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# Lumpy Skin Disease Risk Assessment

**A qualitative assessment on  
unregulated pathways**

Prepared for the Department of  
Agriculture, Fisheries and Forestry  
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## Abbreviations and acronyms

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<b>Abbreviation</b>	<b>Definition</b>
ABS	Australian Bureau of Statistics
AHAW	Animal Health and Welfare
BTV	bluetongue virus
COVID-19	Coronavirus disease 2019
the Department	Department of Agriculture, Water and the Environment
DNA	deoxyribose nucleic acid
FAO	Food and Agriculture Organization
FAOSTAT	FAO database on food and agriculture statistics
HDI	human development index
LSD	lumpy skin disease
LSDV	lumpy skin disease virus
MARS	Maritime Arrivals Reporting System
NAQS	Northern Australia Quarantine Strategy
PNG	Papua New Guinea
Ro-Ro	roll-on, roll-off
SA2	Statistical area level 2
SA4	Statistical area level 4
TSIS	Torres Strait Information System
VCS	Vessel Compliance Scheme
WOAH	World Organisation for Animal Health (formerly the Office International des Épizooties (OIE))

# Executive summary

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## Introduction

Lumpy skin disease (LSD) is a highly contagious disease of cattle and water buffalo caused by the capripoxvirus *Lumpy skin disease virus* (LSDV). While several modes of transmission of LSDV are recognised, it is widely accepted that the primary transmission route is mechanical through arthropods, with longer-distance spread facilitated by the movement of animals (Chihota *et al.*, 2001; Tuppurainen and Oura, 2012; Namazi and Tafti, 2021). Since 2021, LSDV has spread rapidly through Southeast Asia and was reported from Indonesia in 2022, increasing concerns of it entering Australia (World Organisation for Animal Health, 2022).

In a recent expert judgement exercise, specialists estimated there was a 28 percent chance of an LSD outbreak occurring in Australia in the next five years (Centre of Excellence for Biosecurity Risk Analysis, 2022). Given the complexity of entry and exposure pathways, as well as the magnitude of the consequences, it is prudent to further assess the risk of LSDV being introduced to Australia.

While several risk mitigation measures have already been, and continue to be, implemented, formal risk assessment allows for targeting of approaches, ensuring that available resources are allocated most efficiently and that the risk is systematically assessed. With this in mind, Ausvet Pty Ltd was commissioned to conduct a qualitative risk assessment on four specific unregulated pathways (including 'leakage' from regulated pathways) for entry of and exposure of LSDV in Australia. The four selected pathways were: 1) windborne dispersal of arthropod vectors, 2) commercial vessels carrying hitchhiker arthropod vectors (excluding live export vessels), 3) returning live export vessels carrying hitchhiker arthropod vectors, and 4) Torres Strait Treaty movements carrying hitchhiker arthropod vectors (Figure 1).

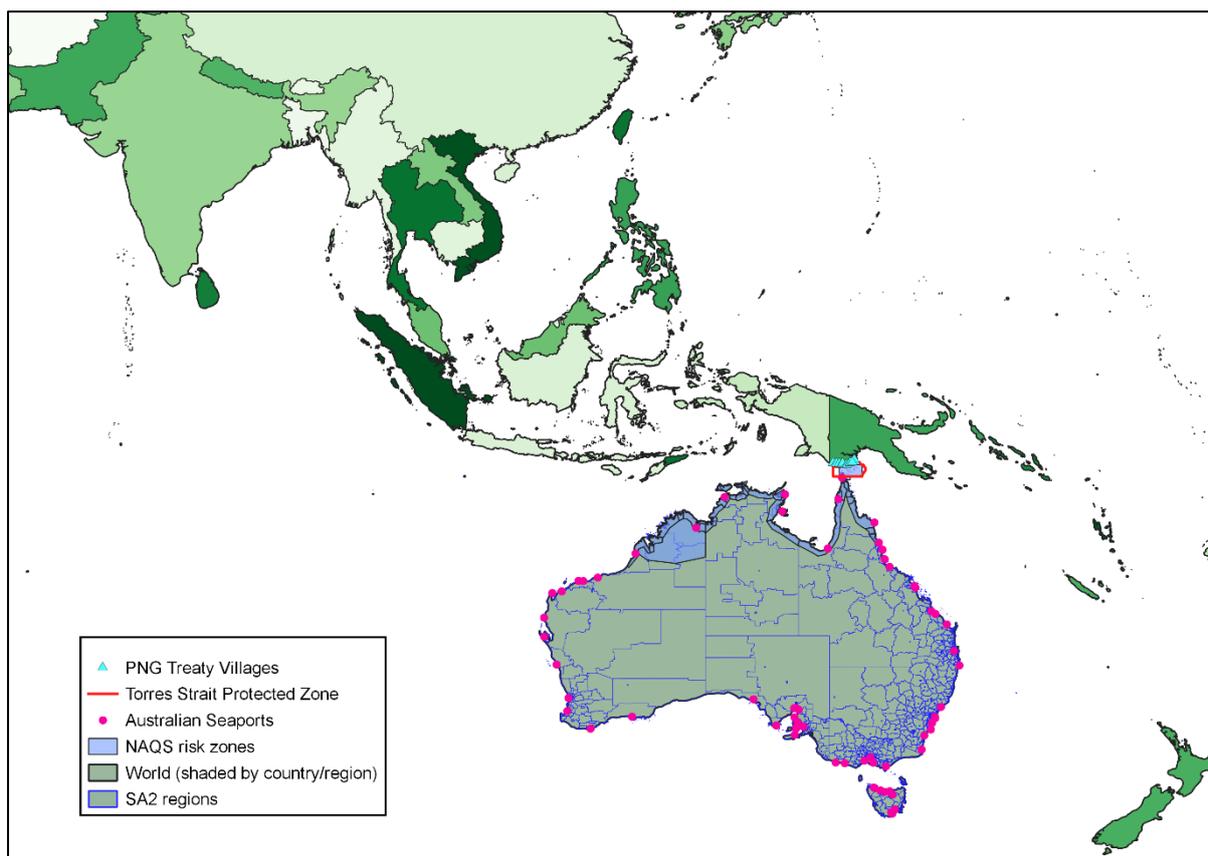


Figure 1 Map showing region of interest for this analysis.<sup>1</sup>

## Methodology

We consulted several expert entomologists and additional subject matter experts and conducted a systematic literature review on LSDV and approaches to animal health risk assessment before designing our methodology. The four pathways selected were chosen after extensive consultation with staff of the Department of Agriculture, Water and the Environment (DAWE).

We determined that three specific vector groups could potentially carry LSDV into Australia: midges, mosquitoes and ‘heavy fliers’ (principally, *Stomoxys* spp. but also *Musca* spp. and tabanids). We used spatial analysis to select countries of origin and destinations of entry based on distances derived from expert opinion and the published literature. For example, for windborne dispersal, expert entomologist opinion informed by the literature suggested that the realistic maximum dispersal distance for any vector capable of transmitting LSDV was 500 km. While reports in the literature have suggested longer-distance dispersal, particularly of *Culicoides* midges (Ducheyne *et al.*, 2007; Eagles *et al.*, 2014), we used the range

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<sup>1</sup> Individual countries are shown in different shades of green. Indonesia is subdivided into western, central and eastern regions. Torres Strait Treaty villages (in PNG) are shown as cyan triangles. The boundary of the Torres Strait Protected Zone is shown in red. Australian seaports are represented by pink dots. NAQS risk zones are shown as blue filled areas. Blue outlines within Australia represent SA2 boundaries.

suggested by the expert entomologists for this assessment. Thus, we included all countries within 500 km of the Australian mainland.

Scenario trees were developed for each of the four potential pathways and data were sought to inform the allocation of a qualitative likelihood at each node, reflecting the probability of each event of the scenario tree occurring. The qualitative likelihood categories were negligible, extremely low, very low, low, moderate or high.

Qualitative likelihoods for each pathway were combined using a matrix approach, modified from those described previously (European Food Safety Authority, 2007a; Peeler and Thrush, 2009a). Likelihoods at each node were iteratively combined to derive a final combined likelihood for each combination of origin country, arrival destination and vector category for each pathway.

Results from preliminary qualitative analysis indicated significant range compression (Peeler and Thrush 2009), largely due to the insensitivity of the qualitative categories and conditional dependence of each node on a pathway to the preceding node, so a semi-quantitative approach to combining qualitative likelihoods was also taken.

