which are imported for breeding, compared to animals which are imported for direct slaughter upon arrival.

4.5. Overall rate of introduction



Risk scores: very low rate of introduction: 0–0.2; low rate of introduction: 0.2–0.4; moderate rate of introduction: 0.4–0.6, high rate of introduction: 0.6–0.8, very high rate of introduction: > 0.8. The overall introduction score is a logarithmic translation of the rate of introduction of new epidemics. A score of 1 translates to 10 epidemics starting each year, a score of 0.8 translates to one epidemic per year, 0.6 translates to 1 epidemic every 10 years, etc. The overall introduction score (sc) translates into the number of new epidemics/year (No. epidemics/year) using the following formula: No. epidemics/year = 10^[5 × (sc − 0.8)]. AHSV: African horse sickness virus; ASFV: African swine fever virus; AINOV: Aino virus; AKAV: Akabane virus; AHFV: Alkhurma haemorrhagic fever virus; BHAV: Bhanja virus; BTV: Bluetongue virus; BEFV: Bovine ephemeral fever virus; CVV: Bunyamwera virus; CCHFV: Crimean Congo haemorrhagic fever virus; EEEV: Eastern equine encephalitis virus; EHDV: Epizootic haemorrhagic disease virus; EEV: Equine encephalosis virus; GETV: Getah virus; Cowdr: Heartwater (Cowdriosis); Hepat: Hepatozoonis; (*H. canis*); HJV: Highlands J. virus; JEV: Japanese encephalitis virus; KOTV: Kotonkan virus; CanL: Leishmaniosis (*L. infantum*); MDV: Main Drain virus; MIDV: Middelburg virus; NSDV: Nairobi sheep disease virus; KASV: Palyam virus; PHSV: Peruvian horse sickness virus; RVFV: Rift Valley fever virus; SLEV: Saint Louis encephalitis virus; SBV: Schmallenberg virus; SHUV: Shuni virus; THOV: Thogoto virus; VEE: Venezuelan equine encephalitis virus; VSV: Vesicular stomatitis virus; WSLV: Wesselsbron virus; WNV: West Nile fever virus; WEEV: Western equine encephalitis virus; YUOV: Yunnan orbivirus virus.

Figure 16: Overall rate of introduction of vector-borne diseases in the four regions in the EU (excluding VBDs with rate of introduction = 0 in all 4 VBDs)

CanL, CCHFV, BTV, WNV, SBV, Hepat, CanL and CVV and HJV have an overall rate of introduction that is more than 0.001 overall introductions per year (or a score > 0.2). For these disease agents, the annual extent of spread needed to be assessed.

In contrast, it was observed that some VBD-agents with a very high to moderate rate of entry, such as BHAV, THOV, KASV, VEE, VSV or SLEV, had an overall rate of introduction that was very low, either because there were no potential vectors present, or because the probability of exposure between the vector and the susceptible host was too low, leading to a very low probability of establishment.

4.5.1. Conclusions

- According to the model, pathogens with a very high to risk of overall introduction are BTV, CanL and CCHFV but not in the whole EU. Other pathogens such as WNV and SBV have moderate risk of overall introduction.
- The model estimated that Crimean-Congo haemorrhagic fever virus, bluetongue virus, West Nile virus, Schmallenberg virus, *Hepatozoon canis, L. infantum*, Bunyamwera virus and Highlands J. virus have more than 0.001 overall introductions per year (or a score > 0.2). The rate of introduction of all the other VBD-agents is lower.

5. Annual extent of spread of vector-borne diseases (ToR 2 and ToR 5)

5.1. Methodology to assess the annual extent of spread

There were six questions that needed to be answered to assess the annual extent of spread (Figure 17) in the EFSA-VBD_RISK model (Step 4 of the risk assessment framework, see Figure 4). Only for those VBDs for which the model estimated to be introduced (i.e. entered, transmitted and established) at least once every 1,000 years, the annual rate of spread was estimated.

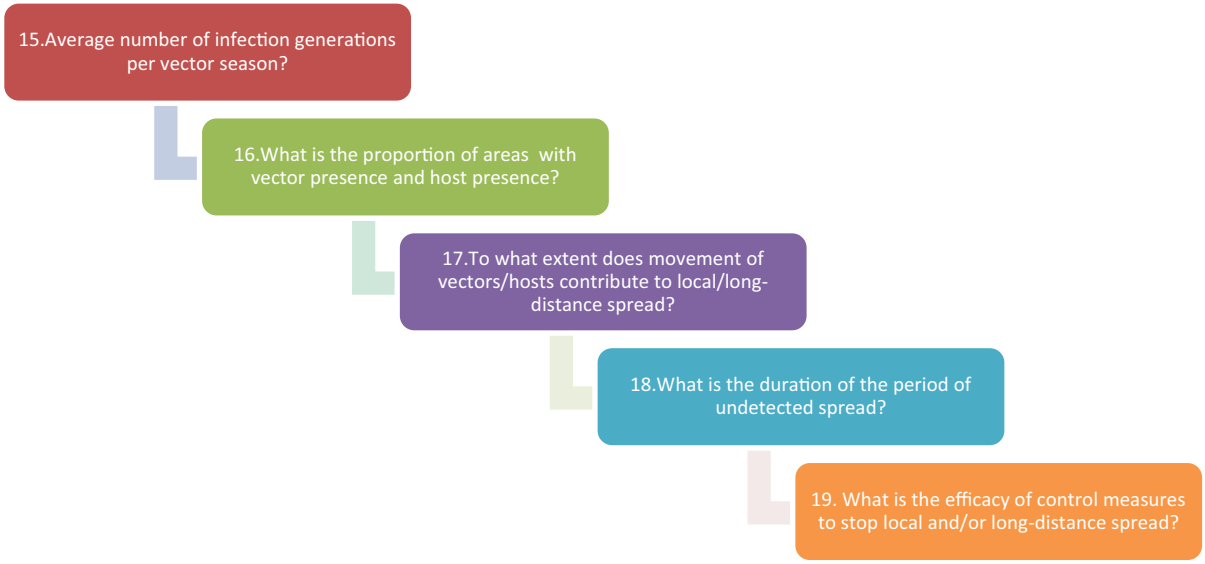


Figure 17: Questions to assess the extent of spread of a VBD-agent

5.1.1. Methodology to assess the average number of infection generations per vector season

The average number of vector infection generations in the vector season per UN region was estimated by the following equation:

Average number of vector infection generations = number of days in active vector season/(extrinsic incubation period (EIP)) + the latent period (host) + 0.5 × (infectious periods of the vector) + 0.5 × (infectious period the host)). For *L. infantum*, which can cause a very long infectious period in the host, the infectious period in the host was replaced by the duration of the vector season- latent period.

For example, for Schmallenberg virus, in the W-EU region, with an average number of days in the active vector season of Schmallenberg virus of 259.25 days per year, an average EIP of 10.29 days, an average latent period of 2 days, an average lifetime of 14 days and an average infectious period in the host of 6 days, the average number of infection generations in the vector season would be = = (259.25)/(10.29 + 2 + ((14 − 10.29)/2) + (6/2)) = 15.12 generations per year.

5.1.2. Methodology to assess the proportion of areas with vector presence and host presence

See second step of the establishment (Section 4.4.1.2).

5.1.3. Methodology to assess to what extent vectors/hosts movement does contribute to short/long-distance spread

Both the active dispersal of vectors species and the animal movements in the EU reported to EUROSTAT and TRACES were taken into account when addressing the extent of spread. The numbers of susceptible host species moved between the EU regions are large, and it was assumed that they will contribute to long distance spread of the VBD-agent when not controlled. The calculated probabilities were then evaluated against the ranges provided in the EFSA-VBD_RISK model: Very low (< 1 km), Low (1–3 km), Moderate (3–10 km), High (10–30 km) or Very high (> 30 km).

5.1.4. Methodology to assess the duration of the period of undetected spread

See Section 4.1.1.4.

5.1.5. Methodology to assess the relevant control measures and the impact of each on local and on long-distance spread (ToR 5)

To assess the impact of the relevant control measures on the spread, measure has to be implemented in case of an outbreak according to the EU legislation. Then, the expected coverage or implementation of the measure (Ci) in the outbreak area was multiplied with its efficacy (Ei) to obtain the reduction of a given measure (Ri = 1/1 − (Qi × Ei)). As data on the coverage or implementation of the measures are scarce, these figures were based on expert opinion. The total reduction of R_0 of all possible measures together was considered to be an approximation of 1/the maximum reduction of all the Ri (Table 6). The outcome of this evaluation was compared with the classes of the EFSA-VBD_RISK model: Very low (< 0.15), Low (15–50%), Moderate (15–50%), High (75–90%), Very high (> 90%).

Table 6: Implementation of different control measures and their efficacy to reduce spread in case of a VBD outbreak

Measure	Implementation/ coverage	Efficacy	Reduction of transmission
Restriction of movement	C1	E1	1 − (C1 × E1) = R1
Culling	C2	E2	1 − (C2 × E2) = R2
Vector control	C3	E3	1 − C3 × E3) = R3
Vaccination	C4	E4	1 − (C4 × E4) = R4
Treatments	C5	E5	1 − (C5 × E5) = R5

5.2. Data to assess the annual extent of spread

To answer the six questions in the EFSA-VBD_RISK model to assess the extent of spread the data items described below were collected. A summary of the data that was used as input for the model is provided in the supporting material.

5.2.1. Data to assess the average number of infection generations per vector season

- Duration of the vector season: see Section 4.4.2.1.
- Intrinsic incubation period: see Section 4.2.2.2.
- Extrinsic incubation period: see Section 4.3.2.2.

- Infectious period of host: see Section 4.2.2.2.
- Infectious period of vector (~ life span of the vector): see Section 4.3.2.2.

5.2.2. Data to assess the proportion of areas with vector presence and host presence

Vector distribution: See Section 4.3.2.1.

5.2.3. Data to assess to what extent movement of vectors/hosts does contribute to short/long-distance spread

Animal movements: See Section 4.2.2.1.

Active movements of vectors were reported by Braks et al. (2017a) up to 10 m for ticks, up to 100 m for sandflies, up to 1 km for biting midges and more than 1 km for mosquitoes.

5.2.4. Data to assess the duration of the period of undetected spread

See Section 4.1.2.4.

5.2.5. Data to assess the relevant control measures and the impact of each on local and on long-distance spread

- The EU legislation for control measures after confirmation of an outbreak: the applicable EU legislation was reviewed and information was obtained for which VBD specific control measures, such as movement restrictions and culling, are regulated see Section 4.2.2.3.
- Vaccine efficacy: A systematic literature review was conducted looking into the efficacy of vaccines authorised for vaccinating animals in the EU (see Dórea et al., 2017, for review protocol).
- Vector control measures: An extensive literature review was carried out to look into the active substances that are approved by the European Environmental Agency concerning their target species, their application and efficacy (see Annex 2).
- Treatment efficacy: A systematic literature review was carried looking into the efficacy of preventive and curative pharmaceutical treatments that are authorised for treating animals in the EU (see Dórea et al., 2017, for review protocol).

5.3. Assessment of the annual extent of spread (ToR 2)

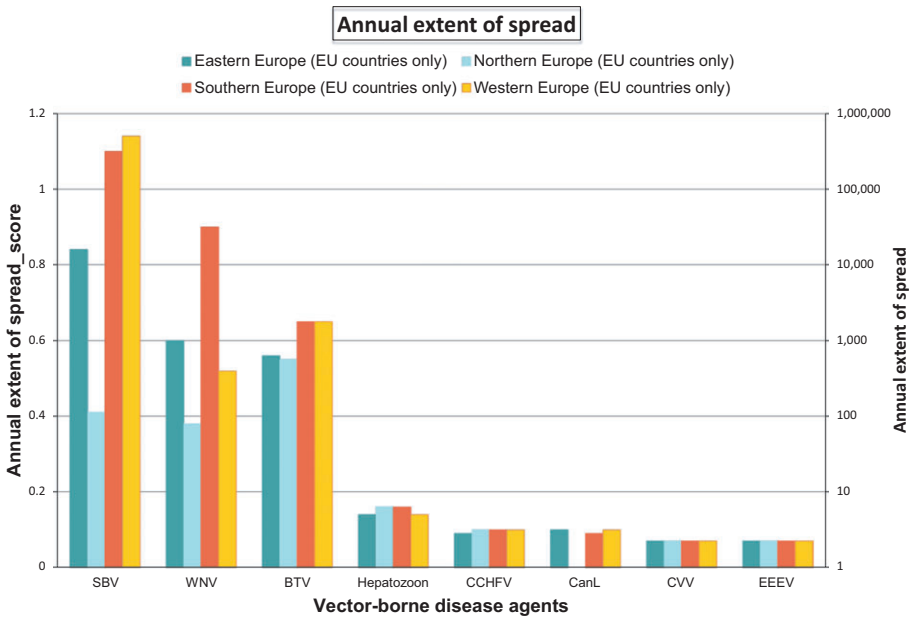
Figure 18 shows the model's estimates for the annual extent of spread after introduction of a VBD in a previously free area. Only BTV, WNV and SBV were estimated to have a moderate to very high annual extent of spread, depending on the region, whereas the other disease outbreaks would stay more localised**.** Results of BTV, WNV and SBV were mainly due to the high number of infection generations, and the high overlap of high abundance host and vector areas.

For tick-borne diseases, such as CCHF and *Hepatozoon canis*, mainly the low number of infection generations limits the extent of spread in the first year after introduction. Also, for CanL, the estimated number of infection generations per season was relatively low, but also the proportion of the overlapping areas with high density of hosts and vector was estimated to be very low, leading to a low spread. Finally, the combination of the application of topical insecticide together with vaccination was considered to keep the spread of CanL low.

Issues to be taken into account when interpreting the results

It should be taken into account that to assess the potential extent of spread, it was assumed that all available control measures were implemented. So the graph below should be interpreted, that even when vaccinating and applying insecticides at the moment of suspicion and confirmation of the outbreak, BTV, WNV and SBV will still have a high to very high spread.

Additionally, it should be noted that there is a high uncertainty concerning the efficacy of the prevention and control measures of VBDs such as CVV, CCHF and HEPA. The confidence intervals around the outputs values visualised in Figure 18 can be found in Table D.1 in Appendix D.



Risk scores: very low annual extent of spread: 0–0.2; low annual extent of spread: 0.2–0.4; moderate annual extent of spread: 0.4–0.6, high annual extent of spread: 0.6–0.8, very high annual extent of spread: > 0.8. The annual extent of spread is a logarithmic translation of the number of infected hosts that is expected to develop within one year. A risk score of 0 translates to 1 host, a score of 0.2 translates to 10 hosts, a score of 0.4 translates to 100 hosts, etc. and a score of 1 translates to 100,000 hosts. The annual extent of spread score (sc) translates into the number of infected hosts (units)/year (# infected hosts/year) using the following formula: # infected hosts/year = 10^[5 × sc]. BTV: Bluetongue virus; CVV: Bunyamwera virus; CCHFV: Crimean Congo haemorrhagic fever virus; EEEV: Eastern equine encephalitis virus; Hepatozoonis; *(H. canis)*; CanL: Leishmaniosis (*L. infantum*); SBV: Schmallenberg virus; WNV: West Nile virus.

Figure 18: Annual extent of spread of vector-borne diseases in the four regions in the EU

5.4. Conclusions

- The model estimated that the annual extent of spread after introduction of bluetongue virus, West Nile virus and Schmallenberg virus in a previously free area would be moderate to very high, depending on the region.
- The model estimated that the annual extent of spread after introduction of *Hepatozoon canis*, Crimean-Congo haemorrhagic fever virus, *L. infantum*, Bunyamwera virus and Eastern equine encephalitis virus in a previously free area would be very low.

6. Probability of overwintering of selected vector-borne diseases (ToR 4)

6.1. Methodology to assess the probability of overwintering

There were five questions that needed to be answered to assess the probability of overwintering (Figure 19) in the EFSA-VBD_RISK model (Step 5 of the risk assessment framework, see Figure 4).

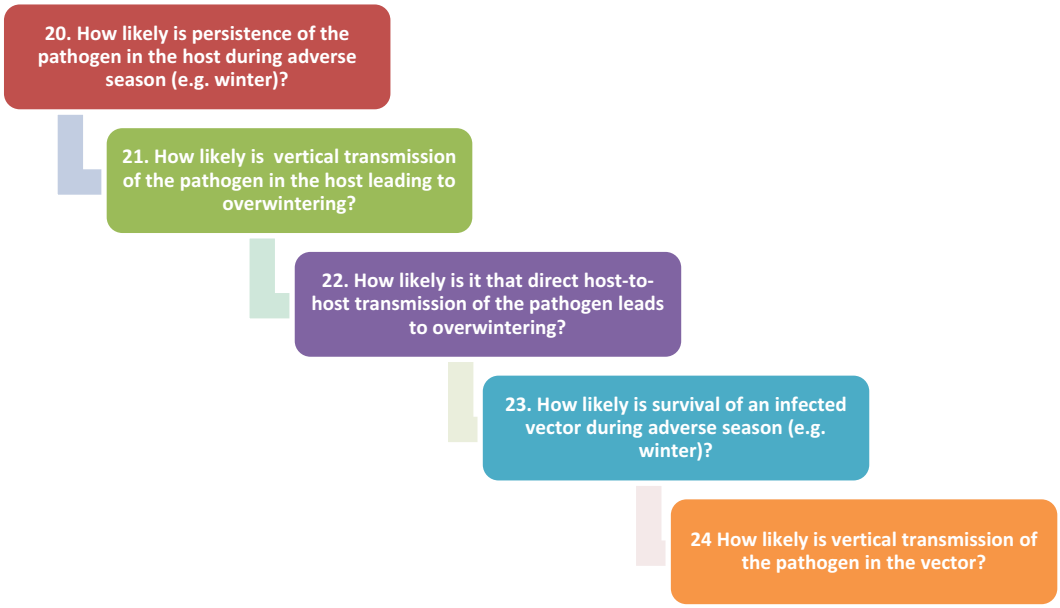


Figure 19: Questions to assess the probability of overwintering of a VBD-agent

6.1.1. Methodology to assess the likelihood of overwintering of the pathogen in the host during adverse season

The overwintering of the pathogen in the host was considered as the median duration of the infectious period divided by the median duration of the adverse season. This proportion was compared with the available classes in the EFSA-VBD_RISK model: Very low (< 0.1%), Low (0.1–1%), Moderate (1–10%), High (10–80%) and Very high (> 80%).

6.1.2. Methodology to assess the likelihood of vertical transmission of the pathogen in the host leading to overwintering

This likelihood was calculated as the (the prevalence) × (probability of vertical transmission) × (the probability of being pregnant in the last trimester). When scientific evidence of vertical transmission was found in scientific literature, an arbitrary probability of vertical transmission of '0.9' was chosen. The probability of being pregnant in the third trimester was chosen as the average number of pregnancies per year for a given species, divided by 3. The outcome of the calculated probability of vertical transmission was then compared with the available classes in the EFSA-VBD_RISK model: Very low (< 0.1%), Low (0.1–1%), Moderate (1–10%), High (10–80%) and Very high (> 80%).

6.1.3. Methodology to assess the likelihood of direct host-to-host transmission of the pathogen leading to overwintering

When evidence was found of direct host-to host transmission of the VBD-agent in scientific literature, the highest class was chosen from the available classes in the EFSA-VBD_RISK model: Very high (> 80%). When there was no evidence of direct host-to-host transmission the lowest class was chosen: Very low (< 0.1%).

6.1.4. Methodology to assess the how likely is survival of an infected vector during the adverse season

The probability of overwintering of vectors was calculated as the duration of the adverse season over the life span of the vector. The outcome of the calculated probability of vertical transmission was then compared with the available classes in the EFSA-VBD_RISK model: Very low (< 0.1%), Low (0.1–1%), Moderate (1–10%), High (10–80%) and Very high (> 80%).

6.1.5. Methodology to assess the likelihood of vertical transmission of the pathogen in the vector

The probability of vertical transmission of the pathogen in the vector was reviewed by VectorNet for the most important vector species for each VBD-agent (VectorNet, 2016). The probability was based on expert opinion and compared with the classes provided in the EFSA-VBD_RISK model: Very low (< 0.1%), Low (0.1–1%), Moderate (1–10%), High (10–80%) and Very high (> 80%).

6.2. Data to assess the probability of overwintering

To answer the five questions in the EFSA-VBD_RISK model to assess the probability of overwintering the data items described below were collected. A summary of the data that was used as input for the model is provided in the supporting material.

6.2.1. Data used to assess the likelihood of overwintering of the pathogen in the host during adverse season

- Infectious period: see Section 4.2.2.2.
- Adverse season: see Section 4.4.2.1.

6.2.2. Data used to assess the likelihood of vertical transmission of the pathogen in the host leading to overwintering

- Prevalence: see Section 4.1.2.1.
- Probability of vertical transmission in the host: see Section 4.2.2.2.
- Average number of pregnancies per year.

6.2.3. Data used to assess the likelihood of host-to-host transmission of the pathogen leading to overwintering

- Results of contact transmission studies: see Section 4.2.2.2.

6.2.4. Data used to assess the likelihood of survival of an infected vector during the adverse season

- Duration of the adverse season: see Section 4.4.2.1.
- Duration of the life span of the vector: see Section 4.3.2.2.

6.2.5. Data used to assess the likelihood of vertical transmission of the pathogen in the vector

- Vertical transmission in vectors: see Section 4.3.2.2.

6.3. Assessment of the probability of overwintering(ToR 4)

The model estimated the probability of overwintering of CCHFV and WNV to be very high in the four regions of the EU (Figure 20). This was mainly because for CCHFV direct transmission between hosts was estimated to lead to a high probability of overwintering of the virus. Further, vertical transmission in the vectors has been proven for both viruses and this mechanism is estimated to lead to a high probability of overwintering of both pathogens.

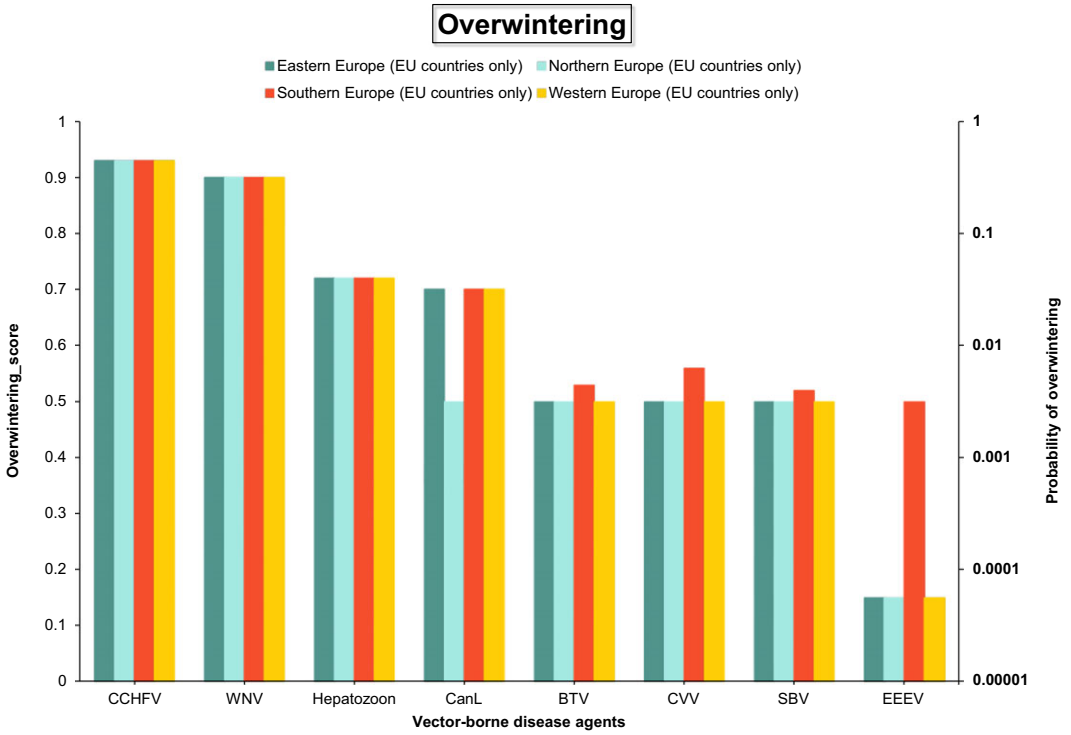
The model estimated the probability of overwintering of HEPAT and CanL to be high in the four regions of the EU. For CanL, both the persistence of the pathogen in the host, as well as vertical transmission of the pathogen in the host was estimated to possibly lead to overwintering. For HEPAT, both the persistence of the pathogen in the host, as well as the survival of the pathogen in the ticks could lead to overwintering.

For BTV, CVV and SBV, the model estimated a moderate probability of overwintering. This was mainly due to the possibility of vertical transmission in the host and the potential survival of the vector in the adverse season (the latter only in S-EU).

Issues to be taken into account when interpreting the results:

There is a high uncertainty accompanied with some of the possible overwintering mechanisms. More in particular, there was no published information on the vertical transmission of CCHFV and

HEPAT in the host. Also, concerning vertical transmission of CVV in the vectors was no information found. The confidence intervals around the outputs values visualised in Figure 20 are reported in Table D.1 in Appendix D.



Risk scores: very low probability of overwintering: 0-0.2; low probability of overwintering: 0.2–0.4; moderate probability of overwintering: 0.4–0.6, high probability of overwintering: 0.6–0.8, very high probability of overwintering: > 0.8. The overwintering score translates into a probability that the infection will persist through the winter. An overwintering score of 0.8 stands for nearly certain persistence through the winter, if the epidemic enters the winter with about 100 infected hosts/vectors, a score of 0.6 stands for a probability of 10%, a score of 0.4 stands for a probability of 1%. The overwintering score (sc) translates into the overwintering probability using the following formula: overwintering probability = 10^[5 × (sc − 1)]. BTV: Bluetongue virus; CVV: Bunyamwera virus; CCHFV: Crimean Congo haemorrhagic fever virus; EEEV: Eastern equine encephalitis virus; Hepatozoonis; *(H. canis*); CanL: Leishmaniosis (*L. infantum*); SBV: Schmallenberg virus; WNV: West Nile virus.

Figure 20: Probability of overwintering of vector-borne diseases in the four regions in the EU

6.3.1. Conclusions

- The model estimated the probability of overwintering of Crimean-Congo haemorrhagic fever virus and West Nile virus to be very high in the four regions of the EU.
- The model estimated the probability of overwintering of *H. canis* and *L. infantum* to be high in the four regions of the EU.
- The model estimated the probability of overwintering of Schmallenberg virus, Bunyamwera virus and bluetongue virus to be moderate in the four regions of the EU.
- For EEEV, only in S-EU, the model estimated the probability of overwintering to be moderate

7. Impact (ToR 3)

There were three questions that needed to be answered to assess the impact (Figure 21) in the EFSA-VBD_RISK model (Step 6 of the risk assessment framework, see Figure 4).

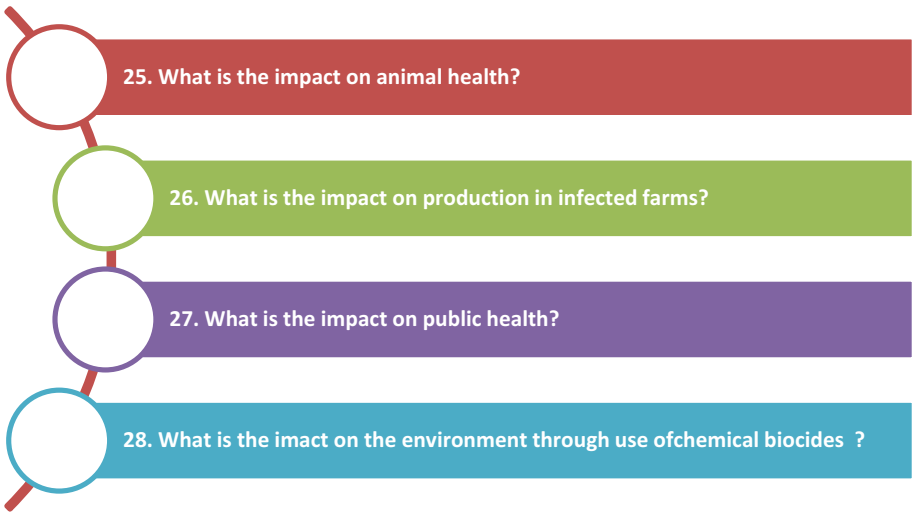


Figure 21: Questions to assess the impact of a VBD-agent

7.1. Impact on Animal Health and Welfare

7.1.1. Methodology to assess the predicted impact on animal health and welfare

Currently, there is internationally a lack of consensus on methodologies to assess or quantify the impact on animal health. In an attempt to provide and evidence based assessment, clinical signs as extracted from the experimental infection studies (see Section 4.2.2.2 and Dórea et al., 2017 were categorised by the AHAW Panel as either very severe, severe, moderate, mild, and very mild for an example of clinical signs of BTV in sheep). In addition, 'death' was added as a separate category indicating the biggest possible impact on animal health.

To enable the comparison of the impact on animal health and welfare of the different VBDs, a severity score was calculated for each VBD. That is, for disease 'a' reporting n_{a,i} groups with clinical signs 'i', the associated weight w_{a,i} was computed as: w_{a,i} = n_{a,i}/[sum of all n_{a,i} over all disease (index a)]

The severity score (=aggregated severity over all clinical signs) for a disease 'a' was obtained by S_a = [sum of C_i × w_{a,i} over all clinical signs (index i)]/[sum of all w_{a,i} over all clinical signs (index i)], where C_i is the severity assigned to each clinical sign. The severity scores were then inserted in the EFSA VBD risk assessment model as following: very mild (0.00–0.02), mild (0.02–0.07), moderate (0.07–0.19), severe (0.19–0.44) and very severe (0.44–1.00).

These classes were chosen to reflect the understanding of a non-linear increase between subsequent levels of severity of clinical signs e.g. severe clinics towards dead (see Appendix B). The calculation used an exponential curve to define the increase with the exponent (here being 4) was adapted to the most plausible understanding of severity levels for the animals.

It should be noted that there are still challenges to further standardise the approach. More in particular, the assignment of clinical signs to the different categories of severity was merely guided by expert opinion. Further, the way of reporting clinical signs in scientific literature is highly heterogeneous, at time very detailed on the individual animal level, and at times general, on the animal group level, using nonspecific terminology. Consequently, here we could only use signs reported at the group level.

7.1.2. Data to assess the impact on animal health and welfare

- See Section 4.2.2.2 for data collection on clinical signs and Appendix C

7.1.3. Assessment of the impact on animal health and welfare

After calculating the severity score (see Appendix C) of the eight VBDs, which had an overall rate of introduction that was higher than 0.001 per year, this score was combined with the epidemic size (which is a combination of the extent of spread and the possibility of overwintering), to obtain a score for the impact on animal health and welfare (see Figure 22).

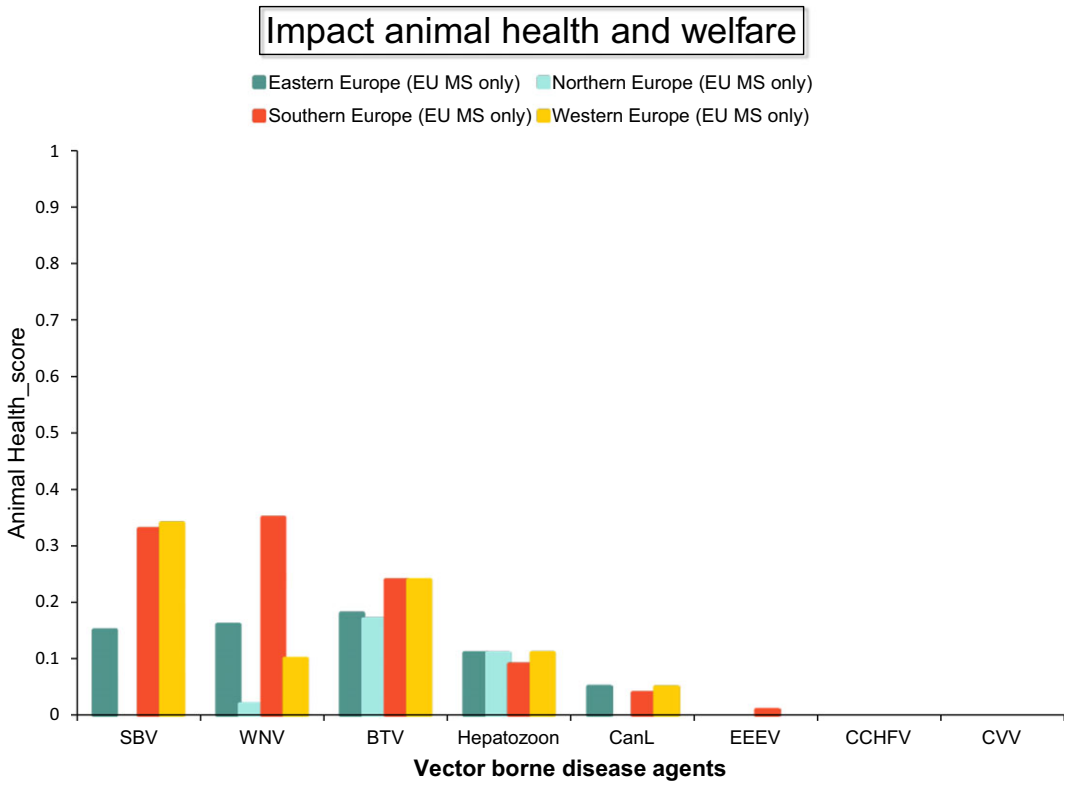
The model estimated SBV and BTV to have a low impact on animal health and welfare in the W-EU and S-EU regions, whereas the impact was estimated to be very low in the other two regions of the EU for these VBD-agents (Figure 22). It should be noted that the impact on animal health is the combination of the severity score (being an indication of the severity of the clinical signs) combined with the estimated epidemic size. The estimated epidemic size is a combination of the spread and possible duration of the epidemic over more than 1 vector season (overwintering). Thus, the very mild and moderate severity of a potential infection with SBV and BTV, respectively, were combined by the model with the moderate to very large spread of the virus in previously uninfected areas (depending on the EU region) and the moderate probability of overwintering in these areas for the two VBD-agents, resulting in the low impact in the W-EU and S-EU regions, and very low in the other two regions of the EU.

For canine leishmaniosis (infections which can lead to severe clinical signs depending on the stage of infection), the model estimated that the impact on animal health and welfare would be very low. This was because the model estimated that the spread of the parasite in the hereto free areas would be very low. The latter assumed the application of preventive measures (e.g. treatments with topical insecticides or vaccination and curative treatments of infected dogs) after detection of the outbreaks.

For the other six VBD-agents, the impact was absent to very low everywhere in the EU, mainly due to the limited spread predicted by the model and or the absence of clinical signs.

Issues to be taken into account when interpreting the results

Additionally, it should be noted that the uncertainty related to any of the previous steps will also add up to the uncertainty related to the impact of the outbreaks on animal health and welfare as it depends on the estimated size of the epidemic. Additionally, the uncertainty around the severity score would reduce if clinical signs in animal experiments would be reported on an individual animal level using specific terminology, instead of on the animal group level. The confidence intervals around the outputs values visualised in Figure 18 can be found in Table D.1 in Appendix D.



Impact scores: very low impact: 0–0.2; low impact: 0.2–0.4; moderate impact: 0.4–0.6, high impact: 0.6–0.8, very high impact: > 0.8. BTV: Bluetongue virus; CVV: Bunyamwera virus; CCHFV: Crimean Congo haemorrhagic fever virus; EEEV: Eastern equine encephalitis virus; Hepatozoonis; *(H. canis)*; CanL: Leishmaniosis (*L. infantum*); SBV: Schmallenberg virus; WNV: West Nile virus.

Figure 22: Impact on animals health and welfare of 8 VBDs with an overall rate of introduction that was higher than 0.001 per year

7.1.4. Conclusions

- When combining the size of the epidemic with the severity of the infections, Schmallenberg virus and bluetongue virus introductions were estimated by the model to cause a low impact on animal health and welfare in S-EU and W-EU, and WNF in S- EU.
- For *H. canis, L. infantum*, Eastern equine encephalitis virus, Crimean-Congo haemorrhagic fever virus, Bunyamwera virus and West Nile virus, the model estimated the impact on animal health and welfare to be very low everywhere in the EU.

7.2. Impact on production in infected farms

7.2.1. Methodology to assess the possible production losses due to the infection in case farms

Based on the information collected about production losses (Table 7) during outbreaks, an expert judgement was made, classifying the case farm production losses according to the classes in the EFSA-VBD_RISK model and Table 7. Note that the production losses can be more than 100% because they are not only the marginal losses to the infection but the infection could also result in culling of other animals, or long-lasting economic losses, higher than the value of the farm at the moment of infection. The economic impact due to the restrictions on trade or due to the costs of prevention and control measures was not considered. Although these aspects can result in major economic consequences, their impact assessment is resource intensive and was not within the scope of this mandate.