To conduct semi-quantitative analyses, qualitative likelihood categories were deterministically assigned a maximum probability based on the respective qualitative risk category, derived from a previously reported conversion table (Biosecurity Australia, 2004). The probabilities associated with each node on a pathway were multiplied down the pathway to obtain a combined semi-quantitative likelihood for each pathway for each combination of origin country, arrival destination and vector category (Mauroy *et al.*, 2021).

Given the uncertainty associated with the assigned qualitative and semi-quantitative values, sensitivity analysis was performed by modifying key nodes within each pathway to assess how the likelihood of an LSDV incursion would change based on alternative parameter estimates (Delahay, Smith and Hutchings, 2009).

Overall, we determined that climate change projections were not likely to unequivocally increase any of the parameter estimates in our qualitative model. Thus, we did not re-evaluate our assessment for future climate scenarios.

## Results

### Qualitative

There were 108 unique combinations of origin country, arrival destination and vector category for the windborne dispersal pathway, 2,139 combinations for the commercial shipping (excluding live exports) pathway, 1,428 combinations for the returning live export vessels pathway and nine combinations for entry of insects via the Torres Strait Treaty pathway. All combinations across all four pathways returned a negligible likelihood of LSDV incursion using a matrix approach to combine qualitative likelihoods in the 3,684 individual pathways.

This finding (negligible for all pathways) is a direct result of:

- the low or very low likelihood of any one herd in a country of origin being symptomatically infected with LSDV at one time, noting that current evidence suggests that asymptomatic animals contribute minimally to vector-borne transmission of LSDV due to low titres of virus in the blood and skin (Sanz-Bernardo *et al.*, 2021)
- the low to moderate likelihood that a vector becomes infectious after taking a protein meal, noting that the entomology experts made this assessment after consulting peer-reviewed transmission studies (Carn and Kitching, 1995a; Chihota *et al.*, 2001, 2003; Sohler *et al.*, 2019; Issimov *et al.*, 2020; Sanz-Bernardo *et al.*, 2021). This likelihood varies between different vector categories.

- the negligible to extremely low bovine densities in regions of northern Australia where wind-dispersed vectors may be deposited
- the negligible cattle densities in Papua New Guinea (PNG), our closest neighbour
- the low likelihood that an infectious vector would land on a ship bound for Australia
- the very low to extremely low likelihood that an infectious vector would be able to disembark in an Australian port without detection
- the lack of biological transmission of LSDV, resulting in decreasing viral loads in vectors over time and no vertical transmission in vectors.

Figure 2 shows how iteratively combining nodes along each pathway (using a matrix approach) resulted in all pathways becoming negligible by the final node.

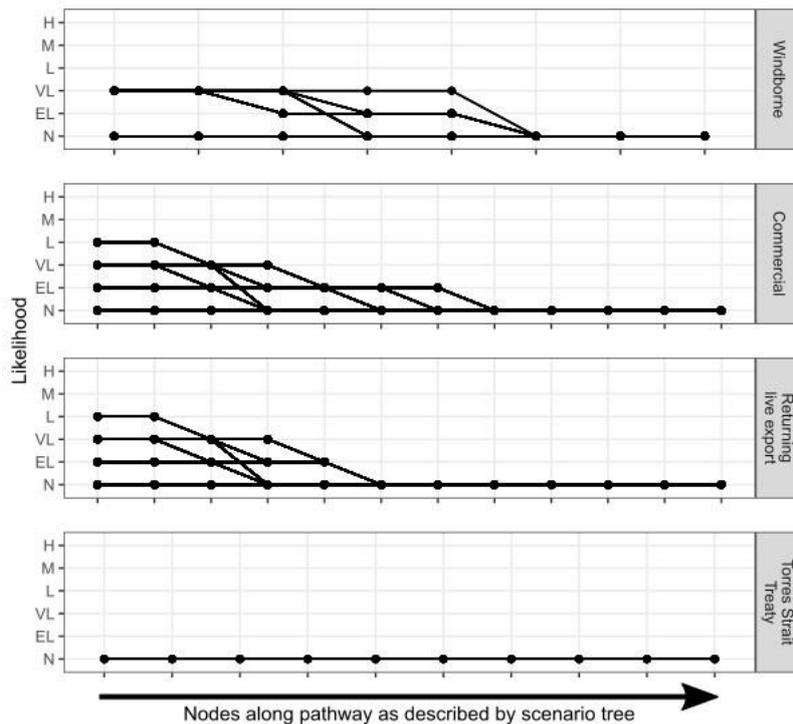


Figure 2 Cumulative qualitative likelihood at each node, by pathway<sup>2</sup>

Many of our individual node assessments had high levels of uncertainty, so to assess the sensitivity of our results we modified parameters at key nodes and re-evaluated the resulting qualitative likelihood outcomes.

Only for the windborne dispersal pathway did the final cumulative likelihood of LSDV importation change under our alternative scenarios. We explored the impacts of increasing cattle densities in the

<sup>2</sup> Qualitative likelihoods were iteratively combined over each node using the matrix described in the Methodology. The combined likelihood going into each node is shown. N negligible; EL extremely low; VL very low; L low; M moderate; H high. Some nodes are absent from the windborne dispersal pathway and Torres Strait Treaty pathway (see full results section for more information).

destination Northern Australian Quarantine Strategy (NAQS) risk zones to simulate local heterogeneities in cattle populations in these regions. When we increased livestock densities in every region by two categories, the following combinations yielded a cumulative qualitative likelihood of LSDV incursion of ‘extremely low’:

- midges from central Indonesia to W3, W4, W5
- midges from eastern Indonesia to N10, N1a, N8a, N8b, N9, Q6a
- heavy fliers from eastern Indonesia to Q1a, Q1b, Q2.

When we increased livestock density by three categories, the following combinations were associated with an extremely low risk (in addition to those just described):

- midges from eastern Indonesia to N2a, N2b, N3, N4, N5, N6, N7, Q1a, Q1b, Q2, Q3, Q4a, Q4b, Q5a, Q6b, Q6c
- midges from Timor-Leste to N7
- heavy fliers from eastern Indonesia to N3, N5, N6, N7, Q3, Q4a, Q6b, Q6c.

Even when increasing livestock density by three likelihood categories, the LSDV incursion risk by windborne dispersal did not exceed ‘extremely low’.

### **Semi-quantitative**

To better discriminate between the different combinations of origin country, destination and vector category within a pathway, we assigned maximum probabilities to qualitative likelihood categories and multiplied these to give differential risk rankings (a semi-quantitative approach). Results from different pathways cannot be objectively compared because longer pathways will always give lower results due to the mathematics of multiplying proportions. However, results within each pathway can be compared to determine the vector group, origin and destination associated with the greatest risk.

In summary, pertinent findings for the four pathways when assessed semi-quantitatively were:

#### **Windborne dispersal**

- Likelihood estimates were higher for midges, relative to mosquitoes and heavy fliers, due to midges being assessed as more likely to be transported via wind.
- NAQS risk zones W3, W4, W5, N10, N1a, N8a and b, N9 and Q6a were found to be the destinations at highest risk, due to higher cattle densities in these areas.
- Q1a, Q1b and Q2 were identified as destinations of higher risk for heavy fliers only, due to heavy fliers being considered more likely to bite cattle and for this bite to result in viral transmission, as well as the short travel distance to PNG from these risk zones.
- There were more NAQS risk zones within a 500 km radius of eastern Indonesia than for the other regions assessed.
- Notably, NAQS risk zones are confined to the coastline and vectors may be dispersed further inland.

#### **Commercial shipping (excluding live export)**

- Likelihood estimates were broadly similar across all vector categories but varied depending on country of origin.
- Timor-Leste, India, Viet Nam, Thailand, Cambodia, the Philippines, Myanmar, Laos, Indonesia and Sri Lanka generally were the countries of origin associated with the highest risk. These are the closer countries to Australia, with the exception of PNG where the lower cattle population downgraded the associated risk.
- It was difficult to compare destination seaports as the analysis did not account for the volume of shipping traffic between origin country and destination, so ports that were in statistical areas with

higher cattle densities ranked highly, even if they don't receive many international arrivals, e.g. Launceston and Hobart.