Table 7: EFSA-VBD_RISK model classes for the impact on case farm production losses

Impact on case-farm production (e.g. due to reduced milk production, growth, mortality, etc.)	Qualitative	Classes for impact on production losses in case farms
0% of annual farm production is lost due to disease	No impact	0
Up to 3% of annual farm production is lost due to disease	Very Low impact	0–0.03
3–10% of annual farm production is lost due to disease	Low impact	0.03–0.1
10–30% of annual farm production is lost due to disease	Moderate	0.1–0.3
30–100% of annual farm production is lost due to disease	High	0.3–1
More than 100% of annual farm production is lost due to disease	Very High impact	> 1
Unknown	Unknown	

7.2.2. Data to assess the impact on production losses

Case farm production losses: a narrative literature review on production losses during outbreaks (i.e. early culling, reduced milk production, weight loss and reproduction losses) was carried out.

7.2.3. Assessment of the impact on production in infected farms

Table 8 summarises the relative direct production losses on infected farms due to the VBD-agent infection, which have been found in the scientific literature. Although for both BTV and SBV the production losses on infected farms due to the disease were considered to be moderate, for all the other diseases there were either no production losses due to the disease (WNF and CCHF), or the disease did not affect production animals (CanL or Hepat), or there was no information found.

Table 8: Results of narrative review on direct production losses in VBD infected farms

VBD-agent	Impact on case-farm production (direct losses due to disease)	Ref	Mintrisk range	Uncertainty
BTV	Between 0.3% and 0.9% loss of the annual milk yield due to disease in cattle	Santman-Berends et al. (2011)	Very low	Low
BTV	3.4% loss of the annual milk yield due to disease in cattle	Nusinovici et al. (2013)	Low	Low
BTV	20% loss of the annual milk yield due to disease in cattle and sheep	Velthuis et al. (2010)	Moderate	Low

VBD-agent	Impact on case-farm production (direct losses due to disease)	Ref	Mintrisk range	Uncertainty
BTV	0–3% early culling due to disease in cattle and sheep	Velthuis et al. (2010)	Very Low	Low
BTV	7–8.1% weight loss due to disease in cattle and sheep	Velthuis et al. (2010)	Low	Low
BTV	2.6–6.7% reduced birth weight due to disease in cattle	Velthuis et al. (2010)	Low	Low
BTV	2–6.2% abortion due to disease in cattle and sheep	Velthuis et al. (2010)	Very Low	Low
BTV	0–53.5% postponed gestation due to disease in cattle and sheep	Velthuis et al. (2010)	High	Low
BTV	Overall production losses due to disease in infected farm	Expert opinion	Moderate	Moderate
CanL	Not applicable (dogs)	Expert opinion	No impact	Low
CCHFV	Unapparent infection in most other vertebrate hosts than humans	Expert opinion	No impact	Low
CVV	Not found		Unknown	High
EEEV	Not found		Unknown	High
Hepat	Not applicable (dogs)	Expert opinion	No impact	LOW
SBV	5–16% reduction of the gross margin due to disease, mainly due to the costs of heifers and steers not produced	Raboisson et al. (2014)	Moderate	Low
SBV	2–10% Median morbidity rate in cattle and small ruminants	Martinelle et al. (2014)	Low	Low
SBV	53.3% increased rate of lamb mortality in first week due to disease in sheep	Saegerman et al. (2014)	High	Low
SBV	8.1% increased rate of malformations due to disease in born lambs	Saegerman et al. (2014)	Low	Low
SBV	3.5% increased rate of abortions due to disease in sheep	Saegerman et al. (2014)	Low	Low
SBV	0–53.5% postponed gestation due to disease in sheep	Saegerman et al. (2014)	High	Low
SBV	50 decreased prolificacy due to disease in sheep	Saegerman et al. (2014)	High	Low
SBV	Overall production losses due to disease in infected farm	Expert opinion	Moderate	Moderate
WNV	Up to 3% early culling due to disease in horses based on the following information ($0.1 \times 0.35 \times 0.28 = 0.01$)		Very low	Low
	10% Horse morbidity rate (infected horses that will develop clinical signs of disease)	Leblond et al. (2007)		
	35% Hospitalisation rate for neurological cases	Weese et al. (2003)		
	28% Horse case fatality rate (mortality among neurological cases; the most severe cases being hospitalised)	Murgue et al. (2001)		
WNV	Overall production losses due to disease in infected farm	Expert opinion	Very low	Moderate

The score of the overall production losses of each disease was then combined with the estimated epidemic size to obtain the impact on production in the infected farms (Figure 23).

The impact on production losses of BTV was estimated to be low in the four regions of the EU. The impact of SBV was estimated to be moderate in S-EU and W-EU, low in E-EU and very low in N-EU. For all the other VBDs, there was either no impact, or there were no data available.

Issues to be taken into account when interpreting the results

It should be noted that for CVV and for EEEV there was no published information found about direct production losses in infected farms. For those diseases where some peer-reviewed studies were available, the uncertainty around the on farm production losses was moderate, due to the pooled estimated of different production parameters. The confidence intervals around the outputs values visualised in Figure 18 can be found in Table D.1 in Appendix D.

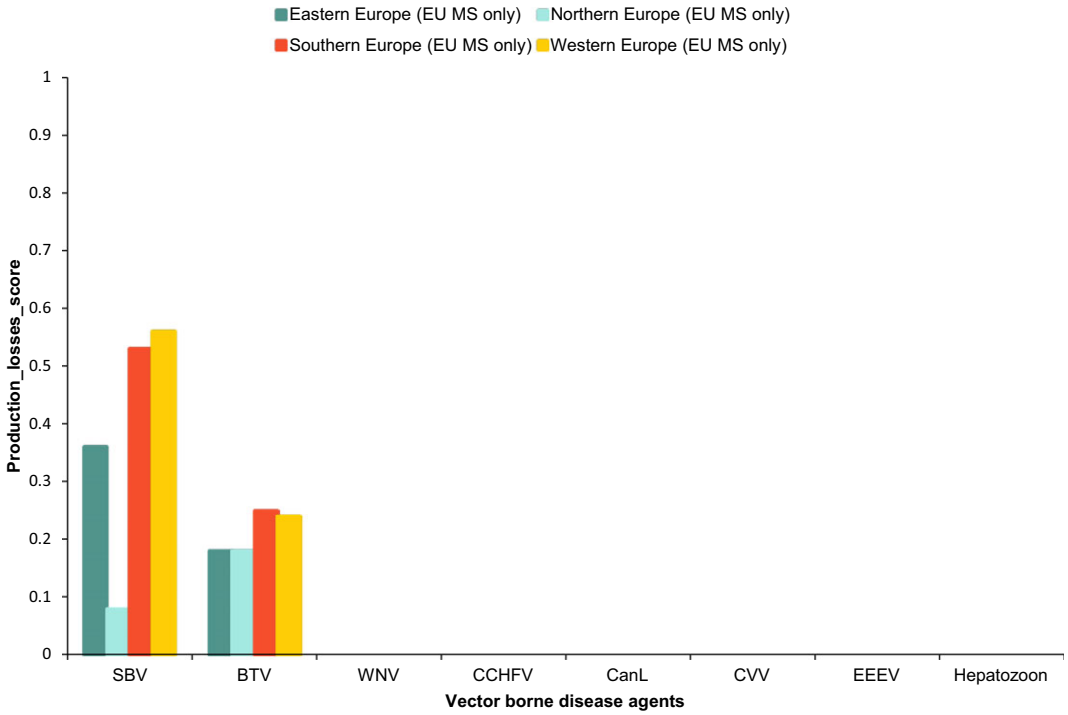


Figure 23: Possible production losses on infected farms with VBDs with an overall rate of introduction that was higher than 0.001 per year

7.2.4. Conclusions

- Possible production losses due to bluetongue outbreaks were estimated to be very low to low depending on the region in the EU. The impact of Schmallenberg outbreaks was estimated to be moderate in S-EU and W-EU, low in E-EU and very low in N-EU.
- For all the other VBD-agents, there was either no impact on production in the infected farms (CanL, Hepat, CCHF and WNV) or there was no information available on the production losses in infected farms (CVV and EEEV).

7.3. What is the impact on public health?

7.3.1. Methodology to assess the predicted impact on public health

Disability-adjusted life years (DALYs) are calculated to estimate the burden of disease by adding years of life lost (YLLs) and years lived with disability (YLDs). YLLs represent the life years lost due to death and are calculated by multiplying the number of deaths by a standardised expectation of remaining life years at the age of death due to the disease. YLDs represent the life years lost due to disability, adjusted for the severity of the disability. YLDs are computed for a given health outcome by multiplying the prevalence of that outcome by a disability weight that has a value between 0 (equivalent to full health) and 1 (equivalent to death) (Mangen et al., 2013).

DALYs calculated to estimate the burden of disease for vector-borne diseases that affect public health in other infected countries in the EU or elsewhere were used to judge on the possible burden of disease in case a VBD-agent would enter, spread and possibly persist in a currently free region in Europe. The DALY's were then compared with the classes of the EFSA-VBD_RISK model for impact on public health: Not zoonotic (0), Very low (< 3), Low (3–10), Moderate (10–30), High (30–100), Very

High (> 100). This estimate was assigned a high uncertainty due to different life expectancy, immune status and health care facilities in the EU compared to the already endemic areas.

7.3.2. Data to assess the impact on public health

A narrative literature review was carried out to find published information of possible outcomes of DALY estimates (on 100,000 inhabitants) for those diseases that had an overall rate of introduction that was higher than 0.001 per year and to provide an short description of the symptoms in humans.

7.3.3. Assessment of the impact on public health

Fifteen of 36 VBD could potentially affect humans (see Section 3 for the characterisation of the diseases, including a brief section of the public health impact). For only five of those, the EFSA VBD risk assessment model predicted an overall rate of introduction of more than 0.001 per year. Those were WNV, CCHFV, CanL, CCV and EEEV. Up to date, only for cutaneous leishmaniosis scientific literature could be found estimating the global burden of cutaneous leishmaniosis in DALYs, being 0.58 (0.26–1.12) per 100,000 people (Karimkhani et al., 2016), or very low when using the EFSA-VBD_RISK model classes. For the other four zoonoses, the global public health impact is currently unknown.

Issues to be taken into account when interpreting the results

Although several studies are available on the clinical impact and the occurrence of these diseases, there is currently no global assessment available combining the quantitative data on the incidence of the diseases and the morbidity and mortality rates (with the exception of CanL). It should be stressed, however, that the absence of studies calculating the burden of a disease does not mean that there is no impact of the disease, but it has not been quantified so far. Therefore, the provision of a meaningful model output on public health impact was at this stage not yet possible for these diseases.

7.3.4. Conclusions

The impact of the introduction of *L. infantum* in previously free areas on public health was estimated to be very low. For the other diseases (Crimean-Congo haemorrhagic fever virus, West Nile virus, Bunyamwera virus and Eastern equine encephalitis virus), there were either not sufficient data available to make any conclusion on the public health impact of new introductions of these diseases in previously free areas.

7.4. Impact on the environment

7.4.1. Methodology to assess the predicted impact on the environment through the use of chemical biocides

All biocidal products require an authorisation before they can be placed on the market, and the active substances contained in that biocidal product must be previously approved by the ECHA. A summary was provided on the biocidal products approved by ECHA but an environmental impact assessment of their use was not considered within the scope of this mandate.

7.4.2. Data to assess the environmental impact

Information was extracted from ECHA's website on approved active substances which may be used for controlling the relevant vector species such as information on the target species, intended uses (e.g. indoor/outdoor, professional/non-professional use), application/dose rate (i.e. efficacy), hazard class category and risk characterisation ratios (RCRs) (see Appendix D for more details).

7.4.3. Assessment of the impact on the environment through the use of chemical biocides

The information collected as described in Section 7.4.2 and summarised in Appendix D defines the specific intended uses and doses to be applied for the specified target species of the approved biocidal products and the Hazard Statements and Risk Characterisation Ratios. Most of the products indicate no risk for the environment, particularly those that intended for indoor use. The most frequent risk is that of impact on aquatic organism if some of the products are not properly used and result in contact with aquatic environments (i.e. Lambda-cyhalothrin and deltamethrin). Other products, such as insect

growth regulators insecticides may also impact environment if contact with water bodies is not avoided (i.e. diflubenzuron and pyriproxyfen). Some products massively used for controlling mosquitoes, such as *Bacillus thuringiensis* (Bti) (200 tonnes annually worldwide, Becker, 1998) have shown no significant negative impact on the environment (Lagadic et al., 2014, 2016). Some indirect effects have been observed in trophic chains, such as those between Diptera (i.e. Chironomida and Culicidae) and Odonata (Jakob and Poulin, 2016). However, apart from the extensive literature on Bti, there is no published data about the impact on the environment of general procedures conducted in regular basis for vector control, particularly for chemical products (i.e. chemical treatments in stable, animals and environment). However, since some of the products are also used in agricultural pest control programs (i.e. deltamethrine), we could expect to have similar effects when those chemicals are applied in a general way to the environment. Any potential impact on the environment of the use of biocidal products beyond the intended uses, doses and target species as evaluated by ECHA is unknown.

7.4.4. Conclusions

- The Hazard Statements and Risk Characterisation Ratios of approved biocidal products indicate the possible impact on the environment and non- targeted organism (i.e. soil biota, aquatic organism, etc.) of the active ingredients according to its chemical composition, targeted species and way of application.
- Any potential impact on the environment of the use of biocidal products beyond the intended uses, doses and target species as evaluated by ECHA is unknown.

8. Overall conclusions

Table 9: Qualitative model outputs for the steps pre-introduction

EU region	Worldwide occurrence	Rate of entry	Level of transmission	Probability of establishment	Overall rate of introduction	Annual extent of spread	Probability of overwintering	Impact on animal health and welfare	Impact on farm production
AHFV E-EU	H/VH	L	M	VL/L	VL				
AHFV N-EU	H/VH	L	M	VL/L	VL				
AHFV S-EU	H/VH	L	M	VL/L	VL				
AHFV W-EU	H/VH	L	VL	VL/L	VL				
AHSV E-EU	VL	VL	M	VL/L	VL				
AHSV N-EU	VL	VL	M	VL/L	VL				
AHSV S-EU	VL	VL	M	VL/L	VL				
AHSV W-EU	VL	VL	M	VL/L	VL				
AINOV E-EU	H/VH	VL	M	VL	VL				
AINOV N-EU	H/VH	VL	M	VL	VL				
AINOV S-EU	H/VH	VL	M	M/H	VL				
AINOV	H/VH	VL	M	H/VH	VL				
AKAV E-EU	M/H	VL	M	H/VH	VL				
AKAV N-EU	M/H	VL	M	H/VH	VL				
AKAV S-EU	M/H	VL	M	H/VH	VL				
AKAV	M/H	VL	M	H/VH	VL				
ASFV E-EU	VL	H	M	VL/L	VL				
ASFV N-EU	VL	L	M	VL/L	VL				
ASFV S-EU	VL	H	M	VL/L	VL				
ASFV	VL	M	M	VL/L	VL				
BEFV E-EU	H/VH	VL	M	VL	VL				
BEFV N-EU	H/VH	VL	M	VL	VL				
BEFV S-EU	H/VH	VL	M	VL	VL				
BEFV	H/VH	VL	M	VL	VL				
BHAV E-EU	H/VH	VH	VL/L	M/H	VL				
BHAV N-EU	H/VH	VH	M	VL	VL				
BHAV S-EU	H/VH	VH	VL/L	M/H	VL				
BHAV	H/VH	VH	M	VL	VL				
BTV E-EU	M	VH	H	H/VH	VH	M/H	M	VL/L	VL/L
BTV N-EU	M	VH	H	H/VH	H/VH	M/H	M	VL/L	VL/L
BTV S-EU	M	VH	H	H/VH	VH	H	M	VL/L	L
BTV	M	VH	H	H/VH	H/VH	H	M	VL/L	VL/L
CanL E-EU	VH	VH	M	VL	VL	VL	H	VL	VL
CanL N-EU	VH	VH	VL	VL	VL	VL	M	VL	VL
CanL S-EU	VH	VH	M	M/H	L/M	VL/L	H	VL	VL
CanL	VH	VH	M	VL/L	VL	VL	H	VL	VL
CCHFV E-EU	M/H	VH	M	H/VH	VL/L	VL	VH	VL	VL
CCHFV N-EU	M/H	M	M	H/VH	L	VL	VH	VL	VL
CCHFV S-EU	M/H	VH	M	H/VH	H/VH	VL	VH	VL	VL
CCHFV	M/H	VH	M	H/VH	H	VL	VH	VL	VL

Cowdr E-EU	M	L	VL	H/VH	VL				
Cowdr N-EU	M	L	M	VL/L	VL				
Cowdr S-EU	M	L	M	VL/L	VL				
Cowdr	M	L	VL	VL/L	VL				
CVV E-EU	H/VH	VL	L	VL	VL/L	VL	M	VL	VL
CVV N-EU	H/VH	M	L	VL	VL/L	VL	M	VL	VL
CVV S-EU	H/VH	VL/L	L	M/H	VL/L	VL	H	VL	VL
CVV	H/VH	H/VH	L	VL	VL/L	VL	M	VL	VL
EEEV E-EU	L/M	H/VH	L	H/VH	L	VL	VL/L	VL	VL
EEEV N-EU	L/M	H/VH	L	H/VH	VL/L	VL	VL/L	VL	VL
EEEV S-EU	L/M	H/VH	L	H/VH	VL/L	VL	M	VL	VL
EEEV	L/M	M	L	H/VH	L	VL	VL/L	VL	VL
EEV E-EU	H/VH	M/H	H	VL	VL				
EEV N-EU	H/VH	H/VH	H	VL	VL				
EEV S-EU	H/VH	M/H	H	VL	VL				
EEV	H/VH	H/VH	H	VL	VL				
EHD E-EU	L	VL	H	H/VH	VL				
EHD N-EU	L	VL	H	H/VH	VL				
EHD S-EU	L	VL	H	H/VH	VL				
EHD	L	VL	H	H/VH	VL				
GETV E-EU	M/H	VL	VL	M/H	VL				
GETV N-EU	M/H	VL	VL	M/H	VL				
GETV S-EU	M/H	VL	VL	M/H	VL				
GETV	M/H	VL	VL	H/VH	VL				
Hepat E-EU	H/VH	VH	M	VL/L	VL	VL	H	VL	VL
Hepat N-EU	H/VH	VH	M	VL/L	L/M	VL/L	H	VL	VL
Hepat_S-EU	H/VH	VH	M	VL/L	L	VL/L	H	VL	VL
Hepat W-EU	H/VH	VH	M	VL/L	L/M	VL	H	VL	VL
HJV E-EU	H/VH	M	VL	VL/L	v				
HJV N-EU	H/VH	L	VL	VL/L	VL				
HJV S-EU	H/VH	VL	VL	VL/L	VL				
HJV	H/VH	H	VL	VL/L	VL				
JEV E-EU	VL/L	VL	M	M/H	VL				
JEV N-EU	VL/L	VL	M	M/H	VL				
JEV S-EU	VL/L	VL	M	M/H	VL				
JEV	VL/L	VL	M	H/VH	VL				
KASV E-EU	H/VH	M/H	H	VL/L	VL				
KASV N-EU	H/VH	M/H	H	VL/L	VL				
KASV S-EU	H/VH	M/H	H	VL/L	VL				
KASV	H/VH	M/H	H	VL/L	VL				
KOTV E-EU	H/VH	VL	M	VL/L	VL				
KOTV N-EU	H/VH	VL	M	VL/L	VL				
KOTV S-EU	H/VH	VL	M	VL/L	VL				
KOTV	H/VH	VL	M	VL/L	VL				