### **Returning live export vessels**

- Combinations associated with higher risk were similar to those seen in the commercial shipping (excluding live export) pathway.
- Overall, likelihoods for the returning live export vessels pathway were slightly lower than those estimated for the commercial shipping (excluding live export vessels) pathway. This was driven by the 'extremely low' likelihood of vectors disembarking without being detected, due to the inspections and decontamination procedures in place for these vessels. Other commercial ships were classified as 'very low' since cleaning protocols are less stringent on these vessels. This highlights the importance of the risk mitigation procedures already in place for returning live export vessels.

### **Torres Strait Treaty**

- The cattle density in PNG is very low, and was considered 'negligible' by our criteria.
- The highest likelihoods in this pathway were associated with heavy fliers, followed by midges and then mosquitoes.
- All NAQS risk zones assessed returned the same likelihoods, since cattle densities are negligible in all three zones.

## **Discussion**

Based on our qualitative risk assessment methodology, the risk of LSDV entry into Australia via the four pathways assessed was found to be negligible. This finding is encouraging, but contrasts with a recent expert judgement exercise where the probability of an incursion in the next five years (from any pathway) was estimated to be 28 percent (Centre of Excellence for Biosecurity Risk Analysis, 2022). Importantly, in contrast to viruses such as bluetongue virus (BTV), which undergo biological replication within the insect host, it is unlikely that the introduction of a single infectious vector would result in LSDV establishing in Australia because a swarm of insects is widely considered to be necessary to initiate a bovine infection (Yeruham *et al.*, 1995; Chihota *et al.*, 2003; Kahana-Sutin *et al.*, 2017; Sohler *et al.*, 2019; Issimov *et al.*, 2020; Sanz-Bernardo *et al.*, 2021).

Critically, this analysis formally assesses the likelihood of a single event leading to an introduction. Practically speaking, if a large enough number of vectors are imported, even an event with a negligible likelihood of occurrence may still occur. This qualitative risk assessment does not consider the volume of vectors imported because, once volumes are introduced, the analysis becomes quantitative and more detailed data are required. Given the magnitude of the consequences for an LSDV introduction, a quantitative analysis that accounts for annual vector volumes and therefore provides a meaningful unit of measure is recommended. We are currently conducting a quantitative analysis that will incorporate vector volumes by using data such as shipping numbers and modelling approaches such as HYSPLIT to investigate patterns of windborne dispersal.

Because of the range compression that occurred in our qualitative risk assessment, we also conducted a semi-quantitative assessment. Semi-quantitative approaches may offer a more consistent way of evaluating risks compared to a qualitative approach, avoiding some of the ambiguities and range compression without requiring the detailed data or mathematical skills needed for a quantitative approach (European Food Safety Authority *et al.*, 2020). We based our methodology on a previous semi-quantitative analysis for the introduction of African swine fever virus into Belgium (Mauroy *et al.*, 2021). However, we chose to use probability values, rather than a Likert scale as previously reported, because of the known limitations to combining ordinal values (Krisper, 2021). We note that the distribution of probability

ranges that we used is arbitrary and applied equally to all parameters, which may not represent the underlying processes appropriately (Krisper, 2021). In addition, this semi-quantitative approach also does not account for ‘the weakest link’ concept. Practically speaking, an event at a specific node is contingent on outcome of the previous nodes. However, in this semi-quantitative analysis the nodes are simply multiplied together. Therefore, if the likelihood of one event in the chain is negligible but the likelihood of other events in the chain are high, the overall likelihood score may be overestimated, when in reality the pathway is negligible because the ‘weakest link’ in the pathway has a negligible likelihood of occurring.

Lastly, we noted considerable uncertainty around several parameters. Any risk assessment is only as robust as the data used to inform it. For this reason, we identified several priority areas for future research. These included a better understanding of:

- the role of single insects in LSDV transmission. In other words, answering the question ‘is a single infectious vector sufficient to transmit LSDV to a bovine?’
- the true prevalence of symptomatic LSD in both endemic regions and over the course of an outbreak to define how many insects are likely to be infectious over a given time period
- the likelihood of vector species travelling long distances by wind and the likelihood that these vectors would survive such a journey
- the frequency with which arthropods of different species disperse to ports and land on ships
- livestock numbers in NAQs risk zones or equivalent regions with more relevance to animal health (as opposed to the statistical areas used by the Australian Bureau of Statistics)
- the strengths and limitations of semi-quantitative risk assessment.

## Conclusion

Using qualitative and semi-quantitative approaches, the risk of a LSDV incursion into Australia via the four pathways assessed appears to be limited. This is especially true in the current context where the disease burden in neighbouring countries is low.

It is important to note that the parameters used in this assessment are subject to uncertainty and may change over time because of changes in circumstance and context and as new data become available.

Current mitigation measures, such as insecticide treatments of incoming vessels, contribute to the management of this risk and must be maintained and adapted as the disease situation changes in potential origin countries.

# 1 Introduction

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## 1.1 Background

Lumpy skin disease (LSD) is a highly contagious disease of cattle and water buffalo caused by *Lumpy skin disease virus* (LSDV), a double-stranded DNA virus in the family *Poxviridae*, genus *Capripoxvirus* (Tuppurainen *et al.*, 2017; Issimov *et al.*, 2020). Clinically, the disease is characterised by generalised nodular skin lesions, fever, lymph node enlargement, a drop in milk production and poor reproductive performance (Khan *et al.*, 2021). Affected farmers experience severe economic losses through a sharp decline in milk yield, reduced milk quality, hide damage, reduction in body weight, abortion, infertility and, in rare cases, death of animals (Babiuk *et al.*, 2008). Typically, morbidity in diseased herds is low to moderate, ranging from 5–20%; however, rarely it can approach 100% (Woods, 1988; World Organisation for Animal Health, 2010; Tuppurainen and Oura, 2012).

For many years, LSD could be attributed to two distinct genetic lineages of the virus: field isolates and live attenuated vaccine strains (Calistri *et al.*, 2018). However, in Russia in 2017 and 2019 recombinant variants were found comprising genomic regions of both the Neethling vaccine strain and field isolates, which highlighted concerns with the use of live attenuated vaccines (Sprygin *et al.*, 2018, 2020; Aleksandr *et al.*, 2020). The impact of the recombination on the virulence and transmission capacity of LSDV remains unclear and is the subject of ongoing work (Sprygin *et al.*, 2018).

LSD was first reported in Zambia in 1929 but spread quickly within Africa (Morris, 1930; Khan *et al.*, 2021). The virus was largely contained to the African continent until 1984 when it moved into the Middle East (House *et al.*, 1990; Davies, 1991; Tuppurainen and Oura, 2012). In 1989 the virus spread to Israel, and over the following years, the virus continued to spread across contiguous countries throughout the Middle East, moving westerly into Iran and into other central Asian countries (Yeruham *et al.*, 1995; European Food Safety AHAW Panel, 2016). In 2015, the disease first emerged in Europe, spreading to several countries, but it was effectively controlled through mass vaccination (European Food Safety, 2018). Since 2017, Russia is the only country on the European continent to report outbreaks of LSD (World Organisation for Animal Health, 2022).

Since 2019, the spread of LSDV has increased in Asia. China reported its first outbreak in August 2019, with the virus later spreading to Taiwan by unknown means (Gupta *et al.*, 2020; Lu *et al.*, 2021). Outbreaks occurred in feral cattle in Hong Kong in October 2020 (Flannery *et al.*, 2021). In southern Asia, India first reported the disease in August 2019 (Gupta *et al.*, 2020; Kumar *et al.*, 2021). Similarly, Bangladesh reported the disease in July and September of 2019 (Gupta *et al.*, 2020). Nepal experienced their first outbreak of LSD in June 2020 (Acharya and Subedi, 2020). Sri Lanka and Bhutan reported outbreaks in September 2020 (Azeem *et al.*, 2022).

In Southeast Asia, the disease was reported for the first time in Laos, Thailand, Cambodia, Viet Nam and Malaysia in 2021 (World Organisation for Animal Health, 2022). Indonesia reported their first outbreak on 2 March, 2022 (World Organisation for Animal Health, 2022). In most cases, anecdotal reports preceded official reports, a typical occurrence in the region (Smith *et al.*, 2015). The Indonesian outbreak has thus far been restricted to Java, to the authors' knowledge. Presumably, LSDV spread across the narrow Malacca straight from Malaysia to Indonesia via windborne dispersal of vectors and/or movement of infected animals. Although the key drivers of cattle movements are typically from east to west, from rural areas to central locations like Jakarta on Java Island (M. Patching, Boralis group, pers. comm.), spread of other notable livestock diseases (such as classical swine fever) in the past has been observed from west to east (Sawford, 2015). Singapore also reported the disease for the first time in 2022 (World

Organisation for Animal Health, 2022), despite being considered to be at negligible risk of incursion with low uncertainty, based on a qualitative risk assessment conducted by the Food and Agriculture Organization (FAO) in 2020 (Roche *et al.*, 2020).