MDV E-EU	M/H	VL	M	VL/L	VL				
MDV N-EU	M/H	VL	M	VL/L	VL				
MDV S-EU	M/H	VL	M	VL/L	VL				
MDV	M/H	L	M	VL/L	VL				
MIDV E-EU	H/VH	VL	VL	VL/L	VL				
MIDV N-EU	H/VH	VL	VL	VL/L	VL				
MIDV S-EU	H/VH	VL	VL	VL/L	VL				
MIDV	H/VH	VL	VL	VL/L	VL				
NSD E-EU	M/H	VL	VL	VL/L	VL				
NSD N-EU	M/H	VL	VL	VL/L	VL				
NSD S-EU	M/H	VL	M	VL/L	VL				
NSD	M/H	VL	VL	VL/L	VL				
PHSV E-EU	H/VH	L	M	VL/L	VL				
PHSV N-EU	H/VH	M	M	VL/L	VL				
PHSV S-EU	H/VH	L	M	VL/L	VL				
PHSV	H/VH	M	M	VL/L	VL				
VL	VL	VL	VL	VL	VL				
RFV N-EU	VL	VL	M	H/VH	VL				
RFV S-EU	VL	VL	M	H/VH	VL				
RFV	VL	VL	M	H/VH	VL				
SBV E-EU	H/VH	VH	M	H/VH	L/M	H/VH	M	VL	L/M
SBV N-EU	H/VH	VH	M	H/VH	L/M	L/M	M	VL	VL
SBV S-EU	H/VH	VH	M	H/VH	M/H	H	M	L	M
SBV	H/VH	VH	M	H/VH	M/H	VH	M	L	M/H
SHU E-EU	H/VH	VL	VL/L	VL	VL/L				
SHU N-EU	H/VH	VL	VL	VL	VL				
SHU S-EU	H/VH	VL	VL/L	VL	VL/L				
SHU	H/VH	VL	VL/L	VL	VL/L				
SLEV E-EU	M/H	M	M	VL/L	VL				
SLEV N-EU	M/H	M	M	VL/L	VL				
SLEV S-EU	M/H	M	M	VL/L	VL				
SLEV	M/H	H	M	VL/L	VL				
THOV E-EU	H/VH	VH	M	VL/L	VL				
THOV N-EU	H/VH	VH	M	VL/L	VL				
THOV S-EU	H/VH	VH	M	VL/L	VL/L				
THOV	H/VH	VH	VL	VL/L	VL				
VEE E-EU	L/M	L/M	VL/L	VL	VL/L				
VEE N-EU	L/M	H	VL	VL	VL				
VEE S-EU	L/M	L/M	VL/L	VL	VL/L				
VEE	L/M	VH	VL/L	VL	VL/L				
VSV E-EU	H	M	M	VL/L	VL				
VSV N-EU	H	H	M	VL/L	VL				
VSV S-EU	H	M	M	VL/L	VL				
VSV	H	H	M	VL/L	VL				
WEEV E-EU	M/H	L	VL/L	H/VH	VL/L				
WEEV N-EU	M/H	VL	VL/L	H/VH	VL/L				
WEEV S-EU	M/H	VL	VL/L	H/VH	VL/L				
WEEV	M/H	M	VL/L	H/VH	VL/L				

WNV E-EU	VL/L	VH	M	H/VH	M	M/H	VH	VL	VL
WNV N-EU	VL/L	VH	M	H/VH	M	L/M	VH	VL	VL
WNV S-EU	VL/L	VH	M	VH	M/H	VH	VH	VL/L	VL/L
WNV	VL/L	VH	M	VH	M	M	VH	VL	VL
WSLV E-EU	H/VH	VL	VL	VL/L	VL				
WSLV N-EU	H/VH	VL	VL	VL/L	VL				
WSLV S-EU	H/VH	VL	VL	VL/L	VL				
WSLV	H/VH	VL	VL	VL/L	VL				
YUOV E-EU	H/VH	L	M	VL	VL				
YUOV N-EU	H/VH	M	VL	VL	VL				
YUOV S-EU	H/VH	L	M	VL/L	VL				
YUOV	H/VH	M	VL	VL	VL				

- According to the model, there is a moderate/high to very high rate of entry (1 entry per 10 years to 1 entry per year) of CanL, Hepat, BTV, BHAV, WNV, SBV, THOV, CCHFV, EEV and KASV in all four EU regions through movement of livestock or pets from infected regions in or outside the EU.
- The expected level of vector transmission of epizootic haemorrhagic disease virus, Palyam virus, bluetongue virus and equine encephalosis virus was estimated to be high in the four regions of the EU, with R0 values between 3 and 10.
- The level of vector transmission was estimated to be low to very low for Bunyamwera virus, Eastern equine encephalitis virus, Shuni virus, Venezuelan equine encephalitis virus, Western equine encephalitis virus, Getah virus, Highlands J. virus and Middelburg virus everywhere in the EU with R_0 values smaller than 0.3.
- For all the other VBD-agents, the level of transmission was expected to be moderate everywhere in the EU (R_0 between 1 and 3), except in W-EU where the level of transmission of Alkhurma haemorrhagic fever virus, Ehrlichia ruminantium, Nairobi sheep disease virus, Thogoto virus and YUOV was estimated to be very low; in E-EU (very low level of Bhanja virus, *E. ruminantium*, Nairobi sheep disease virus); in S-EU (very low level of transmission of Alkhurma haemorrhagic fever virus); and in N-EU very low level of transmission of *Leishmania infantum, Nairobi sheep disease virus and Yunnan orbivirus).*
- The model estimated the probability of establishment of Akabane virus, bluetongue virus, Crimean-Congo haemorrhagic fever virus, Eastern equine encephalitis virus, epizootic haemorrhagic disease virus, Schmallenberg virus, West Nile virus, Getah virus and Japanese encephalitis virus to be high to very high (with a probability of 0.1–1 per introduction), depending on the region of the EU.
- For most of the other diseases, the probability of establishment is estimated to be low to very low.
- In general, there is a much higher probability of establishment after introduction by animals which are imported for breeding, compared to animals which are imported for direct slaughter upon arrival.
- The model estimated that Crimean-Congo haemorrhagic fever virus, bluetongue virus, West Nile virus, Schmallenberg virus, *H. canis*, *L. infantum*, Bunyamwera virus and Highlands J. virus have more than 0.001 overall introductions per year (or a score > 0.2). The rate of introduction of all the other VBD-agents is lower.
- The model estimated that the annual extent of spread after introduction of bluetongue virus, West Nile virus and Schmallenberg virus in a previously free area would be moderate to very high, depending on the region.
- The model estimated that the annual extent of spread after introduction of *H. canis*, Crimean-Congo haemorrhagic fever virus, *L. infantum*, Bunyamwera virus and Eastern equine encephalitis virus in a previously free area would be very low.
- The model estimated the probability of overwintering of Crimean-Congo haemorrhagic fever virus and West Nile virus to be very high in the four regions of the EU.
- The model estimated the probability of overwintering of *H. canis* and *L. infantum* to be high in the four regions of the EU.

- The model estimated the probability of overwintering of Schmallenberg virus, Bunyamwera virus and bluetongue virus to be moderate in the four regions of the EU.
- For EEEV, only in S-EU, the model estimated the probability of overwintering to be moderate.
- When combining the size of the epidemic with the severity of the infections, Schmallenberg virus and bluetongue virus introductions were estimated by the model to cause a low impact on animal health and welfare in S-EU and W-EU, and West Nile virus in S-EU.
- For *H. canis, L. infantum*, Eastern equine encephalitis virus, Crimean-Congo haemorrhagic fever virus, Bunyamwera virus and West Nile virus, the model estimated the impact on animal health and welfare to be very low everywhere in the EU.
- Possible production losses due to bluetongue outbreaks were estimated to be very low to low depending on the region in the EU. The impact of Schmallenberg outbreaks was estimated to be moderate in S-EU and W-EU, low in E-EU and very low in N-EU.
- For all the other VBD-agents, there was either no impact on production in the infected farms (CanL, Hepat, CCHF and WNF) or there was no information available on the production losses in infected farms (CVV and EEEV).
- The impact of the introduction of *L. infantum* in previously free areas on public health was estimated to be very low. For the other diseases (Crimean-Congo haemorrhagic fever virus, West Nile virus, Bunyamwera virus and Eastern equine encephalitis virus), there were either not sufficient data available to make any conclusion on the public health impact of new introductions of these diseases in previously free areas.
- Any potential impact on the environment of the use of biocidal products beyond the intended uses, doses and target species as evaluated by ECHA is unknown.

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Abbreviations

AHAW	EFSA Panel on Animal Health and Welfare
DALY	Disability-adjusted life year
E-EU	eastern European Union
ECHA	European Chemicals Agency
EIP	extrinsic incubation period in the vector
FEVER	Framework developed to guide the risk assessment of possible Emerging VEctor-borne disease Risks
GAUL	Global Administrative Unit Layers
IIP	intrinsic incubation period in the host
MINTRISK	Method to INTegrate all relevant RISK aspects
N-EU	northern European Union
NUTS	Nomenclature of territorial units for statistics
OIE	World Organisation for Animal Health
PEC	Predicted Environmental Concentration
PNEC	Predicted No Effect Concentration
R_0	reproduction number
RCR	risk characterisation ratio
S-EU	southern European Union
TOR	Term of Reference
VBD	vector-borne disease
W-EU	western European Union
YLD	years lived with disability
YLL	years of life lost
YUOV	Yunnan orbivirus

Appendix A – Pathways

Table A.1: Species considered for the pathways in the model

Disease agent	Pathways: Species considered in the model*
AHFV	Camel, sheep and goat
AHSV	Equine
AINOV	Cattle, sheep and goat
AKAV	Cattle, sheep, goat and swine
ASFV	Swine
BEFV	Cattle
BHAV	Cattle, sheep, goat
BTV	Cattle, sheep, goat
CanL	Dogs
CCHFV	Cattle, sheep, goat and camel
Cowdr	Cattle, sheep and goat
CVV	Cattle, sheep, goat and equine
EEEV	Birds (domestic turkeys, Live birds (excluding birds of prey, Psittaciformes, parrots, parakeets, macaws, cockatoos, ostriches, emus and pigeons))
EEV	Equine
EHD	Cattle, sheep and goat
GETV	Equine and swine
Hepat	Dogs
HJV	Birds (domestic turkeys, live birds (excluding birds of prey, Psittaciformes, parrots, parakeets, macaws, cockatoos, ostriches, emus and pigeons))
JEV	Swine
KASV	Cattle, sheep and goat
KOTV	Cattle
MDV	Equine
MIDV	Equine, sheep and goats
NSDV	Sheep and goat
PHSV	Equine
RVF	Cattle, sheep, goat and camel
SBV	Cattle, sheep and goat
SHUV	Cattle, sheep, goat and equine
SLEV	Birds (*Gallus domesticus*, domestic turkeys, domestic ducks, pigeons, live birds (excluding birds of prey, Psittaciformes, parrots, parakeets, macaws, cockatoos, ostriches, emus and pigeons))
THOV	Cattle, sheep, goat and camel
VEE	Equine, swine, dogs
VSV	Cattle, sheep, goat, swine, equine and camel
WEEV	Birds (domestic turkeys, domestic ducks, pigeons, live birds (excluding birds of prey, Psittaciformes, parrots, parakeets, macaws, cockatoos, ostriches, emus and pigeons))
WNV	Birds (pigeons, live birds of prey, live domestic guinea fowls, live domestic, live ostriches and emus, live birds (excluding birds of prey, Psittaciformes, parrots, parakeets, macaws, cockatoos, ostriches, emus and pigeons))
WSLV	Cattle, sheep, goat, equine and camel
YUOV	Equine, sheep and goat

*: Dead end hosts were not considered in the pathways.

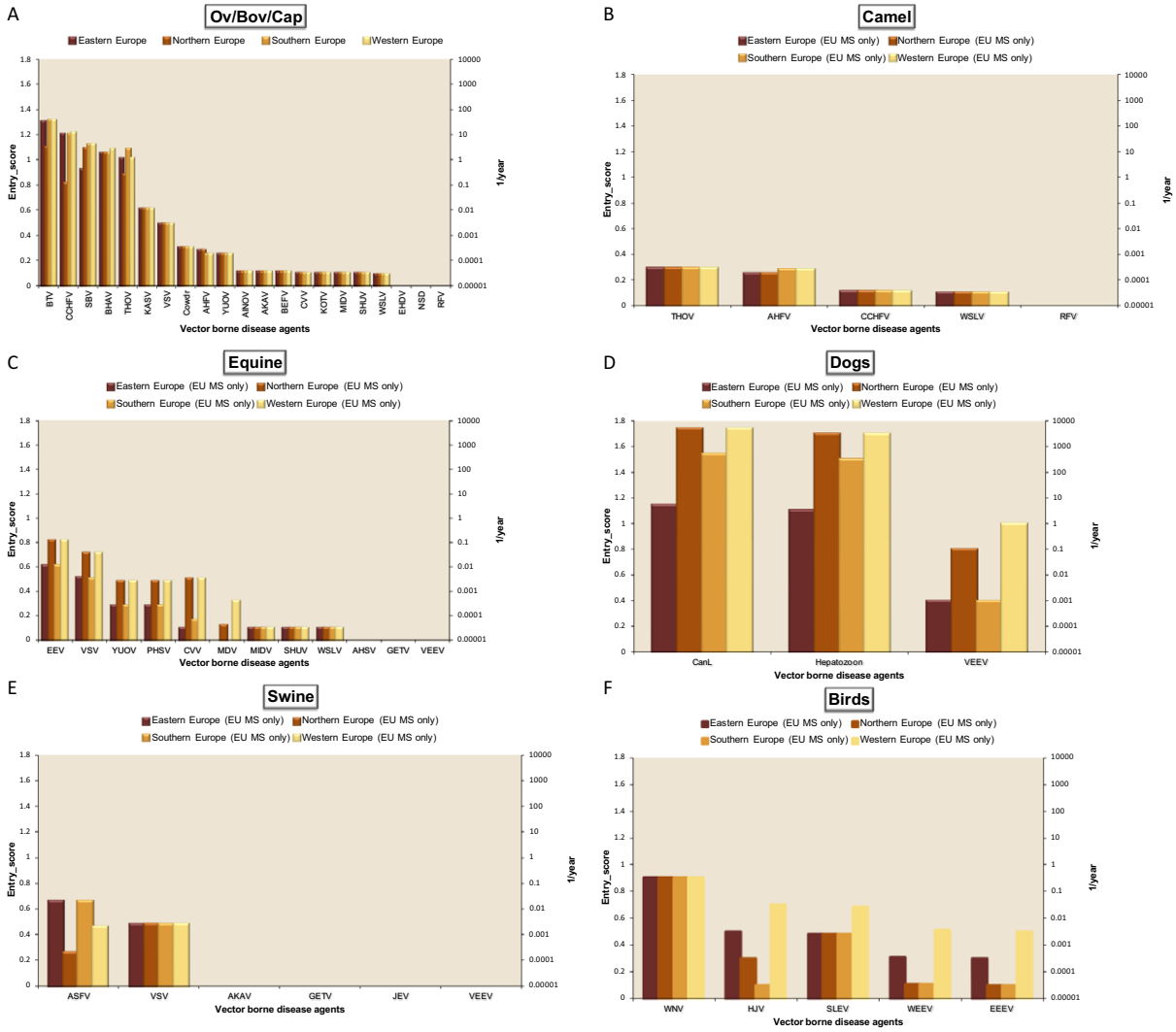

Figure A.1: Rate of entry for the different diseases displayed per species groups

Table A.2: Medians values of parameters observed during experimental infections with VBDs in animals

VBD	Median duration latent period	Median duration of infectious period	Median duration of incubation period	Median duration of clinical signs
AHS	4	10	6.5	9.5
AKAV	2	6	7	7
ASFV	3	12	3	11
BEFV	2	5	3.5	8
BTV	5	27	4	12.5
CanL	7	> 365	120	290
CCHFV	5	12	3	8
Cowdr	13.5	15.25	12	15
CVV	2	2	na	na
EHDV	3	20.5	1	7
EEEV	1	5	na	na
GETV	1	3	1.5	4.5
Hepat	28	43	na	na
HJV	1	2.5	na	na

VBD	Median duration latent period	Median duration of infectious period	Median duration of incubation period	Median duration of clinical signs
JEV	2	4	5	8
RVFV	1	2	2	5
SBV	na	na	4.5	22
SLEV	na	29	na	na
VEE	1	4	1	8
VSV	1	162	2	13
WEEV	2.5	2.5	na	na
WNV	1.5	10	na	1
WSLV	1.5	4	2	5

Source: Dórea et al. (2017).

Appendix B – Data used to estimate the range of the Reproduction Ratio

Table B.1: Reproduction Ratios extracted from literature review (Braks et al., 2017b)

Pathogen	Reproduction number*	Country	Year**	Bibliography
African swine fever	1.58	Russian Federation	2015	Iglesias et al. (2016)
African swine fever	1.07***	Ukraine	NR	Korrenoy et al. (2016)
African horse sickness virus	2.6	United Kingdom	2006	Lo et al. (2013)
Bluetongue virus – serotype 8	2.3	Netherlands	2007	Santman Berends et al. (2013)
Bluetongue virus – serotype 8	6.0	United Kingdom	NR	Gubbins et al. (2012)
Bluetongue virus	4	United Kingdom	NR	Gubbins et al. (2008)
Bluetongue virus	3.4	Austria	2009	Brugger et al. (2016)
Bluetongue virus	4.6	Austria	2009	Brugger and Rubel (2013)
Bluetongue virus – serotype 8	4.0	Belgium	2006	de Koeijer et al. (2011)
Bluetongue virus – serotype 8	4.0	Germany	2006	de Koeijer et al. (2011)
Bluetongue virus – serotype 8	4.0	Netherlands	2006	de Koeijer et al. (2011)
Bluetongue virus – serotype	4.6	Spain	2007	Napp et al. (2016)
Bluetongue virus – serotype 8	22.0	Switzerland	2006	Racloz et al. (2008)
Bluetongue virus	3.1	South Africa	NR	Turner et al. (2013)
Crimean-Congo haemorrhagic fever virus	1.2	Turkey	2013	Hoch et al. (2016)
Japanese encephalitis virus	1.2	Bangladesh	2009	Khan et al. (2014)
Leishmania infantum	1.1	Spain	1992	Amela et al. (1995)
Rift Valley fever virus	2.4	Egypt	NR	Gao et al. (2013)
Rift Valley fever virus	2.3	Unknown	NR	Chitnis et al. (2013)
Rift Valley fever virus	3.7	South Africa	2010	Xue et al. (2012)
Rift Valley fever virus	3.4	Unknown	NR	Mpeshe et al. (2011)
Rift Valley fever virus	6.8	United Republic of Tanzania	2006	Mpeshe et al. (2014)
West Nile virus	7.0	Unknown	NR	Cruz-Pacheco et al. (2005)
West Nile virus	15.3	United States	2004	Kilpatrick et al. (2006)
West Nile virus	89.4	Unknown	NR	Foppa and Spielman (2007)
West Nile virus	1.6	United States	2003	Hartley et al. (2012)
West Nile virus	3.0	United States	2006	Pawelek et al. (2014)

*: For studies using outbreak data, the R_0, calculated for the peak of the vector season were extracted. For those studies that estimated the R_0 based on estimated transmission parameters, the R_0 that was calculated for the most ideal conditions for transmission were extracted.
**: Start of the study.
***: Between-farm R_0.

Table B.2: Calculations of the proxy for the External Incubation Period derived from the literature per disease/pathogen (a) and per vector group (b)

Disease	Number of records	EIP*		
		Max	Min	Mean
African horse sickness virus	9	10	10	10.0
African swine fever virus	3	7	7	7.0
Bluetongue virus	44	12	7	9.9
Cache Valley virus	2	12	12	12.0
Epizootic haemorrhagic disease virus	22	14	10	10.3
Equine encephalosis virus	21	10	10	10.0
Getah virus	2	21	21	21.0
Highlands J virus	3	11	4	6.3
Japanese encephalitis virus	14	18	12	14.0
Leishmania infantum	3	7	5	5.7
Rift Valley fever virus	26	20	5	12.9
Schmallenberg virus	7	14	8	10.3
St. Louis encephalitis virus	10	14	12	13.6
Venezuelan equine encephalitis virus	17	25	10	13.7
Vesicular stomatitis virus	1	7	7	7.0
West Nile virus	120	65	2	15.1
Western equine encephalitis virus	8	14	4	12.3
Total	312			
Vector group	**Number of records**	**EIP**		
		Max	**Min**	**Mean**
Biting midges	105	14	7	10.0
Mosquitoes	199	60	4	14.0
Sand flies	2	5	5	5.0
Ticks	6	65	2	22.2
Total	312			

*: In case the range of the EIP instead of a point value was extracted from the papers, the mean value was considered for computing.
Source: Braks et al., 2017b.

Table B.3: Vector Competence

Pathogen	Average vector competence (%)	References
African horse sickness virus	25	Venter et al. (2000), Venter and Paweska (2007)
African swine fever	100	de Carvalho Ferreira et al. (2014)
Bluetongue virus	22	Baylis et al. (2008), Venter et al. (1998, 2005, 2006), Paweska et al. (2002), Veronesi et al. (2008)
Cache valley virus	60	Reeves and Miller (2013)
Epizootic haemorrhagic disease virus	13	Paweska et al. (2005), Reeves et al. (2009), Ruder et al. (2012)
Equine encephalosis virus	12	Paweska and Venter (2004), Venter et al. (1999, 2002)
Getah virus	80	Takashima et al. (1983)
Highlands J virus	82	Borland et al. (2016)
Japanese encephalitis virus	45	van den Hurk et al. (2003), Kramer et al. (2011), Huber et al. (2014), Samuel et al. (2010), Johnson et al. (2009)
Leishmania infantum	60	Guimaraes et al. (2016), Seblova et al. (2012)

Pathogen	Average vector competence (%)	References
Rift Valley fever virus	17	Jupp et al. (2002), Kading et al. (2014), Moutailler et al. (2007), Turell et al. (2007, 2008, 2010), Ndiaye et al. (2016)
Schmallenberg virus	13	Veronesi et al. (2013), Manley et al. (2015)
St. Louis encephalitis virus	25	Reisen et al. (2005), Richards et al. (2007, 2009, 2012a,b)
Venezuelan equine encephalitis virus	40	Deardorff and Weaver (2010), Moncayo et al. (2008), Smith et al. (2005), Turell et al. (2006)
Vesicular stomatitis virus	36	Drolet et al. (2005)
West Nile virus	62	Alto et al. (2014a,b), Anderson et al. (2010, 2012), Balenghien et al. (2007, 2008), Bolling et al. (2012), Brustolin et al. (2016), Ciota et al. (2013), Dodson et al. (2011, 2012), Eastwood et al. (2011), Erickson et al. (2006), Fall et al. (2014), Fortuna et al. (2015a,b), Fros et al. (2015), Goddard et al. (2002), Huber et al. (2014), Hutcheson et al. (2005), Jansen et al. (2008), Jiang et al. (2010), Kilpatrick et al. (2008, 2010), Kramer et al. (2011), Lapointe et al. (2009), Lawrie et al. (2004), Lutomiah et al. (2011), Micieli et al. (2013), Moudy et al. (2007), Reisen et al. (2006a,b, 2008a,b), Richards et al. (2007a, 2010, 2011, 2012a,b, 2014), Sardelis et al. (2001), Sudeep et al. (2014), Turell et al. (2002, 2005), Vaidyanathan and Scott (2007), Vaidyanathan et al. (2008)
Western equine encephalitis virus	50	Mahmood et al. (2006), Reisen et al. (2008a,b), Wang et al. (2010, 2012)

Table B.4: Expert opinion on parameters needed to calculate the Reproduction Ratio

Parameters	Biting midges	Sand flies	Hard ticks	Mosquitoes
Expected number of vector bites per host (the attack rate was used as proxy)	20	5	20	5
Expected number of bites	10	10	3	10
Expected lifespan	14	21	100	21
Biting rate = Expected number of bites/expected lifespan	0.71	0.48	0.03	0.48

Appendix C – Clinical signs in experimentally infected animals with VBDs and calculations of severity score

Table C.1: Clinical signs in experimentally infected animals with VBDs and calculations of severity score (based on Dórea et al., 2017)

VBD	AHS	ASF	AKA	BHA	BT	BEF	CV	CCHF	EEE	Cowdr	EHD	GET	Hepat	JEF	Canl	MD	RV	SB	SLE	VEE	VS	WSL	WN	WEE
Number of independent groups	22	102	11	1	250	6	6	3	5	48	36	13	4	10	59	1	28	16	3	43	56	11	14	2
No of clinical signs reported	4	11	1	0	50	0	3	1	1	8	1	2	3	2	1	0	2	2	0	9	3	0	0	2
Dead	16	48	0	0	48	1	0	0	3	31	12	5	0	0	13	1	9	0	0	19	1	2	1	0
Severe Signs	**Number of groups with at least one animals that shows severe signs**																							
Recumbent	1	3	0	0	3	0	0	0	0	5	4	0	1	0	0	0	0	0	1	0	0	1	0	0
Haemorrhages external	0	0	0	0	7	0	0	0	0	0	6	0	0	0	0	0	1	0	0	0	0	0	0	0
Haemorrhages internal	1	7	0	0	6	0	0	0	0	0	7	0	0	0	0	0	1	0	0	0	0	0	0	0
Tremors	0	0	0	0	0	0	0	0	0	2	0	0	0	5	0	0	0	0	0	0	0	0	1	0
Encephalopathy	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	9	0	0	0	0
Abortion	0	2	4	0	10	0	0	0	0	0	0	0	0	1	0	0	6	0	0	0	0	1	0	0
Hepatitis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0
Opisthotonus	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Depression	6	19	0	0	27	0	0	0	2	6	5	1	0	2	0	0	7	0	0	9	4	2	1	0
Locomotion problems	0	4	0	0	35	2	0	0	0	4	1	0	0	0	0	0	1	0	0	1	5	0	0	0
Respiratory distress	7	14	0	0	32	0	0	0	0	4	2	0	0	0	0	0	4	0	0	0	0	1	0	0
Cyanosis blue tongue	1	2	0	0	8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Behavioural changes	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0
Moderate/severe signs	**Number of groups with at least one animals that shows moderate/severe signs**																							
Dermatitis	0	3	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
Colic	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Neurological signs	0	0	0	0	0	0	0	0	3	5	0	0	0	2	0	0	1	0	0	7	0	0	2	0
Dysentery	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Chronic kidney disease	0	0	0	0	2	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
Vertigo Balance disorder	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

VBD	AHS	ASF	AKA	BHA	BT	BEF	CV	CCHF	EEE	Cowdr	EHD	GET	Hepat	JEF	Canl	MD	RV	SB	SLE	VEE	VS	WSL	WN	WEE
Abscess fistula	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0
Ulcer_vesiculae	0	0	0	0	23	0	0	0	0	0	0	2	0	0	1	0	0	0	0	0	33	0	0	0
Moderate	**Number of groups with at least one animals that shows moderate signs**																							
Fever	15	75	0	1	135	4	0	2	4	37	11	10	1	5	2	0	23	2	1	24	9	10	5	0
Diarrhoea	0	10	0	0	6	0	0	0	1	0	2	1	0	0	1	0	2	2	1	3	1	2	0	0
Coughing	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Muscle atrophy	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
Epithelial sloughing of tongue	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
Splenomegaly	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5	0	0	0	0	0	0	0	0	0
Joint swelling; arthritis	0	5	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0
Lymphadenopathy	0	0	0	0	1	0	0	0	0	0	0	0	0	0	20	0	0	0	0	0	0	0	0	0
Congestion_skin	0	4	0	0	50	0	0	0	0	0	2	2	0	0	18	0	2	0	0	0	2	0	0	0
Oedema	8	0	0	0	49	0	0	0	0	0	3	4	0	0	0	0	0	0	0	0	2	1	0	0
Anorexia	1	22	0	0	22	2	0	0	1	6	7	4	0	3	13	0	7	0	1	9	0	2	0	0
Erythema	0	2	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Rhinitis	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Hyperesthesia	0	0	0	0	0	0	0	0	0	2	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Mild	**Number of groups with at least one animals that shows mild signs**																							
Pale mucosa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
Red mucosa	1	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Shivering	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
Onychogryphosis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
Foaming mouth	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Lachrymation	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Regurgitation	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Anaemia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
Nasal discharge	4	2	0	0	37	2	0	0	0	0	1	3	0	0	0	0	1	1	0	1	0	1	0	0
Salivation	0	0	0	0	14	1	0	0	0	0	6	0	0	0	0	0	0	0	1	0	7	0	0	0
Conjunctivitis	3	3	0	0	25	1	0	0	0	0	5	0	0	0	6	0	1	0	0	0	0	1	0	0
Fur changes	0	0	0	0	2	0	0	0	0	0	7	0	0	0	3	0	0	0	0	0	0	2	0	0

VBD	AHS	ASF	AKA	BHA	BT	BEF	CV	CCHF	EEE	Cowdr	EHD	GET	Hepat	JEF	Canl	MD	RV	SB	SLE	VEE	VS	WSL	WN	WEE
No of clinical signs	**Number of groups with only animals that show no clinical signs**																							
No of clinical signs	**6**	**5**	**9**	**0**	**61**	**1**	**3**	**0**	**0**	**3**	**18**	**0**	**0**	**1**	**7**	**0**	**3**	**12**	**2**	**3**	**8**	**0**	**6**	**0**
	Total groups per severity class = sum of all n_{a,i}																							
Dead	16	48	0	0	48	1	0	0	3	31	12	5	0	0	13	1	9	0	0	19	1	2	1	0
Very severe (VS)	16	51	4	0	128	3	0	0	3	22	25	1	1	8	1	0	21	0	1	19	12	5	2	0
Severe (S)	1	6	0	0	25	0	0	0	3	5	0	4	0	2	3	0	1	0	0	7	33	0	2	0
Moderate (MOD)	24	118	0	1	268	6	0	2	6	45	25	21	2	8	61	0	35	4	3	36	15	16	5	0
Mild (Mild)	9	7	0	0	81	4	0	0	0	0	20	3	0	0	15	0	3	1	2	1	7	4	0	0
Very mild (VM)	6	5	9	0	61	1	3	0	0	3	18	0	0	1	7	0	3	12	2	3	8	0	6	0
Ci	**w_{a,i} = n_{a,i}/[sum of all n_{a,i}**																							
C _Dead = 1	0.1	0.2	0.0	0.0	0.2	0.0	0.0	0.0	0.0	0.1	0.1	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0
C _very severe = 0.44	0.0	0.2	0.0	0.0	0.4	0.0	0.0	0.0	0.0	0.1	0.1	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.1	0.0	0.0	0.0	0.0
C _Severe = 0.19	0.0	0.1	0.0	0.0	0.3	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.4	0.0	0.0	0.0
C _Moderate = 0.07	0.0	0.2	0.0	0.0	0.4	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0
C _Mild = 0.02	0.1	0.0	0.0	0.0	0.5	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
C _very mild = 0.00	0.0	0.0	0.1	0.0	0.4	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.1	0.0	0.0	0.0
VBD	**AHS**	**ASF**	**AKA**	**BHA**	**BT**	**BEF**	**CV**	**CCHF**	**EEE**	**Cowdr**	**EHD**	**GET**	**Hepat**	**JEF**	**Canl**	**MD**	**RV**	**SB**	**SLE**	**VEE**	**VS**	**WSL**	**WN**	**WEE**
SEVERITY SCORE[a]	**0.39**	**0.46**	**0.07**	**0.07**	**0.22**	**0.18**	**0.00**	**0.07**	**0.39**	**0.54**	**0.23**	**0.30**	**0.26**	**0.24**	**0.24**	**1.00**	**0.37**	**0.01**	**0.06**	**0.44**	**0.17**	**0.25**	**0.15**	
ORDINAL SCORE[b]	**S**	**VS**	**VM**	**mod**	**mod**	**mod**	**VM**	**mod**	**S**	**VS**	**S**	**S**	**S**	**S**	**S**	**VS**	**S**	**VM**	**mild**	**VS**	**mod**	**mod**	**mild**	

ASFV: African swine fever virus; CCHFV: Crimean-Congo haemorrhagic fever virus; NSDV: Nairobi sheep disease virus; AINOV: Aino virus; AKAV: Akabane virus; CVV: Bunyamwera virus; MDV: Main drain virus; SBV: Schmallenberg virus; SHUV: Shuni virus; RVFV: Rift Valley fever virus; BHAV: Bhanja virus; JEV: Japanese encephalitis virus; SLEV; St. Louis encephalitis virus; WSLV: Wesselsbron virus; WNV: West Nile virus; AHFV: Alkhurma haemorrhagic fever virus; Hepat: *Hepatozoon canis*: THOV: Thogoto virus; AHSV: African horse sickness virus; BTV: Bluetongue virus; EHDV: Epizootic haemorrhagic disease virus; EEV: Equine encephalosis virus; KASV: Palyam virus; PHSV: Peruvian horse sickness virus; YUOV: Yunnan orbivirus; BEFV: Bovine ephemeral fever virus; KOTV: Kotonkon virus; VSV: Vesicular stomatitis virus; Cowdr: Ehrlichia ruminantium; EEEV: Eastern equine encephalitis virus; GETV: Getah virus; HJV: Highlands J virus; MIDV: Middelburg virus; VEE: Venezuelan equine encephalitis virus; WEEV: Western equine encephalitis virus; CanL: Leishmania infantum.
Red font: rate of introduction for this pathogen was higher than 0.001 per year.
(a): Severity score = [sum of C_i × w_{a,i}]/[sum of all w_{a,i}.
(b): Ordinal score: Very severe (VS) = (0.44 – 1.00); Severe (S) = (0.19 – 0.44); Moderate (MOD) = (0.07 – 0.19); Mild (Mild) = (0.02 – 0.07); Very mild (VM) = (0.00 – 0.02).