Since the earliest outbreaks of LSD in Africa, the movement of infected cattle along roads and railways and on foot has been associated with long-distance dispersal (Sprygin *et al.*, 2019). Concurrently, it was observed relatively early in southern Africa that outbreaks often occurred in isolated herds in the absence of any cattle movements, suggesting an alternative means of short-distance spread (Tuppurainen and Oura, 2012). It is now understood that transmission between animals can occur mechanically through arthropods, indirectly via contaminated feed and water, and through direct routes such as contact with saliva, secretions and semen (Namazi and Tafti, 2021). There is also limited evidence of intrauterine transmission (Rouby and Aboulsoud, 2016). Despite the diverse modes of transmission, it is widely accepted that the main route of transmission is via mechanical carriage in ectoparasitic arthropods, with longer-distance spread facilitated by the movement of infectious animals (Chihota *et al.*, 2001; Tuppurainen and Oura, 2012; Namazi and Tafti, 2021).

The importance of different arthropod vectors in the transmission of LSDV is likely to vary in different regions, depending on climate, season, humidity and vegetation (Berg *et al.*, 2015; Tuppurainen *et al.*, 2017). Interrupted feeders that regularly parasitise cattle and are found in high abundance are the best candidates for transmitting LSDV, but any protein-feeding arthropod species could play a role (Berg *et al.*, 2015). Midges, mosquitoes, heavy fliers (such as tabanids, *Musca* spp. and *Stomoxys calcitrans*) and ticks have all been suggested as potential vectors. There has been much work on identifying specific vectors capable of transmitting LSDV; however, the current scientific consensus is that the virus can be transmitted by most haematophagous insects. When assessing the risk of LSDV entering and establishing in the United Kingdom, Horigan *et al.* (2018) observed that

Whilst the competency of vectors in the [United Kingdom] is currently unknown, the fact that the disease has moved steadily up from southern African through many different climatic zones involving potentially many different vectors suggests that it is also likely to be transmitted by vectors present in the [United Kingdom].

Since this was written, the disease has also spread through Asia, further demonstrating that, in a practical sense, most countries (including Australia) are likely to have vector species capable of transmitting the disease.

The potential for wind-assisted spread of LSDV through long-distance dispersal of vectors has been proposed, especially following the LSD outbreaks that occurred in Israel in 1989 and 2006 (Yeruham *et al.*, 1995; Magori-Cohen *et al.*, 2012; Klausner, Fattal and Klement, 2017). In both outbreaks, Egypt was suffering from an exceptionally severe epizootic of LSD at a similar time and no other outbreaks were identified in the broader geographic region (Klausner, Fattal and Klement, 2017). Most cattle herds in Israel are closed and the borders are tightly controlled, due to conflict, so introduction of the disease through movement of infected cattle was considered highly unlikely (Klausner, Fattal and Klement, 2017). Phylogenetic analysis reportedly demonstrated that the Israeli isolate from the 2006 outbreak was identical to an isolate analysed from the 1989 outbreak in Egypt (Klausner, Fattal and Klement, 2017), although it seems unlikely that even a poxvirus would remain genetically stable over such a long period of time. As the sequences are not publicly available, it is not possible to verify this or to identify either the region of the genome that was sequenced or the length of the sequence fragment, both of which would affect the inferences that could be made from these data. Nonetheless, this work led the authors to suggest that these Israeli outbreaks occurred as a result of long-distance windborne spread of vectors (Klausner, Fattal and Klement, 2017).

There are several examples of long-distance transmission of other viruses through wind-assisted dispersal of vectors. Ritchie and Rochester et al. (2001) proposed that Japanese encephalitis virus was introduced to Australia by wind-blown *Culex* spp.. Others have suggested that bovine ephemeral fever spread from Korea to Japan via wind and that wind assisted in the spread of BTV in Europe (Shirakawa, Ishibashi and Ogawa, 1994; Hendrickx *et al.*, 2008). Eagles et al. (2014) reported the detection of several exotic *Culicoides* species associated with isolates of novel BTV from the ‘Top End’ of the Northern Territory. These specimens, collected as part of an active arbovirus surveillance program, were used to assess the plausibility of dispersal from neighbouring countries. A likely dispersal event was identified for five of the six cases examined with the source locations varying from Lombok to Timor-Leste and southern PNG (Eagles *et al.*, 2014). The detection of two exotic *Culicoides* species from Douglas Daly shows that dispersal beyond the Northern Australia Quarantine Strategy (NAQS) risk zones and closer to the seasonally variable National Arbovirus Monitoring Program *Culicoides* line is possible. However, no origin source outside Australia could be identified for this incursion, raising the possibility of spread from an initial undetected incursion site within Australia.

Ecological conditions favouring the spread of LSDV have been modelled using data from field outbreaks (Alkhamis and VanderWaal, 2016; Allepuz, Casal and Beltran-Alcrudo, 2019; Machado *et al.*, 2019). Because of the critical role of protein-feeding arthropods in LSDV transmission, it is no surprise that the distribution and spread of LSDV are heavily influenced by environmental conditions and landscape (Tuppurainen *et al.*, 2013; Abera *et al.*, 2015; Lubinga *et al.*, 2015; Alkhamis and VanderWaal, 2016). For example, temperature and humidity are known to be important factors influencing LSD occurrence, presumably due to the role of vectors in its transmission (Ardestani and Mokhtari, 2020). It is therefore logical to conclude that transmission dynamics of vector-borne diseases like LSDV could be affected by climate change through changes in vector survival, geographical range expansion and changes in vector activity, and host susceptibility to infection due to concurrent physiological stressors (Beebe *et al.*, 2013; Ali, Carlile and Giasuddin, 2020). Extreme weather events may also play a role, such as cyclones assisting windborne movement (Thornton *et al.*, 2009). Therefore, a consideration of the impacts of climate change is critical in assessing the risk of LSDV being introduced to new regions in the future.

## 1.2 Purpose of this risk assessment

The potential for LSDV to enter and establish in Australia is dependent on the probability of entry, along with environmental conditions and agricultural and landscape factors conducive to exposure at the point of entry (including livestock density). The probability of LSDV entry into Australia will increase as the disease spreads through our northern neighbours.

Like most countries, Australia is likely to have vector species capable of transmitting the disease. Furthermore, there are sufficient bovine populations and favourable environmental conditions to facilitate exposure and wider spread. Given the implications for trade, as well as the effects on production, the consequence of entry and exposure is assumed to be extreme.

Notably, bovine densities are relatively low in northern Australia; livestock trade and movement into Australia is stringently controlled and animal health surveillance systems are comparatively stronger than those seen in many Southeast Asian countries. Furthermore, a series of events (or steps along a risk pathway) would need to occur for entry and exposure to transpire.

Given the complexity of entry and exposure pathways, as well as the magnitude of the consequences, it is prudent to formally assess the risk of LSDV being introduced to Australia. To date, there is no risk assessment for LSDV being introduced to Australia. While several risk mitigation measures have already been, and continue to be, implemented, formal risk assessment allows for targeting of approaches and

ensures that the resources available are allocated most efficiently. In particular, risk assessment facilitates the systematic assessment of risk and implementation of risk-based surveillance.

## 2 Overall approach

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### 2.1 Risk analysis

#### 2.1.1 Theory of risk analysis

Risk analysis is an established discipline. In animal health, the key principles of risk analysis largely come from import risk analysis. However, these principles can be applied to other types of risk analysis, such as that associated with informal risk pathways.

Risk analysis has four related components: hazard identification, risk assessment, risk management and risk communication (Figure 3).

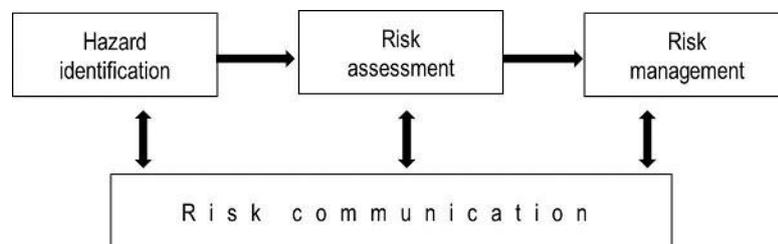


Figure 3 The four components of risk analysis (from the WOAH Terrestrial Animal Health Code)

Whilst hazard identification, risk assessment and risk management occur sequentially, risk communication should occur throughout the risk analysis process. This project concentrates on risk assessment for the hazard LSD.

#### 2.1.2 Risk assessment

Like risk analysis, risk assessment also has four components: entry assessment, establishment assessment, consequence assessment and risk estimation.

Entry assessment consists of describing the pathways necessary for the introduction of a hazard or pathogen into a new environment, and estimating the probability associated with those pathways. In the case of LSDV, this would involve describing the steps necessary for LSDV to enter Australia and estimating a probability of these steps occurring.

Exposure assessment consists of describing the pathways necessary for exposure of animals to the hazard or pathogen after entry and estimating the associated probability. For example, in the case of LSDV, exposure assessment may describe how a fly, fomite or infected animal carrying LSDV that has entered Australia could infect a susceptible species (e.g., cattle, buffalo, banteng), and the probabilities associated with this.

Consequence assessment involves evaluating the consequence of entry and exposure to the hazard or pathogen. Consequences can be direct (such as production losses) or indirect (such as the cost associated with a control or elimination program). For our assessment we have assumed, without conducting formal economic analyses, that introduction of LSD would have severe consequences for Australia's beef industry.

### 2.1.3 Qualitative and quantitative risk assessment

In qualitative risk assessment, likelihoods of an event and/or the magnitude of the consequences is expressed using qualitative descriptors such as ‘high’, ‘moderate’ or ‘low’. These are relatively simple to understand and easy to implement. Qualitative risk assessments are sufficient in most cases and can be followed by a quantitative assessment where further detailed insights are required (Murray and World Organisation for Animal Health, 2010).

In quantitative risk assessment, the likelihood of occurrence is expressed in numerical terms, such as ‘one disease introduction every 100 years’. Quantitative risk assessment requires additional quantitative data and can provide more detailed insights in circumstances where there are high levels of complexity and uncertainty. However, numerical results are often mistakenly considered to be highly precise, when the quality of the underlying data may in fact be comparable for qualitative and quantitative analyses. Thus, results of quantitative risk assessment should always be interpreted with caution (Murray and World Organisation for Animal Health, 2010). Often quantitative assessments encourage a more rigorous assessment by the requirement to outline specific probabilities at individual steps through the entry and exposure pathways. It is important for both qualitative and quantitative risk assessments to be transparent and to fully describe the underlying assumptions and data sources used for the analysis (Murray and World Organisation for Animal Health, 2010).

Semi-quantitative risk assessments involve assigning numbers to qualitative categories and combining these to generate an overall estimate of risk (Murray and World Organisation for Animal Health, 2010). Various approaches to semi-quantitative analysis have been published, however there are as yet no clear guidelines for semi-quantitative methodologies as there are for qualitative and quantitative assessments (Murray and World Organisation for Animal Health, 2010; De Vos *et al.*, 2019). While this method of quantification is generally no more objective or precise than a qualitative assessment, it is often considered very useful by risk managers because of the additional resolution provided over qualitative assessments (De Vos *et al.*, 2019).

## 2.2 Requirements of the Department of Agriculture, Water and the Environment

Originally, this project had two broad objectives: to develop a qualitative risk assessment for the entry of LSD into Australia via non-regulated pathways and to develop a general risk assessment framework for disease incursion. It was the intention of the Department of Agriculture, Water and the Environment (the Department) that the NAQS could use the general risk assessment framework to guide ongoing, regular risk assessments that inform their surveillance. Hence, it was originally intended that the framework be rigorous but free of complex software or methodologies that could not be routinely used by government epidemiologists.

When responding to the tender documentation, Ausvet Pty Ltd provided several options for additional, complimentary work, including simulation modelling of pathways for quantitative risk assessment. During the completion of this work, LSDV was detected in both Indonesia and Singapore, prompting the Department to request more detailed quantitative analyses. In addition, results from preliminary qualitative analysis indicated noteworthy range compression (Section 4.7.1) (Krisper, 2021), encouraging the authors to additionally provide a semi-quantitative assessment. Lastly, when pathways selected for analysis were explored in depth, the assessment was seen to have considerable complexity, requiring automation and coding beyond that originally intended.

### 2.2.1 Pathway selection

Potential pathways for the entry of LSDV are numerous and include both those that are heavily regulated, such as the importation of bovine products, and those that are less regulated or non-regulated, such as the movement of people, vessels and insects between Papua New Guinea (PNG) and northern Australia under the Torres Strait Treaty. Risk mitigation measures (including disease surveillance) can be more difficult, complex and expensive to implement on non-regulated pathways. Risk assessment of non-regulated pathways is therefore critical in appropriately allocating resources for risk mitigation activities. For these reasons, the Department determined that this risk assessment should focus on non-regulated pathways or so-called ‘leakage’ pathways; that is, the risk associated with gaps in regulated pathways. Since live animals and animal products are rarely transported into Australia and are strongly regulated, the risk pathways chosen focussed on the entry of infected arthropod vectors.

In consultation with the Department and NAQS, four pathways were selected for inclusions in this risk assessment:

1. windborne dispersal of arthropod vectors
2. commercial vessels (excluding live export vessels) carrying hitchhiker arthropod vectors
3. returning live export vessels carrying hitchhiker arthropod vectors
4. Torres Strait Treaty movements carrying hitchhiker arthropod vectors.

For more detail on how these pathways were selected, see Section 3.1.

### 2.2.2 Risk question

In this assessment we aimed to answer the following question.

‘Assuming a situation where LSDV is endemic throughout Asia (including Indonesia and Timor-Leste) and in PNG, what is the likelihood of it entering Australia through the four pathways outlined above?’

Although the risk question is ultimately based on a future scenario, we used current (or the most recently available) data for parameters such as bovine density and present risk mitigation approaches.

The resultant likelihoods expressed do not assume a specified and measurable unit, but rather a ‘hypothetical risk unit’ (MacDiarmid and Pharo, 2003). The likelihoods expressed can therefore only be compared to each other. Additional, quantitative analysis is required to determine a specific and measurable unit or rate of introduction.

## 2.3 Overall assumptions

From the outset, we assumed the consequences of entry and establishment of LSD in Australia to be extreme, due to its marked impacts on production and trade; therefore, in our proposal to the Department we proposed not conducting a specific consequence assessment. This scope was agreed by the Department.

As of May 2022, the nearest reports of LSDV to Australia were from Java Island, Indonesia. Many other parts of Indonesia, Timor-Leste and PNG remain free of LSDV. The risk of LSDV arriving from a country or region that is free from the disease is negligible. While the main risk pathways for long-distance spread are widely considered to be informal movements of infected live animals (Tuppurainen and Oura, 2012), most livestock movements in Indonesia occur when livestock from outer regions are transported to Jakarta (M. Patching, Boralis group, pers. comm.). This would presumably slow the spread of LSDV to our closer neighbouring regions, such as Timor-Leste and PNG, but we assume that these areas will be affected in time (Roche *et al.*, 2020). For example, classical swine fever virus spread from Malaysia down to Sumatra, Java, Kalimantan and other central Indonesia islands, and down into Timor-

Leste and PNG between 1994 and 2007 (Sawford, 2015). Therefore, we have conducted this assessment based on the assumption of disease being endemic throughout Southeast Asia and PNG.

We excluded Pacific Island countries (except PNG) and territories and island nations with a land area of <3000 km<sup>2</sup> from the analysis. We assume the risk of LSDV arriving in island countries of <3000 km<sup>2</sup> to be negligible (and therefore chose to exclude them from the analysis), partly because we know that ocean borders and relatively low livestock populations and trade volumes have historically kept these nations free of many infectious diseases of livestock (Brioude, 2016).

## 2.4 Definitions and terminology

For the purpose of this report, we use the following definitions for key terms:

**Risk** refers to the likelihood of occurrence and the likely magnitude of the biological and economic consequences of an adverse event or effect to animal or human health. This definition is presented in the Terrestrial Animal Health Code of the World Organisation for Animal Health (WOAH). The various components of risk analysis are discussed above.

**Probability** is a more general term that refers to how likely an event is to occur. In binomial probabilities, the likelihood of an event occurring summed with the likelihood of it not occurring is one (i.e. there are only two possible outcomes). However, there can be a different probability of the event occurring or not occurring, captured in our assessment with qualitative and semi-quantitative descriptors.