Appendix D – Model outputs and their confidence intervals

Table D.1: Quantitative model outputs for the steps pre-introduction

Area potentially at risk	Worldwide occurrence	Rate of entry	Level of transmission	Probability of establishment	Overall rate of introduction
AHFV_Eastern_EU	0.81 (0.2; 1.38)	0.28 (-0.69; 1.19)	0.5(0.03; 0.97)	0.17(-0.6; 0.89)	-0.03(-1.79; 0.4)
AHFV_Northern_EU	0.8 (0.22; 1.37)	0.25 (-0.68; 1.23)	0.5(0.03; 0.98)	0.16(-0.58; 0.9)	-0.22(-1.85; 0.39)
AHFV_Southern_EU	0.8 (0.22; 1.37)	0.25 (-0.68; 1.23)	0.5(0.03; 0.98)	0.16(-0.58; 0.9)	-0.22(-1.85; 0.39)
AHFV_Western_EU	0.81 (0.2; 1.38)	0.28 (-0.69; 1.19)	-6(-6; -6)	0.17(-0.6; 0.89)	-6(-6; -6)
AHSV_Eastern_EU	0.1 (-0.16; 0.35)	-0.6 (-0.89; -0.3)	0.5(0.27; 0.73)	0.2(0.08; 0.32)	-1.53(-1.9; 0.38)
AHSV_Northern_EU	0.1 (-0.16; 0.35)	-0.6 (-0.89; -0.3)	0.5(0.42; 0.58)	0.2(0.08; 0.32)	-1.59(-1.92; -1.28)
AHSV_Southern_EU	0.1 (-0.16; 0.35)	-0.6 (-0.89; -0.3)	0.5(0.27; 0.73)	0.2(0.08; 0.32)	-1.53(-1.9; 0.38)
AHSV_Western_EU	0.1 (-0.16; 0.35)	-0.6 (-0.89; -0.3)	0.5(0.27; 0.73)	0.2(0.08; 0.32)	-1.53(-1.9; 0.38)
AINOV_Eastern_EU	0.81 (0.43; 1.16)	0.11 (-0.26; 0.49)	0.5(0.27; 0.73)	0(-0.12; 0.12)	-1.01(-1.46; 0.38)
AINOV_Northern_EU	0.8 (;)	0.1 (;)	0.5(0.27; 0.73)	-0.4(;)	-1.5(;)
AINOV_Southern_EU	0.8 (;)	0.1 (;)	0.5(0.27; 0.73)	0.6(;)	-0.5(;)
AINOV_Western_EU	0.8 (;)	0.1 (;)	0.5(0.27; 0.73)	0.8(;)	-0.3(;)
AKAV_Eastern_EU	0.6 (;)	-0.1 (;)	0.5(0.27;0.73)	0.8(;)	-0.5(;)
AKAV_Northern_EU	0.6 (;)	-0.1 (;)	0.5(0.27;0.74)	0.8(;)	-0.5(;)
AKAV_Southern_EU	0.6 (;)	-0.1 (;)	0.5(0.27;0.73)	0.8(;)	-0.5(;)
AKAV_Western_EU	0.6 (;)	-0.1 (;)	0.5(0.27;0.73)	0.8(;)	-0.5(;)
ASFV_Eastern_EU	0.06 (-0.13; 0.28)	0.66 (0.46; 0.91)	0.5(0.42; 0.58)	0.17(-0.6; 0.89)	-0.36(-1.17; 0.42)
ASFV_Northern_EU	0.06 (-0.13; 0.28)	0.26 (0.06; 0.51)	0.5(0.27; 0.73)	0.17(-0.6; 0.89)	-0.6(-1.51; 0.38)
ASFV_Southern_EU	0.06 (-0.13; 0.28)	0.66 (0.46; 0.91)	0.5(0.27; 0.73)	0.17(-0.6; 0.89)	-0.2(-1.11; 0.4)
ASFV_Western_EU	0.06 (-0.13; 0.28)	0.46 (0.26; 0.71)	0.5(0.27; 0.73)	0.17(-0.6; 0.89)	-0.4(-1.31; 0.38)
BEFV_Eastern_EU	0.81 (0.43; 1.16)	0.11 (-0.26; 0.49)	0.5(0.03; 0.97)	-0.6(-0.72; -0.48)	-1.46(-2.04; 0.37)
BEFV_Northern_EU	0.81 (0.43; 1.16)	0.11 (-0.26; 0.49)	0.5(0.03; 0.97)	-0.6(-0.72; -0.48)	-1.46(-2.04; 0.37)
BEFV_Southern_EU	0.81 (0.43; 1.16)	0.11 (-0.26; 0.49)	0.5(0.03; 0.97)	-0.2(-0.32; -0.08)	-1.06(-1.64; 0.37)
BEFV_Western_EU	0.81 (0.43; 1.16)	0.11 (-0.26; 0.49)	0.5(0.03; 0.97)	-0.2(-0.32; -0.08)	-1.06(-1.64; 0.37)
BHAV_Eastern_EU	0.8 (0.22; 1.37)	1.05 (0.12; 2.03)	0.17(-0.6; 0.92)	0.6(0.49; 0.71)	0.12(-0.61; 1.15)
BHAV_Northern_EU	0.8 (0.22; 1.37)	1.05 (0.12; 2.03)	0.5(0.03; 0.98)	-0.6(-0.71; -0.49)	-0.29(-1.58; 0.37)
BHAV_Southern_EU	0.8 (0.22; 1.37)	1.05 (0.12; 2.03)	0.17(-0.6; 0.92)	0.6(0.49; 0.71)	0.12(-0.61; 1.15)
BHAV_Western_EU	0.8 (0.22; 1.37)	1.05 (0.12; 2.03)	0.5(0.03; 0.98)	-0.2(-0.31; -0.09)	0.03(-1.18; 0.5)
BTV_Eastern_EU	0.5 (0.26; 0.74)	1.3 (1.03; 1.57)	0.68(0.42; 0.93)	0.8(0.69; 0.91)	0.89(0.57; 1.18)
BTV_Northern_EU	0.51 (0.26; 0.73)	0.91 (0.64; 1.15)	0.68(0.55; 0.78)	0.2(0.08; 0.31)	-0.1(-0.39; 0.18)
BTV_Southern_EU	0.5 (0.26; 0.74)	1.3 (1.03; 1.57)	0.68(0.54; 0.78)	0.8(0.69; 0.91)	0.89(0.62; 1.19)
BTV_Western_EU	0.51 (0.26; 0.73)	1.31 (1.04; 1.55)	0.7(0.62; 0.78)	0.2(0.08; 0.31)	0.3(0.01; 0.58)
CanL_Eastern_EU	0.95 (0.61; 1.24)	1.04 (0.71; 1.35)	0.5(0.27; 0.73)	0(-0.12; 0.12)	-0.08(-0.5; 0.38)
CanL_Eastern_EU	0.84 (0.63; 1.02)	1.14 (0.91; 1.36)	0.5(0.27; 0.74)	0(-0.11; 0.11)	-0.02(-0.3; 0.38)
CanL_Northern_EU	0.95 (0.61; 1.24)	1.24 (0.91; 1.55)	-6(-6; -6)	-0.6(-0.72; -0.48)	-6(-6; -6)
CanL_Southern_EU	0.95 (0.61; 1.24)	1.04 (0.71; 1.35)	0.5(0.42; 0.58)	0.6(0.48; 0.72)	0.44(0.09; 0.79)
CanL_Western_EU	0.95 (0.61; 1.24)	1.04 (0.71; 1.35)	0.5(0.27; 0.73)	0.2(0.08; 0.32)	0.12(-0.3; 0.39)
CCHFV_Eastern_EU	0.61 (0.15; 1.07)	1.2 (0.74; 1.68)	0.5(0.22; 0.73)	0.8(0.69; 0.91)	0.68(0.21; 1.26)
CCHFV_Northern_EU	0.61 (0.15; 1.07)	0.6 (0.14; 1.08)	0.5(0.69; 0.91)	0.8(0.69; 0.91)	0.27(-0.26; 0.67)
CCHFV_Southern_EU	0.61 (0.15; 1.07)	1.2 (0.74; 1.68)	0.5(0.42; 0.58)	0.8(0.69; 0.91)	0.8(0.33; 1.3)
CCHFV_Western_EU	0.61 (0.15; 1.07)	1.2 (0.74; 1.68)	0.5(0.27; 0.74)	0.8(0.69; 0.91)	0.71(0.25; 1.27)
Cowdr_Eastern_EU	0.51 (0.11; 0.89)	0.3 (-0.09; 0.71)	-6(-6; -6)	0.16(-0.58; 0.9)	-6(-6; -6)
Cowdr_Northern_EU	0.51 (0.11; 0.89)	0.3 (-0.09; 0.71)	0.5(0.03; 0.98)	0.16(-0.58; 0.9)	-0.32(-1.47; 0.37)
Cowdr_Southern_EU	0.51 (0.11; 0.89)	0.3 (-0.09; 0.71)	0.5(0.03; 0.98)	0.16(-0.58; 0.9)	-0.32(-1.47; 0.37)
Cowdr_Western_EU	0.5 (0.14; 0.88)	0.3 (-0.07; 0.7)	-6(-6; -6)	0.17(-0.6; 0.89)	-6(-6; -6)
CVV_Eastern_EU	0.81 (0.2; 1.38)	0.1 (-0.49; 0.7)	0.3(0.07; 0.53)	-0.4(-0.52; -0.28)	0.22(-1.84; 0.39)
CVV_Northern_EU	0.81 (0.2; 1.38)	0.5 (-0.09; 1.1)	0.3(0.07; 0.53)	-0.6(-0.72; -0.48)	0.22(-1.64; 0.39)
CVV_Southern_EU	0.8 (0.22; 1.37)	0.16 (-0.45; 0.78)	0.3(0.07; 0.54)	0.6(0.49; 0.71)	0.22(-0.85; 0.39)
CVV_Western_EU	0.8 (0.22; 1.37)	0.5 (-0.09; 1.1)	0.3(0.07; 0.54)	-0.2(-0.31; -0.09)	0.22(-1.32; 0.39)
EEEV_Eastern_EU	0.4 (0.04; 0.78)	0.3 (-0.09;0.71)	0.3(0.07; 0.53)	0.8(0.68; 0.91)	0.23 (-0.33;0.39)

EEEV_Northern_EU	0.4 (0.04; 0.78)	0.1 (-0.29; 0.51)	0.3(0.07; 0.53)	0.8(0.68; 0.91)	0.22(-0.53; 0.39)
EEEV_Southern_EU	0.4 (0.04; 0.78)	0.1 (-0.29; 0.51)	0.3(0.07; 0.53)	0.8(0.68; 0.91)	0.22(-0.53; 0.39)
EEEV_Western_EU	0.4 (0.04; 0.78)	0.5 (0.11; 0.91)	0.3(0.07; 0.53)	0.8(0.68; 0.91)	0.25(-0.13; 0.4)
EEV_Eastern_EU	0.81 (0.2; 1.38)	0.61 (0; 1.21)	0.7(0.47; 0.93)	-0.6(-0.72; -0.48)	-1.19(-1.81; -0.6)
EEV_Northern_EU	0.81 (0.2; 1.38)	0.81 (0.2; 1.41)	0.7(0.47; 0.93)	-0.6(-0.72; -0.48)	-0.99(-1.61; -0.4)
EEV_Southern_EU	0.81 (0.2; 1.38)	0.61 (0; 1.21)	0.7(0.47; 0.93)	-0.2(-0.32; -0.08)	-0.79(-1.41; -0.2)
EEV_Western_EU	0.81 (0.2; 1.38)	0.81 (0.2; 1.41)	0.7(0.47; 0.93)	-0.6(-0.72; -0.48)	-0.99(-1.61; -0.4)
EHD_Eastern_EU	0.3 (0.04; 0.56)	-0.1 (-0.4; 0.19)	0.7(0.62; 0.78)	0.8(0.69; 0.91)	-0.51(-0.81; -0.19)
EHD_Northern_EU	0.3 (0.04; 0.55)	-0.1 (-0.38; 0.19)	0.7(0.62; 0.78)	0.8(0.68; 0.91)	-0.49(-0.81; -0.2)
EHD_Southern_EU	0.3 (0.04; 0.56)	-0.1 (-0.4; 0.19)	0.7(0.62; 0.78)	0.8(0.69; 0.91)	-0.51(-0.81; -0.19)
EHD_Western_EU	0.3 (0.04; 0.55)	-0.1 (-0.38; 0.19)	0.7(0.62; 0.78)	0.8(0.68; 0.91)	-0.49(-0.81; -0.2)
GETV_Eastern_EU	0.61 (0.23; 0.96)	-0.1 (-0.46;0.29)	0.16(0.03;0.34)	0.6(49; 0.71)	0.16(0.03;0.35)
GETV_Northern_EU	0.61 (0.23; 0.96)	-0.1 (-0.46;0.29)	0.16(0.03;0.35)	0.6(49; 0.71)	0.16(0.03;0.35)
GETV_Southern_EU	0.61 (0.23; 0.96)	-0.1 (-0.46;0.29)	0.16(0.03;0.34)	0.6(49; 0.71)	0.16(0.03;0.35)
GETV_Western_EU	0.61 (0.23; 0.96)	-0.1 (-0.46;0.29)	0.16(0.03;0.35)	0.8(0.68;0.91)	0.16(0.03;0.35)
Hepatozoon_Eastern_EU	0.8 (0.46; 1.16)	1.1 (0.74; 1.46)	0.48(-0.01; 0.98)	0.16(-0.58; 0.9)	0.13(-0.68; 0.75)
Hepatozoon_Northern_EU	0.8 (0.46; 1.16)	1.7 (1.34; 2.06)	0.5(0.03; 0.98)	0.16(-0.58; 0.9)	0.36(-0.08; 1.35)
Hepatozoon_Southern	0.8 (0.46; 1.16)	1.5 (1.14; 1.86)	0.5(0.03; 0.98)	0.16(-0.58; 0.9)	0.28(-0.28; 1.15)
Hepatozoon_Western	0.8 (0.46; 1.16)	1.7 (1.34; 2.06)	0.48(-0.01; 0.98)	0.16(-0.58; 0.9)	0.35(-0.09; 1.35)
HJV_Eastern_EU	0.81 (0.2; 1.38)	0.5 (-0.09; 1.1)	0.1(0.02; 0.18)	0.2(0.08; 0.32)	0.1(0.02; 0.18)
HJV_Northern_EU	0.81 (0.2; 1.38)	0.3 (-0.29; 0.9)	0.1(0.02; 0.18)	0.2(0.08; 0.32)	0.1(0.02; 0.18)
HJV_Southern_EU	0.81 (0.2; 1.38)	0.1 (-0.49; 0.7)	0.1(0.02; 0.18)	0.2(0.08; 0.32)	0.1(0.02; 0.18)
HJV_Western_EU	0.81 (0.2; 1.38)	0.7 (0.11; 1.3)	0.1(0.02; 0.18)	0.2(0.08; 0.32)	0.1(0.02; 0.18)
JEV_Eastern_EU	0.22 (-0.06; 0.46)	-0.48 (-0.8; -0.2)	0.5(0.27; 0.73)	0.6(0.48; 0.72)	-1.01(-1.41; 0.38)
JEV_Northern_EU	0.22 (-0.06; 0.46)	-0.48 (-0.8; -0.2)	0.5(0.27; 0.73)	0.6(0.48; 0.72)	-1.01(-1.41; 0.38)
JEV_Southern_EU	0.22 (-0.06; 0.46)	-0.48 (-0.8; -0.2)	0.5(0.27; 0.73)	0.6(0.48; 0.72)	-1.01(-1.41; 0.38)
JEV_Western_EU	0.22 (-0.06; 0.46)	-0.48 (-0.8; -0.2)	0.5(0.27; 0.73)	0.8(0.68; 0.91)	-0.81(-1.21; 0.38)
KASV_Eastern_EU	0.81 (0.2; 1.38)	0.61 (0; 1.21)	0.7(0.47; 0.93)	0.17(-0.6; 0.89)	-0.42(-1.42; 0.56)
KASV_Northern_EU	0.81 (0.2; 1.38)	0.61 (0; 1.21)	0.7(0.47; 0.93)	0.17(-0.6; 0.89)	-0.42(-1.42; 0.56)
KASV_Southern_EU	0.81 (0.2; 1.38)	0.61 (0; 1.21)	0.7(0.47; 0.93)	0.17(-0.6; 0.89)	-0.42(-1.42; 0.56)
KASV_Western_EU	0.81 (0.2; 1.38)	0.61 (0; 1.21)	0.7(0.47; 0.93)	0.17(-0.6; 0.89)	-0.42(-1.42; 0.56)
KOTV_Eastern_EU	0.81 (0.2; 1.38)	0.1 (-0.49; 0.7)	0.5(0.03; 0.97)	0.17(-0.6; 0.89)	-0.36(-1.77; 0.37)
KOTV_Northern_EU	0.81 (0.2; 1.38)	0.1 (-0.49; 0.7)	0.5(0.03; 0.97)	0.17(-0.6; 0.89)	-0.36(-1.77; 0.37)
KOTV_Southern_EU	0.81 (0.2; 1.38)	0.1 (-0.49; 0.7)	0.5(0.03; 0.97)	0.17(-0.6; 0.89)	-0.36(-1.77; 0.37)
KOTV_Western_EU	0.81 (0.2; 1.38)	0.1 (-0.49; 0.7)	0.5(0.03; 0.97)	0.17(-0.6; 0.89)	-0.36(-1.77; 0.37)
MDV_Eastern_EU	0.62 (0.34; 0.86)	-0.08 (-0.4; 0.2)	0.5(0.27; 0.73)	0.17(-0.6; 0.89)	-0.94(-1.93; 0.38)
MDV_Northern_EU	0.62 (0.34; 0.86)	0.12 (-0.2; 0.4)	0.5(0.27; 0.73)	0.17(-0.6; 0.89)	-0.74(-1.73; 0.38)
MDV_Southern_EU	0.62 (0.34; 0.86)	-0.08 (-0.4; 0.2)	0.5(0.27; 0.73)	0.17(-0.6; 0.89)	-0.94(-1.93; 0.38)
MDV_Western_EU	0.62 (0.34; 0.86)	0.32 (0; 0.6)	0.5(0.27; 0.73)	0.17(-0.6; 0.89)	-0.54(-1.53; 0.38)
MIDV_Eastern_EU	0.8 (0.22; 1.37)	0.1 (-0.49; 0.7)	-6(-6; -6)	0.16(-0.58; 0.9)	-6(-6; -6)
MIDV_Northern_EU	0.8 (0.22; 1.37)	0.1 (-0.49; 0.7)	-6(-6; -6)	0.16(-0.58; 0.9)	-6(-6; -6)
MIDV_Southern_EU	0.8 (0.22; 1.37)	0.1 (-0.49; 0.7)	-6(-6; -6)	0.16(-0.58; 0.9)	-6(-6; -6)
MIDV_Western_EU	0.8 (0.22; 1.37)	0.1 (-0.49; 0.7)	-6(-6; -6)	0.16(-0.58; 0.9)	-6(-6; -6)
NSD_Eastern_EU	0.61 (-0.07; 1.25)	-0.09 (-0.74; 0.56)	-6(-6; -6)	0.17(-0.6; 0.89)	-6(-6; -6)
NSD_Northern_EU	0.61 (-0.07; 1.25)	-0.09 (-0.74; 0.56)	-6(-6; -6)	0.17(-0.6; 0.89)	-6(-6; -6)
NSD_Southern_EU	0.61 (-0.07; 1.25)	-0.09 (-0.74; 0.56)	0.5(0.03; 0.97)	0.17(-0.6; 0.89)	-0.51(-2.04; 0.37)
NSD_Western_EU	0.61 (-0.07; 1.25)	-0.09 (-0.74; 0.56)	-6(-6; -6)	0.17(-0.6; 0.89)	-6(-6; -6)
PHSV_Eastern_EU	0.81 (0.2; 1.38)	0.28 (-0.69; 1.19)	0.5(0.03; 0.97)	0.17(-0.6; 0.89)	-0.03(-1.79; 0.4)
PHSV_Northern_EU	0.81 (0.2; 1.38)	0.48 (-0.49; 1.39)	0.5(0.03; 0.97)	0.17(-0.6; 0.89)	0.03(-1.59; 0.56)