**Regulated pathways** refer to pathways for entry of a hazard that are heavily controlled through official processes, such as the arrival of passenger aircraft. These are excluded from our assessment.

**Non-regulated pathways** refer to pathways for entry of a hazard that are not heavily controlled through official processes or not controlled at all, such as windborne entry of insects. These are the focus of our assessment.

## 3 Methodology

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### 3.1 Determine pathways for inclusion

As discussed in Section 2.2, we took direction from the Department and NAQS on the most appropriate pathways for inclusion in this analysis. As previously discussed, risk assessment of non-regulated or 'leakage' pathways is critical in appropriately allocating resources for risk mitigation activities; hence these formed the basis of this analysis.

We consulted with the Department during the contracting stage of this work and during project inception to clarify pathways for inclusion. We presented draft pathways to a group of NAQS staff during a preliminary consultation meeting on 25 March (see Appendix 1), from which the final pathways were selected. We also conducted a review of the scientific literature to ensure that our pathways were clearly defined and plausible for the transmission of LSDV.

### 3.2 Determine vector categories for inclusion

As previously discussed, the importance of different arthropod vectors in the transmission of LSDV is likely to vary in different regions, depending on climate, season, humidity and vegetation (Berg *et al.*, 2015; Tuppurainen *et al.*, 2017). Interrupted feeders that regularly parasitise cattle and are found in high abundance are the best candidates for transmitting LSDV but any protein-feeding arthropod species may play a role (Berg *et al.*, 2015).

In the literature, categories of vectors are generally divided into brachyceran flies, mosquitoes, midges and hard ticks. Evidence for the involvement of tabanids (e.g., horse flies, soldier flies) in LSDV transmission is limited, while hard ticks are unlikely to be able to travel the distances required to carry LSDV into Australia in the absence of a host animal. For this reason, we limited our analysis to three groups of arthropod vectors: mosquitoes, midges and brachyceran flies (more specifically, 'heavy fliers', which include stable flies, house flies, blowflies, marsh flies and other members of the infraorder *Muscomorpha*). We excluded tabanids as there is limited evidence for their capacity to transmit the virus.

Flies are insects of the order *Diptera*, characterised by the use of only one pair of wings for flight and one for balance. The term 'fly' in common usage refers to any small flying insect, but in entomology the name refers specifically to around 125,000 species of dipterans or 'true' flies, which are distributed throughout the world. Technically, mosquitoes and midges are all part of the order *Diptera* and are therefore considered flies. However, in our analysis we consider 'heavy fliers' as insects of the infraorder *Muscomorpha* that are referred to as common 'flies'. These include *Stomoxys calcitrans* and *Musca* spp.

Mosquitoes are insects within the family *Culicidae*. There are approximately 3,500 species of mosquitoes, several of which transmit pathogens such as Zika virus, *Plasmodium* (which causes malaria) and dengue virus. Mosquitoes live in most parts of the world and are particularly attracted to areas with standing water, because the larval and pupal stages require water with little or no flow to survive (Centre for Disease Control and Prevention, 2022). Mosquitoes have long been suspected of playing a role in transmission of LSDV (Sprygin *et al.*, 2019).

While several families of dipterans are commonly referred to as midges, of most relevance to LSDV transmission is the family *Ceratopogonidae*. This family contains more than 5,000 species, including *Culicoides* spp, and are distributed worldwide on every continent except Antarctica (Boorman, 1993). *Culicoides* species are known vectors of diseases such as African horse sickness virus, BTV and epizootic haemorrhagic disease virus, and can be dispersed long distances by wind (Burgin *et al.*, 2013; Eagles *et al.*,

2014; Paslaru *et al.*, 2022). *Culicoides* midges have also been implicated in LSDV transmission (Chihota *et al.*, 2003; Eagles *et al.*, 2014; Şevik and Doğan, 2017; Sanz-Bernardo *et al.*, 2021).

For further information on studies related to the transmission of LSDV by specific vector categories, see the literature review on lumpy skin disease delivered previously as part of this project.

### 3.3 Use scenario trees to map pathways of interest

We used scenario trees to map the selected pathways of interest. Each node of the tree is binomial; that is, there are two potential outcomes.

We used the same methodology as reported in Biosecurity Australia's Generic Import Risk Analysis for Pig Meat for defining our scenario trees, although we used qualitative methods to combine risk down a pathway (Biosecurity Australia, 2004).

### 3.4 Identify potential data sources

We represented each of the four pathways with a scenario tree and transferred each scenario tree into a tabular format. We then parameterised each table (or pathway). For some nodes there were several systematic possibilities that were repeated across pathways. For example, for vector-related nodes, there were three vector categories repeated across all pathways. This resulted in a different assessment for each vector for several nodes, such as the node 'vector becomes infectious after taking a protein meal'. For the origin node, there were different countries based on geographical proximity to Australia. This led to complexity in the number of assessments, with each risk pathway requiring assessment for different combinations of vector category, origin and destination.

Data were sought to inform the probability of occurrence at each node, based on each combination of country of origin, arrival destination and vector category over the four pathways. Diverse sources of data were used including the Australian Bureau of Statistics (ABS) 2016 agricultural census, published peer-reviewed and grey literature and publicly available information such as trade volumes. These are documented in the Results.

Where data were absent, expert opinion was sought. In particular, we consulted three entomologists: Dr Glenn Bellis, Dr Angus Sly and Dr Mike Muller. These experts were provided with a list of questions preceding a semi-structured interview. These questions asked for detailed probability estimates, which were then converted to qualitative likelihoods (Section 3.6, Appendix 2). The detailed probability estimates will also be available for quantitative assessment.

### 3.5 Spatial analysis

We used spatial analysis to select countries of origin and arrival destinations based on distances derived from expert opinion and the published literature. For example, for the windborne dispersal pathway expert entomologist opinion suggested that the realistic maximum long-distance dispersal range for midges was 500 km. Entomologists estimated mosquitoes and heavy fliers to have shorter maximum flight distances, at 180 km and 225 km, respectively (Hogsette and Ruff, 1985; Yeruham *et al.*, 1995; Showler and Osbrink, 2020). Thus, we considered all countries with a land border within 500 km of the Australian mainland to be potential points of origin for windborne transmission. We used NAQS risk zones as potential arrival destinations for the windborne dispersal pathway since these are of most relevance to surveillance and mitigation actions. A proximity table was generated to determine all countries within 500 km of a NAQS risk zone, based on the closest point between country/region

boundaries (not midpoints) and using ArcGIS Pro (version 2.8.6, geoprocessing tool ‘Generate Near Table’).

For commercial vessels, including returning live export vessels, expert entomologist opinion was that the most likely maximum arthropod survival time, where a vector would be physically able to bite a susceptible bovine host on arrival and still be infectious, was five days (discussed further in Results). Using a travel speed of 20 knots, we calculated that the maximum distance a returning live export ship could travel in five days (120 hours) is 4444.8 km. For other commercial vessels, using a travel speed of 25 knots, the maximum distance that could be covered is 5555 km. Using ArcGIS Pro’s geoprocessing tool ‘Generate Near Table’, a proximity table was generated to determine all countries within these distances of Australian seaports.

For both spatial analyses, we excluded Australian territories (Norfolk Island, Cocos (Keeling) Islands, Christmas Island, and Heard and McDonald Islands) and Antarctica. We excluded New Zealand because of their current animal disease status, high level of biosecurity controls and historical capacity to manage exotic disease incursions effectively (Davidson, 2002). We also excluded Pacific Island countries and territories and island nations with a land area of <3000 km<sup>2</sup>, with the exception of Singapore where LSDV has already been detected. We assumed the risk of LSDV arriving in island countries of < 3000 km<sup>2</sup> to be negligible, partly because we know that ocean borders and relatively low livestock populations have historically kept these nations free of many infectious livestock diseases (Brioude, 2016). Hong Kong special administrative region, China mainland, Macau and Taiwan were classified together as ‘China and associated autonomous regions’. Indonesia was divided into western, central and eastern regions for improved geographical resolution to enable nuanced risk assessment.