PHSV_Southern_EU	0.81 (0.2; 1.38)	0.28 (-0.69; 1.19)	0.5(0.03; 0.97)	0.17(-0.6; 0.89)	-0.03(-1.79; 0.4)
PHSV_Western_EU	0.81 (0.2; 1.38)	0.48 (-0.49; 1.39)	0.5(0.03; 0.97)	0.17(-0.6; 0.89)	0.03(-1.59; 0.56)
RFV_Eastern_EU	0.1 (-0.05; 0.25)	-0.6 (-0.79; -0.4)	0.5(0.27; 0.73)	0.8(0.68; 0.91)	-0.95(-1.21; 0.38)
RFV_Northern_EU	0.1 (-0.05; 0.25)	-0.6 (-0.79; -0.4)	0.5(0.27; 0.73)	0.8(0.68; 0.91)	-0.95(-1.21; 0.38)
RFV_Southern_EU	0.1 (-0.05; 0.25)	-0.6 (-0.79; -0.4)	0.5(0.42; 0.58)	0.8(0.68; 0.91)	-1(-1.22; -0.76)
RFV_Western_EU	0.1 (-0.05; 0.25)	-0.6 (-0.79; -0.4)	0.5(0.27; 0.73)	0.8(0.68; 0.91)	-0.95(-1.21; 0.38)
SBV_Eastern_EU	0.82 (0.54; 1.06)	0.92 (0.6; 1.2)	0.5(0.27; 0.73)	0.8(0.68; 0.91)	0.44(0.19; 0.82)
SBV_Northern_EU	0.82 (0.54; 1.06)	0.92 (0.6; 1.2)	0.47(0.23; 0.73)	0.8(0.68; 0.91)	0.41(0.18; 0.82)
SBV_Southern_EU	0.82 (0.54; 1.06)	1.12 (0.8; 1.4)	0.47(0.23; 0.73)	0.8(0.68; 0.91)	0.61(0.23; 1.02)
SBV_Western_EU	0.82 (0.54; 1.06)	1.12 (0.8; 1.4)	0.5(0.27; 0.73)	0.8(0.68; 0.91)	0.64(0.27; 1.02)
SHU_Eastern_EU	0.8 (0.22; 1.37)	0.1 (-0.49; 0.7)	0.16(0.03; 0.35)	-0.6(-0.71; -0.49)	0.16(0.03; 0.35)
SHU_Northern_EU	0.81 (0.2; 1.38)	0.1 (-0.49; 0.7)	-6(-6; -6)	-0.6(-0.72; -0.48)	-6(-6; -6)
SHU_Southern_EU	0.81 (0.2; 1.38)	0.1 (-0.49; 0.7)	0.16(0.03; 0.34)	-0.2(-0.32; -0.08)	0.16(0.03; 0.34)
SHU_Western_EU	0.81 (0.2; 1.38)	0.1 (-0.49; 0.7)	0.16(0.03; 0.34)	-0.6(-0.72; -0.48)	0.16(0.03; 0.34)
SLEV_Eastern_EU	0.61 (0.23; 0.96)	0.48 (-0.36; 1.24)	0.5(0.03; 0.97)	0.2(0.08; 0.32)	-0.02(-1.29; 0.38)
SLEV_Northern_EU	0.61 (0.23; 0.96)	0.48 (-0.36; 1.24)	0.5(0.03; 0.97)	0.2(0.08; 0.32)	-0.02(-1.29; 0.38)
SLEV_Southern_EU	0.61 (0.23; 0.96)	0.48 (-0.36; 1.24)	0.5(0.03; 0.97)	0.2(0.08; 0.32)	-0.02(-1.29; 0.38)
SLEV_Western_EU	0.61 (0.23; 0.96)	0.68 (-0.16; 1.44)	0.5(0.03; 0.97)	0.2(0.08; 0.32)	0.04(-1.09; 0.41)
THOV_Eastern_EU	0.81 (0.2; 1.38)	1.01 (0.03; 1.93)	0.5(0.03; 0.97)	0.17(-0.6; 0.89)	0.14(-1.08; 1.12)
THOV_Northern_EU	0.81 (0.2; 1.38)	0.88 (-0.09; 1.79)	0.5(0.03; 0.97)	0.17(-0.6; 0.89)	0.1(-1.19; 0.96)
THOV_Southern_EU	0.81 (0.2; 1.38)	1.08 (0.11; 1.99)	0.5(0.03; 0.97)	0.17(-0.6; 0.89)	0.15(-0.99; 1.16)
THOV_Western_EU	0.81 (0.2; 1.38)	1.08 (0.11; 1.99)	-6(-6; -6)	0.17(-0.6; 0.89)	-6(-6; -6)
VEE_Eastern_EU	0.4 (0.13; 0.67)	0.4 (0.11; 0.68)	0.15(0.03; 0.34)	-0.4(-0.52; -0.29)	0.15(0.03; 0.34)
VEE_Northern_EU	0.4 (0.13; 0.67)	0.8 (0.51; 1.08)	-6(-6; -6)	-0.6(-0.72; -0.49)	-6(-6; -6)
VEE_Southern_EU	0.4 (0.13; 0.67)	0.4 (0.11; 0.68)	0.15(0.03; 0.34)	0(-0.12; 0.11)	0.15(0.03; 0.34)
VEE_Western_EU	0.4 (0.13; 0.67)	1 (0.71; 1.28)	0.15(0.03; 0.34)	0(-0.12; 0.11)	0.15(0.03; 0.34)
VSV_Eastern_EU	0.72 (0.19; 1.19)	0.51 (0; 1.02)	0.5(0.03; 0.97)	0.17(-0.6; 0.89)	0(-1.35; 0.4)
VSV_Northern_EU	0.72 (0.19; 1.19)	0.71 (0.2; 1.22)	0.5(0.03; 0.97)	0.17(-0.6; 0.89)	0.05(-1.15; 0.59)
VSV_Southern_EU	0.72 (0.19; 1.19)	0.5 (-0.15; 1.17)	0.5(0.03; 0.97)	0.17(-0.6; 0.89)	0.01(-1.39; 0.4)
VSV_Western_EU	0.72 (0.19; 1.19)	0.71 (0.2; 1.22)	0.5(0.03; 0.97)	0.17(-0.6; 0.89)	0.05(-1.15; 0.59)
WEEV_Eastern_EU	0.61 (-0.07; 1.25)	0.31 (-0.34; 0.96)	0.16(0.03; 0.34)	0.8(0.68; 0.91)	0.16(0.03; 0.34)
WEEV_Northern_EU	0.61 (-0.07; 1.25)	0.11 (-0.54; 0.76)	0.16(0.03; 0.34)	0.8(0.68; 0.91)	0.16(0.03; 0.34)
WEEV_Southern_EU	0.61 (-0.07; 1.25)	0.11 (-0.54; 0.76)	0.16(0.03; 0.34)	0.8(0.68; 0.91)	0.16(0.03; 0.34)
WEEV_Western_EU	0.61 (-0.07; 1.25)	0.51 (-0.14; 1.16)	0.16(0.03; 0.34)	0.8(0.68; 0.91)	0.16(0.03; 0.34)
WNV_Eastern_EU	0.21 (-0.04; 0.43)	0.9 (0.65; 1.14)	0.5(0.27; 0.73)	0.8(0.68; 0.91)	0.45(0.23; 0.76)
WNV_Northern_EU	0.21 (-0.04; 0.43)	0.9 (0.65; 1.14)	0.5(0.27; 0.73)	0.8(0.68; 0.91)	0.45(0.23; 0.76)
WNV_Southern_EU	0.21 (-0.04; 0.43)	0.9 (0.65; 1.14)	0.5(0.27; 0.73)	0.89(0.81; 0.97)	0.55(0.26; 0.83)
WNV_Western_EU	0.21 (-0.04; 0.43)	0.9 (0.65; 1.14)	0.47(0.23; 0.73)	0.89(0.81; 0.97)	0.52(0.23; 0.82)
WSLV_Eastern_EU	0.79 (0.21; 1.39)	0.09 (-0.51; 0.72)	-6(-6; -6)	0.16(-0.61; 0.89)	-6(-6; -6)
WSLV_Northern_EU	0.81 (0.2; 1.38)	0.1 (-0.49; 0.7)	-6(-6; -6)	0.17(-0.6; 0.89)	-6(-6; -6)
WSLV_Southern_EU	0.81 (0.2; 1.38)	0.1 (-0.49; 0.7)	-6(-6; -6)	0.17(-0.6; 0.89)	-6(-6; -6)
WSLV_Western_EU	0.81 (0.2; 1.38)	0.1 (-0.49; 0.7)	-6(-6; -6)	0.17(-0.6; 0.89)	-6(-6; -6)
YUOV_Eastern_EU	0.81 (0.2; 1.38)	0.28 (-0.69; 1.19)	0.5(0.03; 0.97)	-0.6(-0.72; -0.48)	-0.98(-2.34; 0.37)
YUOV_Northern_EU	0.81 (0.2; 1.38)	0.48 (-0.49; 1.39)	-6(-6; -6)	-0.6(-0.72; -0.48)	-6(-6; -6)
YUOV_Southern_EU	0.8 (0.22; 1.37)	0.25 (-0.68; 1.23)	0.5(0.03; 0.98)	0.2(0.09; 0.31)	-0.29(-1.58; 0.37)
YUOV_Western_EU	0.82 (0.21; 1.39)	0.5 (-0.55; 1.37)	-6(-6; -6)	-0.6(-0.72; -0.49)	-6(-6; -6)

very high	high/very high	high	moderate/high	moderate	
low/moderate	low	very low/low	very low		

Table D.2: Model outputs for the steps post-introduction

Area potentially at risk	Annual extent of spread	Overwintering	Estimated epidemic size	Production losses	Impact on animal welfare
AHFV_Eastern_EU					
AHFV_Northern_EU					
AHFV_Southern_EU					
AHFV_Western_EU					
AHSV_Eastern_EU					
AHSV_Northern_EU					
AHSV_Southern_EU					
AHSV_Western_EU					
AINOV_Eastern_EU					
AINOV_Northern_EU					
AINOV_Southern_EU					
AINOV_Western_EU					
AKAV_Eastern_EU					
AKAV_Northern_EU					
AKAV_Southern_EU					
AKAV_Western_EU					
ASFV_Eastern_EU					
ASFV_Northern_EU					
ASFV_Southern_EU					
ASFV_Western_EU					
BEFV_Eastern_EU					
BEFV_Northern_EU					
BEFV_Southern_EU					
BEFV_Western_EU					
BHAV_Eastern_EU					
BHAV_Northern_EU					
BHAV_Southern_EU					
BHAV_Western_EU					
BTV_Eastern_EU	0.56(0.11; 1.64)	0.5(0.42; 0.58)	0.37(-0.14; 1.79)	0.18(-0.13; 0.88)	0.18(-0.2; 0.9)
BTV_Northern_EU	0.55(0.17; 1.24)	0.5(0.42; 0.58)	0.36(-0.09; 1.26)	0.18(-0.08; 0.64)	0.17(-0.2; 0.9)
BTV_Southern_EU	0.65(0.18; 1.57)	0.53(0.46; 0.59)	0.46(-0.09; 1.72)	0.25(-0.08; 0.86)	0.24(-0.14; 0.87)
BTV_Western_EU	0.65(0.25; 1.28)	0.5(0.42; 0.58)	0.46(0; 1.26)	0.24(-0.04; 0.66)	0.24(-0.09; 0.68)
CanL_Eastern_EU	0.1(0.03; 0.21)	0.7(0.51; 0.93)	-0.03(-0.16; 0.23)	-0.42(-0.49; -0.34)	0.05(-0.05; 0.14)
CanL_Eastern_EU	0.1(0.03; 0.21)	0.7(0.51; 0.93)	-0.03(-0.16; 0.23)	-0.42(-0.49; -0.34)	0.05(-0.05; 0.14)
CanL_Northern_EU	0(0; 0)	0.5(0.42; 0.58)	-0.19(-0.2; -0.18)	-0.53(-0.53; -0.52)	-0.07(-0.12; -0.01)
CanL_Southern_EU	0.09(0.07; 0.14)	0.7(0.51; 0.93)	-0.04(-0.13; 0.11)	-0.43(-0.47; -0.37)	0.04(-0.04; 0.12)
CanL_Western_EU	0.1(0.03; 0.21)	0.7(0.51; 0.93)	-0.03(-0.16; 0.23)	-0.42(-0.49; -0.34)	0.05(-0.05; 0.14)
CCHFV_Eastern_EU	0.09 (0.03; 0.27)	0.93(0.86; 0.99)	-0.05(-0.08; 0.3)	-0.39(-0.43; -0.26)	-0.05(-0.21; 0.13)
CCHFV_Northern_EU	0.1(0.03; 0.28)	0.93(0.86; 0.99)	0.02(-0.05; 0.3)	-0.39(-0.43; -0.26)	-0.05(-0.21; 0.13)
CCHFV_Southern_EU	0.1(0.07; 0.21)	0.93(0.86; 0.99)	0.02(-0.02; 0.16)	-0.39(-0.41; -0.32)	-0.05(-0.2; 0.12)
CCHFV_Western_EU	0.1(0.03; 0.28)	0.93(0.86; 0.99)	0.02(-0.05; 0.3)	-0.39(-0.43; -0.26)	-0.05(-0.12; 0.08)
Cowdr_Eastern_EU					
Cowdr_Northern_EU					
Cowdr_Southern_EU					
Cowdr_Western_EU					
CVV_Eastern_EU	0.07(0.01; 0.8)	0.5(0.12; 0.97)	-0.06(-0.19; 0.96)	-0.09(-0.51; 0.43)	-0.05(-0.45; 0.46)
CVV_Northern_EU	0.07(0.01; 0.47)	0.5(0.12; 0.97)	-0.07(-0.19; 0.5)	-0.12(-0.51; 0.29)	-0.07(-0.45; 0.3)
CVV_Southern_EU	0.07(0.01; 1.43)	0.56(0.43; 0.97)	-0.06(-0.19; 1.77)	-0.07(-0.51; 0.83)	-0.03(-0.45; 0.85)
CVV_Western_EU	0.07(0.01; 1.08)	0.5(0.12; 0.97)	-0.06(-0.19; 0.96)	-0.09(-0.51; 0.43)	-0.05(-0.45; 0.46)

EEEV_Eastern_EU	0.07(0.01; 1.08)	0.15(0.09; 0.19)	-0.2(-0.2; -0.2)	-0.22(-0.53; 0.11)	-0.07(-0.23; 0.09)
EEEV_Northern_EU	0.07(0.01; 0.51)	0.15(0.09; 0.19)	-0.13(-0.19; 0.49)	-0.14(-0.52; 0.3)	0(-0.18; 0.29)
EEEV_Southern_EU	0.07(0.01; 1.35)	0.5(0.42; 0.58)	-0.12(-0.19; 1.72)	-0.1(-0.51; 0.76)	0.01(-0.18; 0.84)
EEEV_Western_EU	0.07(0.01; 0.77)	0.15(0.09; 0.19)	-0.13(-0.19; 0.87)	-0.12(-0.52; 0.42)	0(-0.18; 0.47)
EEV_Eastern_EU					
EEV_Northern_EU					
EEV_Southern_EU					
EEV_Western_EU					
EHD_Eastern_EU					
EHD_Northern_EU					
EHD_Southern_EU					
EHD_Western_EU					
GETV_Eastern_EU					
GETV_Northern_EU					
GETV_Southern_EU					
GETV_Western_EU					
Hepatozoon_Eastern_EU	0.14(0.01; 0.58)	0.72(0.66; 0.78)	0.01(-0.15; 0.49)	-0.39(-0.49; -0.11)	0.11(-0.13; 0.42)
Hepatozoon_Northern_EU	0.14(0.01; 0.58)	0.72(0.66; 0.78)	0.01(-0.15; 0.49)	-0.39(-0.49; -0.11)	0.11(-0.13; 0.42)
Hepatozoon_Southern	0.16(0.01; 0.58)	0.72(0.66; 0.78)	0.03(-0.15; 0.5)	-0.38(-0.49; -0.1)	0.09(-0.05; 0.38)
Hepatozoon_Western	0.16(0.01; 0.58)	0.72(0.66; 0.78)	0.03(-0.15; 0.5)	-0.38(-0.49; -0.1)	0.11(-0.13; 0.43)
HJV_Eastern_EU					
HJV_Northern_EU					
HJV_Southern_EU					
HJV_Western_EU					
JEV_Eastern_EU					
JEV_Northern_EU					
JEV_Southern_EU					
JEV_Western_EU					
KASV_Eastern_EU					
KASV_Northern_EU					
KASV_Southern_EU					
KASV_Western_EU					
KOTV_Eastern_EU					
KOTV_Northern_EU					
KOTV_Southern_EU					
KOTV_Western_EU					
MDV_Eastern_EU					
MDV_Northern_EU					
MDV_Southern_EU					
MDV_Western_EU					
MIDV_Eastern_EU					
MIDV_Northern_EU					
MIDV_Southern_EU					
MIDV_Western_EU					
NSD_Eastern_EU					
NSD_Northern_EU					
NSD_Southern_EU					
NSD_Western_EU					
PHSV_Eastern_EU					

PHSV_Northern_EU					
PHSV_Southern_EU					
PHSV_Western_EU					
RFV_Eastern_EU					
RFV_Northern_EU					
RFV_Southern_EU					
RFV_Western_EU					
SBV_Eastern_EU	0.84(0.05; 2.63)	0.5(0.42; 0.58)	0.65(-0.16; 2.94)	0.36(-0.18; 1.52)	0.15(-0.42; 1.33)
SBV_Northern_EU	0.41(0.04; 1.34)	0.5(0.42; 0.58)	0.22(-0.18; 1.38)	0.08(-0.19; 0.7)	-0.14(-0.45; 0.46)
SBV_Southern_EU	1.1(0.04; 4.04)	0.52(0.46; 0.58)	0.9(-0.18; 4.7)	0.53(-0.19; 2.5)	0.33(-0.44; 2.3)
SBV_Western_EU	1.14(0.05; 3.57)	0.5(0.42; 0.58)	0.95(-0.16; 4.11)	0.56(-0.18; 2.18)	0.34(-0.42; 1.99)
SHU_Eastern_EU					
SHU_Northern_EU					
SHU_Southern_EU					
SHU_Western_EU					
SLEV_Eastern_EU					
SLEV_Northern_EU					
SLEV_Southern_EU					
SLEV_Western_EU					
THOV_Eastern_EU					
THOV_Northern_EU					
THOV_Southern_EU					
THOV_Western_EU					
VEE_Eastern_EU					
VEE_Northern_EU					
VEE_Southern_EU					
VEE_Western_EU					
VSV_Eastern_EU					
VSV_Northern_EU					
VSV_Southern_EU					
VSV_Western_EU					
WEEV_Eastern_EU					
WEEV_Northern_EU					
WEEV_Southern_EU					
WEEV_Western_EU					
WNV_Eastern_EU	0.6 (0.08; 1.87)	0.9(0.82; 0.98)	0.52(-0.03; 2.14)	-0.05(-0.4; 0.79)	0.16(-0.27; 0.99)
WNV_Northern_EU	0.38(0.08; 1.03)	0.9(0.82; 0.98)	0.03(-0.03; 1.11)	-0.2(-0.4; 0.23)	0.02(-0.28; 0.45)
WNV_Southern_EU	0.9 (0.08; 3.05)	0.9(0.82; 0.98)	0.82(-0.03; 2.97)	-0.34(-0.42; 0.86)	0.35(-0.27; 1.28)
WNV_Western_EU	0.52(0.06; 1.84)	0.9(0.82; 0.98)	0.44(-0.06; 2.09)	-0.11(-0.41; 0.77)	0.1 (-0.28; 0.95)
WSLV_Eastern_EU					
WSLV_Northern_EU					
WSLV_Southern_EU					
WSLV_Western_EU					
YUOV_Eastern_EU					
YUOV_Northern_EU					
YUOV_Southern_EU					
YUOV_Western_EU					

very high	high/very high	high	moderate/high	moderate

low/moderate	low	very low/low	very low

Appendix E – Biocidal products

According to Reg (EU) No 528/2012, concerning the making available on the market and use of biocidal products, active substances belonging to product type 18 and 19 are taken into account in this opinion. Product type 18 (i.e. insecticides, acaricides and products to control other arthropods) is used for the control of arthropods (e.g. insects, arachnids and crustaceans) by means other than repulsion or attraction. Similarly product type 19 (i.e. repellents and attractants) is applied to control harmful organisms (invertebrates such as fleas, vertebrates such as birds, fish, rodents), by repelling or attracting, including those that are used for human or veterinary hygiene either directly on the skin or indirectly in the environment of humans or animals.

Table E.1: Overview table of product type 18 and 19 for which an application for approval has been submitted under Directive 98/8/EC (BPD) or Regulation (EU) No 528/2012 (BPR), including 'existing' active substances included in the Review Programme and 'new' active substances, and those already 'approved' and those where the application is on-going ('under review'). Updated version available at http://echa.europa.eu/information-on-chemicals/biocidal-active-substances

Product type	Approved a.s.	Under review a.s.	Not approved a.s.	TOT
PT_18	34	27	1	62
PT_19	8	8	–	16

According to Reg (EU) No 528/2012 Annex VI, the risk characterisation for the environment considers the estimation of the incidence and severity of the adverse effects likely to occur in environmental compartments due to actual or predicted exposure to any active substance or substance of concern in a biocidal product. For any given environmental compartment, the risk characterisation must, as far as possible, entail comparison of the Predicted Environmental Concentration (PEC) with the (Predicted No Effect Concentration (PNEC) so that a PEC/PNEC ratio may be derived. If PEC/PNEC ratio < 1, no risks are identified. If the PEC/PNEC ratio is > 1, the Competent Authority must judge, on the basis of the size of that ratio and on other relevant factors, if further information and/or testing are required to clarify the concern, if risk reduction measures are necessary or if the substance cannot be included in the Union List at all. If it has not been possible to derive a PEC/PNEC ratio, the risk characterisation must entail a qualitative evaluation of the likelihood that an effect is occurring under the current conditions of exposure or will occur under the expected conditions of exposure. Data from the approved active substances that are to be used for controlling the relevant vectors species were extracted, such as information on the target species, intended uses (e.g. indoor/outdoor, professional/non-professional use), application/dose rate (i.e. efficacy), hazard class category and risk characterisation ratios (RCRs).

Table E.2: Data extraction on approved active substances that are to be used for controlling the relevant vectors species

Active substance (product type)	Target species	Intended uses	Application/dose rate (i.e. efficacy*)	Hazard statements (According to Reg. No 1272/2008[(a)]	Risk characterisation ratios (according to REG No 528/ 2012, Annex VI)	Assessment Report (link)
1*R*-trans-phenothrin (18)	German cockroaches (*Blattella germanica*), American cockroaches (*Periplaneta americana*) Oriental Cockroaches (*Blatta orientalis*) House fly (*Musca domestica*); Mosquitoes (Culicidae)	Indoor use only by professional operators in particular in areas such as trains, trucks, hospitals, hotels and other public buildings	20 mg/a.s per m^2	H410: very toxic to aquatic life with long lasting effects	1) Aquatic compartment: **NO risk** 2) Terrestrial compartment: **NO risk** from 1R-trans-phenothrin metabolites following indoor targeted spot application of Sumithrin® 10 SEC and its subsequent emissions to the terrestrial soil environment	http://dissemination.echa.europa.eu/Biocides/ActiveSubstances/0059-18/0059-18_Assessment_Report.pdf
Bacillus thuringiensis subsp. *israelensis* Serotype H14, Strain AM65-52 (18)	Larvae of mosquitoes (*Aedes* spp., *Culex* spp) and black flies + larvae of filter fly midges in sewage treatment plants	Ground application: tractor-mounted or handheld sprayer. Aerial application: fixed wing or helicopter. Applied during the first to the fourth larval instar	Rates up to 500 g/ha (9×10^{12} CFU/ha) (mortality greater than 95% of the control was observed after 48 h)	Limited survival in the environment Limited risk to human health, related only to the possibility to induce sensitization, based on the results obtained on animal models	EED/PNED ratio ** at local level below 1 indicates **NO risk** for the environment	http://dissemination.echa.europa.eu/Biocides/ActiveSubstances/0005-18/0005-18_Assessment_Report.pdf

Active substance (product type)	Target species	Intended uses	Application/dose rate (i.e. efficacy*)	Hazard statements (According to Reg. No 1272/2008[a])	Risk characterisation ratios (according to REG No 528/ 2012, Annex VI)	Assessment Report (link)
Deltamethrin (18)	Indoors: flying insects when at rest (e.g. flies and mosquitoes), black ants, bedbugs, fleas, earwigs, carpet beetles, booklice, and cockroaches, as well as spiders and woodlice Outdoors: ants	Indoors: spray applications, professional users only. Outdoors: directly around the nest entrance, by amateurs	6.25 mg/a.s per m^2 (1 month-low dose rate)** 12.5 mg/a.s per/m^2 (3 month-high dose rate)**	H400/410: Aquatic Chronic H331/H301:Acute tox 3	Aquatic compartment: 1) Surface water: a) **NO risk** if following use in crack and crevice treatments in domestic houses and larger buildings b) RISK if following barrier treatment in domestic houses and larger buildings 2) Sediment: a) **NO risk** if for sediment dwelling organisms following use in crack and crevice treatments in domestic houses and larger buildings b) RISK if following barrier treatment in domestic houses and larger buildings Terrestrial compartment: 1) Soil: **NO risk** 2) Groundwater: **NO risk**	http://dissemination.echa.europa.eu/Biocides/ActiveSubstances/0024-18/0024-18_Assessment_Report.pdf

Active substance (product type)	Target species	Intended uses	Application/dose rate (i.e. efficacy*)	Hazard statements (According to Reg. No 1272/2008[a])	Risk characterisation ratios (according to REG No 528/ 2012, Annex VI)	Assessment Report (link)
Diflubenzuron	Mosquito larvae in water (i.e. gully-holes and septic tanks in urban, suburban and rural areas and storage containers for garden irrigation) and control of fly larvae in farm buildings or in refuse and waste disposal areas	Manual (broad cast) made directly to water surface. Granule formulation, Professional PCO or farmer	Application rate dependent on type of water: • High organic polluted water 1 g a.s./1 m^3 (equivalent to 1 mg a.s./L) • Dirty water 1 g a.s./4 m^3 (equivalent to 0.25 mg a.s./L). • Clear water 1 g a.s./8 m^3 (equivalent to 0.125 mg a.s./L) Minimum interval of 1 month	H400: Aquatic Acute 1 H410: Aquatic Chronic 1	*Scenario1: Mosquito Control in Gully Holes* Aquatic compartment: a) Surface water: RISK b) Sediment: RISK STP (Sewage Treatment Plants): **NO risk** Terrestrial compartment: **NO risk** *Scenario 2: Mosquito control in septic tanks* Aquatic compartment: a) Surface water: **NO risk** b) Sediment: **NO risk** Terrestrial compartment: RISK Groundwater (for metabolite CPU): RISK	http://dissemination.echa.europa.eu/Biocides/factsheet?id=0062-18

Active substance (product type)	Target species	Intended uses	Application/dose rate (i.e. efficacy*)	Hazard statements (According to Reg. No 1272/2008[a])	Risk characterisation ratios (according to REG No 528/ 2012, Annex VI)	Assessment Report (link)
Lambda-cyhalothrin (18)	Flies and other insects in and around animal housing	For fly control, application is as a low pressure spray in areas where flies congregate or settle such as floors, walls, ceilings and around doors and windows. For other insects, the product is applied as a low pressure spray as a crack and crevice treatment	25 mg/a.s. per m^2	H400/410: *Aquatic Chronic* H312: harmful in contact with skin H301 or H300: toxic or fatal/if swallowed H330: fatal if inhaled	Aquatic compartment: 1) Sewage Treatment Plant: **NO risk** 2) Surface water: a) RISK for aquatic organisms at the representative uses of lambda-cyhalothrin in Demand/ICON 10CS that result in emissions to STP b) RISK: aquatic organisms at the indoor use of OXYFLY 10CS in animal houses (poultry) connected to STP c) **NO risk** For aquatic organisms exposed via distribution of manure/ slurry to arable land/grassland	http://dissemination.echa.europa.eu/Biocides/ActiveSubstances/0041-18/0041-18_Assessment_Report.pdf
Metofluthrin (18)	Mosquitoes	Indoor: Heated vaporiser space treatment	0.0217 mg/a.s. per m^3 (effective for 60 days at 12 h use per day)	H412: harmful to aquatic life with long lasting effects. H304 (Asp Tox 1): may be Fatal if swallowed and Enters Airways	1) STP: **NO risk** 2) Surface **waters:** a) **NO** risk (tier 1) b) RISK (tier 2) 3) Sediment: **NO risk** 4) Soil (local): **NO risk** 5) Biota (Avian): **NO risk** 6) Biota (mammal, food chain): **NO risk**	http://dissemination.echa.europa.eu/Biocides/ActiveSubstances/0045-18/0045-18_Assessment_Report.pdf

Active substance (product type)	Target species	Intended uses	Application/dose rate (i.e. efficacy*)	Hazard statements (According to Reg. No 1272/2008[a])	Risk characterisation ratios (according to REG No 528/ 2012, Annex VI)	Assessment Report (link)
Permethrin (18)	Flying insects (e.g. flies and mosquitoes) and crawling insects (e.g. roaches, mites, fleas and ticks)	Indoor use (households* and commercial areas), by professional and non-professional users against flying and crawling insects. Spot treatments	0.0011 mg/a.s. per m^2	H410 (Acute Cat 1; Chronic Cat 1): very toxic to aquatic life with long lasting effects. H317: may cause an allergic skin reaction	1) STP: **NO risk** 2) Surface waters: a) **NO risk** (If the product is restricted to use in dry cleaned areas) b) RISK (if not respected the scenario a) 3) Sediment: a) **NO risk** (If the product is restricted to use in dry cleaned areas) b) RISK (if not respected the scenario a) 4) Soil (local): **NO risk** 5) There is **NO risk** to wildlife when professional/non-professional use is restricted to targeted spot applications in dry cleaned areas or the dry cleaning of areas subject to wetting 6) Secondary poisoning: **NO risk**	http://dissemination.echa.europa.eu/Biocides/ActiveSubstances/1342-18/1342-18_Assessment_Report.pdf

Active substance (product type)	Target species	Intended uses	Application/dose rate (i.e. efficacy*)	Hazard statements (According to Reg. No 1272/2008[a])	Risk characterisation ratios (according to REG No 528/2012, Annex VI)	Assessment Report (link)
Pyriproxyfen (18)	Flies: e.g. house fly – *Musca domestica*, stable fly- *Stomoxys calcitrans* Mosquitoes: including *Culex pipiens*, *Aedes aegypti*, *Aedes albopictus*, *Aedes togoi* and *Anopheles dirus*	1) Controlling flies in farm applications such as cattle pens, pig houses and poultry houses 2) Controlling flies also in waste treatment facilities, i.e. municipal waste tips 3) Controlling mosquitoes in both running and standing water	0.05–0.1 mg/a.s. per L (tested only on *C. pipiens* and *A. togoi* and only in shallow standing water)	H400: Aquatic Acute 1. H410: Aquatic Chronic 1	1) STP: **NO risk** 2) Surface waters: a) NO risk (from indirect emissions via the STP is expected for use in cattle and pig animal housings) b) RISK (if direct application to surface water) c) RISK (in poultry housing with release via the STP to surface water) 3) Sediment: RISK 4) Soil: RISK (if used in running water) 5) Groundwater: **NO risk** 6) Primary poisoning: **NO risk** 7) Secondary poisoning: **NO risk**	http://dissemination.echa.europa.eu/Biocides/ActiveSubstances/0061-18/0061-18_Assessment_Report.pdf

Active substance (product type)	Target species	Intended uses	Application/dose rate (i.e. efficacy*)	Hazard statements (According to Reg. No 1272/2008[a])	Risk characterisation ratios (according to REG No 528/ 2012, Annex VI)	Assessment Report (link)
Transfluthrin (18)	Mosquitoes e.g. *Culex pipiens* (House mosquito), *Aedes aegypti* (Yellow fever mosquito) and *Aedes albopictus* (Tiger mosquito) Adult stages controlled Mosquitoes e.g. *Culex pipiens* (House mosquito), *Aedes aegypti* (Yellow fever mosquito) and *Aedes albopictus* (Tiger mosquito) Adult stages controlled Mosquitoes e.g. *Culex pipiens* (House mosquito), *Aedes aegypti* (Yellow fever mosquito) and *Aedes albopictus* (Tiger mosquito). moth (*Tineola bisselliella*) Adult stages controlled	Indoor/outdoor, Battery-operated fan vaporiser/ Coil	1 mg/a.s. per m^3 (mosquito coil and vaporiser)	H410: very toxic to aquatic life with long-lasting effects	1) STP: **NO risk** 2) Surface water & Sediment: a) RISK (if used raid portable electric and baygon mosquito coil) b) **NO risk** (if used Turbo 4 Seasons) 3) Soil: a) RISK (indoor and outdoor use of raid portable electric and baygon mosquito coil) b) **NO risk** (if used Turbo 4 Seasons) 4) Primary poisoning: **NO risk** 5) Secondary poisoning: **NO risk**	http://dissemination.echa.europa.eu/Biocides/ActiveSubstances/1404-18/1404-18_Assessment_Report.pdf
Decanoic acid (19)	Mosquitos of the family of Culicidae	Ready to use lotion intended for general public (non-professional use, adults) to spread over skin to repel insects and prevent them from biting	0.588 mg a.s./person referring to 6 g b.p./person (applier: adult)	H226: flammable liquid and vapour H319: causes serious eye irritation	1) AIR: **NO risk** 2) STP: **NO risk** 3) Surface water & Sediment: **NO risk** 4) Soil: **NO risk** 5) Secondary poisoning: **NO risk**	http://dissemination.echa.europa.eu/Biocides/ActiveSubstances/1287-19/1287-19_Assessment_Report.pdf

Active substance (product type)	Target species	Intended uses	Application/dose rate (i.e. efficacy*)	Hazard statements (According to Reg. No 1272/2008[(a)]	Risk characterisation ratios (according to REG No 528/ 2012, Annex VI)	Assessment Report (link)
Ethyl butylacetylaminopropionate (19)	Mosquitoes: *Anopheles* sp., *Aedes* sp., *Culex* sp., *Mansonia* sp. Ticks: *Ixodes* sp. Lice: *Pediculus* sp. Flies: *Stomoxys* sp., Simuliidae, Tabanidae, Musca sp., *Phlebotomus* sp. Wasps: *Pollistes* sp.. Bees: *Avis* sp	Direct application to skin by the consumer. Products used for other applications than to human skin (i.e. application to human hair, textiles and insect nets, surfaces households, or to animal skin/fur) may also be relevant for product authorisation	3,000 mg of model formulation is sufficient to cover approximately 50% of the total body surface of an adult	H319: causes serious eye irritation	*ONLY INDOOR SCENARIO* 1) AIR: **NO risk** 2) STP: **NO risk** 3) Aquatic compartment: **NO risk** 4) Groundwater: a) RISK (1st tier) b) **NO risk** (2nd tier)	http://dissemination.echa.europa.eu/Biocides/ActiveSubstances/1320-19/1320-19_Assessment_Report.pdf
Lauric acid (19)	Hard ticks (*Ixodes ricinus*)	Skin treatment with lotion	3,000–4,000 mg a.s./m^2 skin	H400: very toxic to aquatic life H315: causes skin irritation H318: causes serious eye damage	1) AIR: **NO risk** 2) Aquatic Compartment including Sediment: **NO risk** 3) Terrestrial Compartment including Groundwater: **NO risk** 4) Secondary Poisoning: **NO risk**	http://dissemination.echa.europa.eu/Biocides/ActiveSubstances/1323-19/1323-19_Assessment_Report.pdf
N,*N*-diethyl-meta-toluamide (19)	Biting flies, biting midges or black flies (Ceratopogonidae, Simuliidae), chiggers, deer flies, no-see ums, gnats, horse flies (Tabanidae), mosquitoes (Culicidae), fleas	Aerosol spray, direct dermal application	NA	H412: Aquatic Chronic 3 H302: harmful if swallowed H315: causes skin irritation H319: causes serious eye irritation	**NO risk** to any of the environmental compartments	http://dissemination.echa.europa.eu/Biocides/ActiveSubstances/0023-19/0023-19_Assessment_Report.pdf

*: Efficacy of products will be assessed thoroughly at the stage of product authorisation. Moreover the conclusion was reached within the framework of the uses that were proposed and supported by the applicant (see each Assessment Report, Appendix II). Extension of the use pattern beyond those described will require an evaluation at product authorisation level in order to establish whether the proposed extensions of use will satisfy the requirements of Article 5(1) and of the common principles laid down in Annex VI to Directive 98/8/EC).

**: EED= Expected Environmental Density. PNED=predicted no-effect density.

(a): Regulation (EC) No 1272/2008 on classification, labelling and packaging of substances and mixtures, amending and repealing Directives 67/548/EEC and 1999/45/EC, and amending Regulation (EC) No 1907/2006.