### **3.6 Assign qualitative values to nodes**

Based on the respective data sources for each node, data were converted to qualitative likelihood categories based on the descriptors and probabilities outlined in Table 1. Additional details on the assumptions for each node are discussed in the Results. For each node, we also qualitatively assigned the level of uncertainty as either ‘low’, ‘moderate’ or ‘high’. This incorporates both variability, due to the intrinsic stochasticity of the parameters, and uncertainty, stemming from lack of information about the ‘true’ value.

For expert opinions, we elicited ‘minimum’, ‘maximum’, and ‘most likely’ likelihoods for parameters of interest; the choice of value used for relevant parameters is detailed in the Results. Our approach to expert opinion was designed so that results could also be used for future quantitative analysis.

Table 1 Qualitative likelihood categories

Qualitative category	Numerical probability (Biosecurity Australia, 2004)	Description (Rinchen <i>et al.</i> , 2020)
High	0.7–1	Likelihood of an event occurring is very often
Moderate	0.3–0.7	Likelihood of the event occurring is regular
Low	0.05–0.3	Likelihood of the event occurring is occasional
Very low	0.001–0.05	Likelihood of the event occurring is rare but does occur
Extremely low	$10^{-5}$ –0.001	Likelihood of the event occurring is extremely rare but cannot be excluded
Negligible	0– $10^{-5}$	Likelihood of the event occurring is so rare that it does not merit consideration

### 3.7 Determine overall qualitative risk for each pathway

Data were processed in R version 4.1.3 (R Core Team, 2021) using the tidyverse v1.3.1 (Wickham *et al.*, 2019) and scales v1.2.0 (Wickham and Seidel, 2022) packages. The full code is available in Appendix 3.

Data for each of the parameters were cleaned as described in the Results and independent data sources were joined for downstream processing. Data frames were generated for each of the four pathways based on all combinations of origin country, arrival destination, and vector category (n = 2,139 for commercial ships (excluding live export vessels), n = 1,428 for live export ships, n = 108 for windborne dispersal, n = 9 for the Torres Strait Treaty pathway). These data frames were populated with qualitative categories for each node, as detailed in the Results.

#### 3.7.1 Qualitative analysis

Qualitative likelihoods were combined using a matrix approach, modified from those described previously (European Food Safety Authority, 2007b; Peeler and Thrush, 2009b) (Figure 4).

		Likelihood $n$					
		Negligible	Extremely low	Very low	Low	Moderate	High
Likelihood $n + 1$	High	Negligible	Extremely low	Very low	Low	Moderate	High
	Moderate	Negligible	Extremely low	Very low	Very low	Low	Moderate
	Low	Negligible	Extremely low	Extremely low	Very low	Very low	Low
	Very low	Negligible	Negligible	Extremely low	Extremely low	Very low	Very low
	Extremely low	Negligible	Negligible	Negligible	Extremely low	Extremely low	Extremely low
	Negligible	Negligible	Negligible	Negligible	Negligible	Negligible	Negligible

Figure 4 Cumulative likelihood matrix

Likelihoods at each node were iteratively combined to derive a final combined likelihood for each combination of origin country, arrival destination, and vector category for each pathway.

### 3.7.2 Semi-quantitative analysis

For semi-quantitative analysis, qualitative likelihood categories were assigned the maximum numerical probability from Table 1. These probabilities were multiplied together to obtain a semi-quantitative combined likelihood for each combination of origin country, arrival destination, and vector category for each pathway (Mauroy *et al.*, 2021). We chose to use discrete maximum probabilities, rather than the previously reported Likert scale, due to concerns around combining ordinal values (Krisper, 2021).

## 3.8 Sensitivity analysis

Following our initial analyses, we performed a local sensitivity analysis by modifying key nodes within each pathway to assess how the likelihood of an LSDV incursion would change based on alternative parameter estimates (Delahay, Smith and Hutchings, 2009). We specifically looked at nodes that were negligible or extremely low, resulting in a downgrading of cumulative risk early in the scenario tree, or nodes with high uncertainty. Outcomes were descriptively compared to the original outputs.

## 3.9 Potential impacts of climate change

We consulted the literature to better understand how our chosen parameters may change in a future climate scenario. Overall, we determined that climate change projections were unlikely to unequivocally increase any of the parameter estimates in our qualitative model. Thus, we did not re-evaluate our assessment for future climate scenarios.

## 4 Results

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### 4.1 Pathways for inclusion

Through our consultations with the Department and NAQS we identified four unregulated pathways for inclusion in the analysis of LSDV entry into Australia:

1. windborne dispersal of arthropod vectors
2. commercial vessels (excluding returning live export vessels) carrying hitchhiker arthropod vectors
3. returning live export vessels carrying hitchhiker arthropod vectors
4. Torres Strait Treaty movements carrying hitchhiker arthropod vectors.

#### 4.1.1 Windborne dispersal

Windborne transmission of vector-borne diseases is a major concern for northern Australia. This has been discussed in detail in the Background section.

Because of both evidence of other vector-borne diseases entering via wind and speculation that this has occurred with LSDV in other regions, the windborne pathway was included in this risk assessment as an unregulated pathway.

#### 4.1.2 Commercial vessels (excluding returning live export vessels)

Most vessels that arrive in Australia are commercial vessels. These includes bulk carriers, cruise vessels, tankers, container vessels and roll-on, roll-off (Ro-Ro) cargo ships. In this pathway we included all commercial vessels except cruise vessels and live export vessels (the latter was considered separately).

Bulk carriers are ships especially designed to transport unpackaged bulk cargo. They account for around 70 percent of all vessel arrivals into Australia (Inspector General of Biosecurity, 2017). Tankers are ships designed to transport liquids or gas in bulk and account for around 15 percent of vessels arrivals into Australia (Bureau of Infrastructure and Transport Research Economics, 2021). Container vessels are cargo ships that carry their load in truck-size intermodal containers. These make up less than 10 percent of all vessel arrivals in Australia (Bureau of Infrastructure and Transport Research Economics, 2021). Lastly, Ro-Ro cargo ships are designed to carry wheeled cargo, such as cars and trucks. These account for less than five percent of Australian vessel arrivals (Bureau of Infrastructure and Transport Research Economics, 2021).

Foreign fishing vessels and yachts (non-commercial) are assumed to arrive in insufficient volumes to pose a significant threat. Additionally, they spend extended periods of time at sea prior to landing, which is not conducive to arthropod survival.

Although commercial vessel entry is a regulated pathway, because of the potential for hitchhiker carriage of LSDV-infected arthropod vectors this pathway was considered an important potential source of 'leakage'.

#### 4.1.3 Returning live export vessels

We considered returning live export vessels in a separate pathway to commercial shipping, since their risk is likely to be different to other commercial vessels.

In 2021, 211 voyages carried live animals internationally (Australian Government Department of Agriculture, Water and the Environment, 2022). Of these, 185 voyages carried cattle and buffalo, with Indonesia receiving the most vessels of any country (51 vessels). The remaining 134 voyages were made to countries in the Middle East and Asia, with a relatively even distribution. These vessels were required to make return journeys to Australia.

Returning livestock vessels are subject to strict biosecurity risk mitigation measures on re-entry into Australia and hence this could be considered a regulated pathway. Every livestock ship undergoes a pre-arrival inspection and is thoroughly cleaned, disinfected with soda ash, and receives two insecticide treatments on arrival into Australia. However, because of the potential for hitchhiker arthropods to enter undetected, this pathway could be an additional important source of 'leakage'. Notably, returning live export vessels may be more attractive to biting insects than other commercial vessels due to their association with livestock, a source of blood meals.

#### 4.1.4 Torres Strait Treaty movements

The Torres Strait Treaty was implemented in 1985 and defines a border between Australia and PNG that allows for special provisions. One of these provisions is the free movement (without visas or passports) between Australia and PNG for traditional activities. This provision is only for Torres Strait Islanders and coastal people of PNG who live in and maintain traditions of the region. There are 13 PNG villages that have free movement privileges under the Treaty (Figure 5).

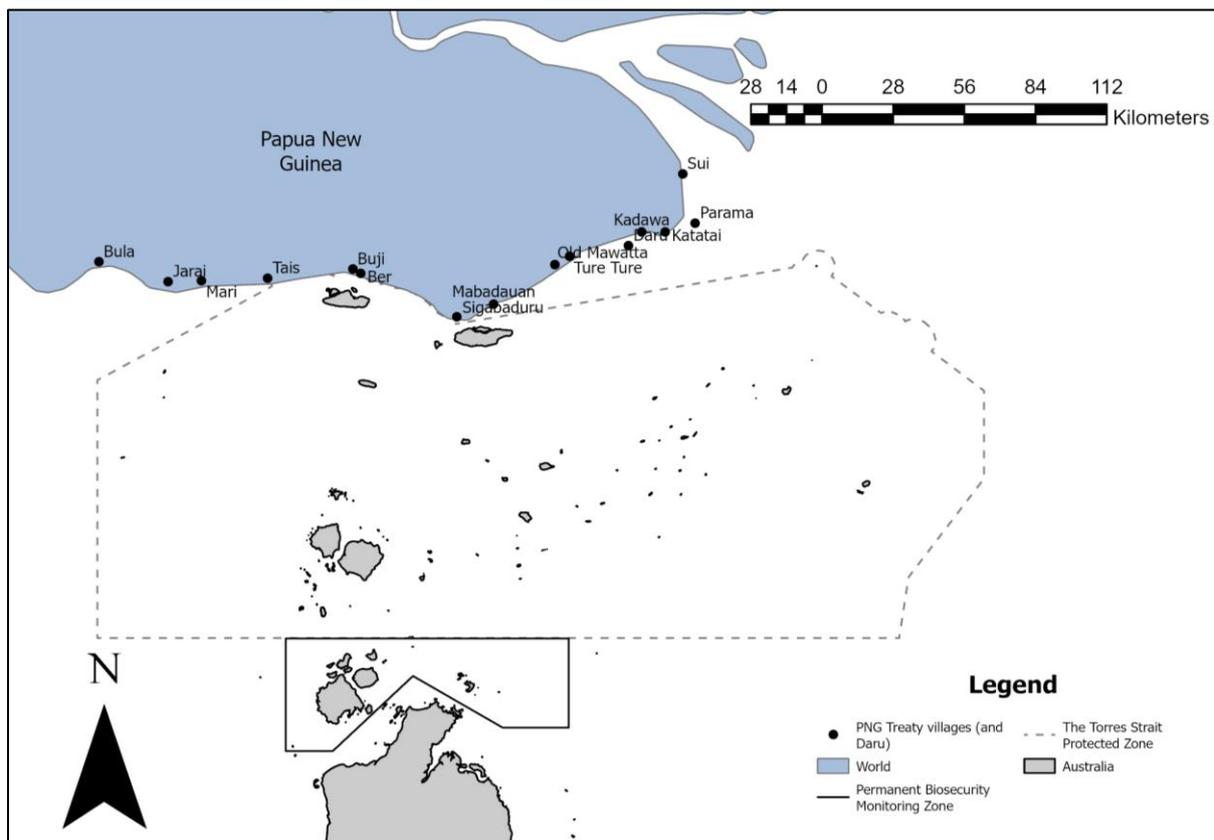


Figure 5 Torres Strait Treaty villages and associated zones

Due to COVID-19 and subsequent border closures, there have been minimal arrivals of people from Treaty villages since September 2021. In general, when these movements take place, a biosecurity officer

in the Torres Strait will inspect vessels and goods upon arrival; however, this pathway was considered a potential source of 'leakage' from an otherwise regulated pathway.

The TSIS (Torres Strait Information System) was first introduced in 2017 to facilitate issuing of permits for the movements of various goods, mainly dogs, soil and some plant material from the Torres Strait Protected Zone and the Torres Strait Permanent Biosecurity Monitoring Zone to mainland Australia. In February 2018 TSIS was expanded to include the recording of inspection data from various inspections from the above legislative zones and including those arrivals from the PNG Treaty villages.

When this pathway was discussed, there was some speculation around the risk of LSDV entering in animal hides brought ashore during these movements and further information was sought. TSIS was first introduced in 2017 to facilitate issuing of permits for the movement of various goods, mainly dogs, soil and some plant material from the Torres Strait Protected Zone and the Torres Strait Permanent Biosecurity Monitoring Zone to mainland Australia (A. Smith, DAWE, pers. comm.). In February 2018, TSIS was expanded to include recording of inspection data. Since the system was introduced in 2018, no bovine hides have been seized from PNG Treaty village arrivals (A. Smith, DAWE, pers. comm.). Hence LSDV entering in animal hides related to Treaty movements was not included as a potential pathway. Instead hitchhiking of insects was considered as the only plausible method.

## **4.2 Vector categories**

We chose to include three categories of vectors: mosquitoes, midges and heavy fliers. This was based on a review of the literature and discussion with the Department. Definitions of these categories and reasons for their selection are described in Section 3.2.

### 4.3 Scenario trees

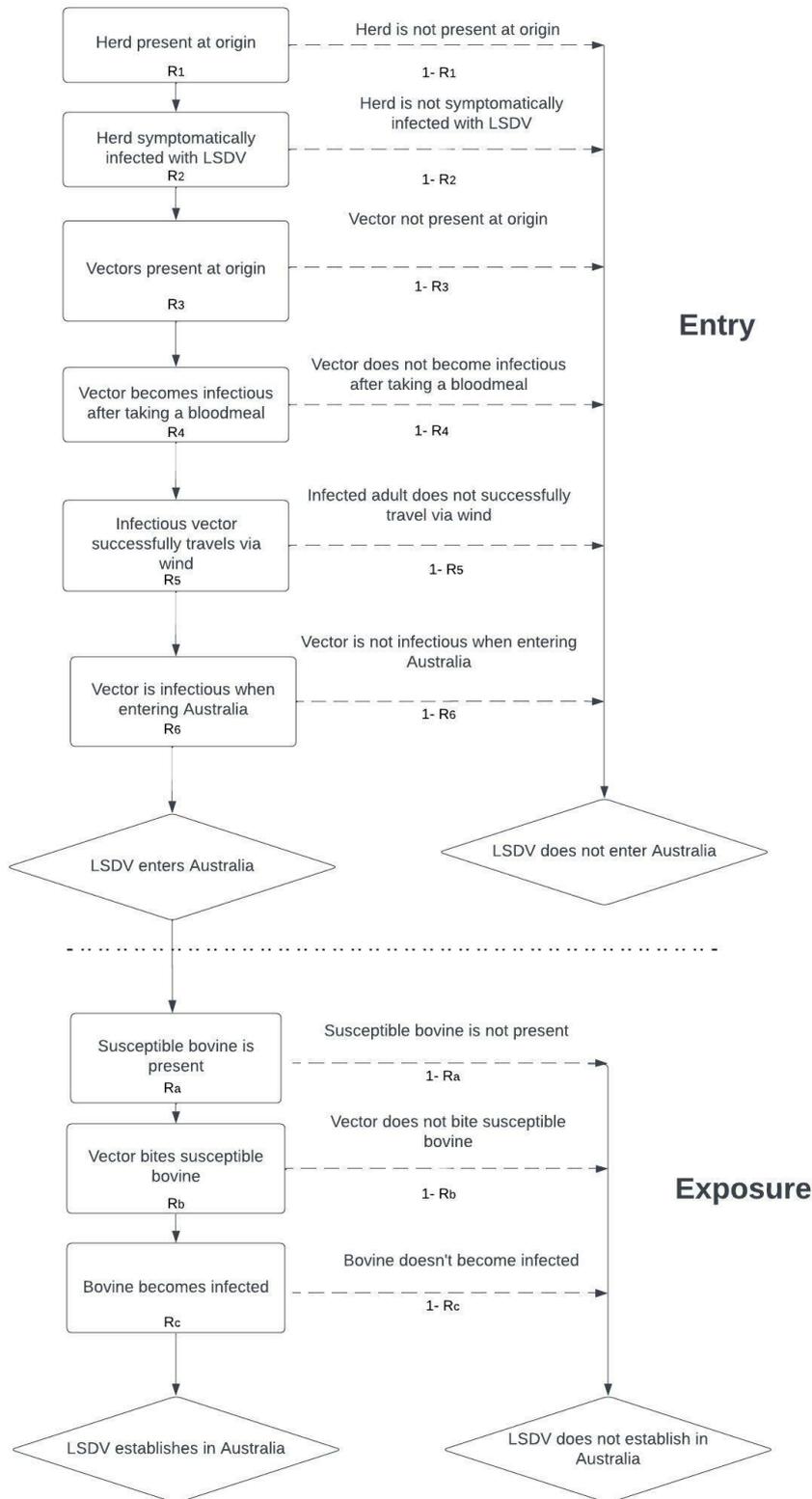


Figure 6 Scenario tree for windborne dispersal of LSDV-carrying arthropods into Australia

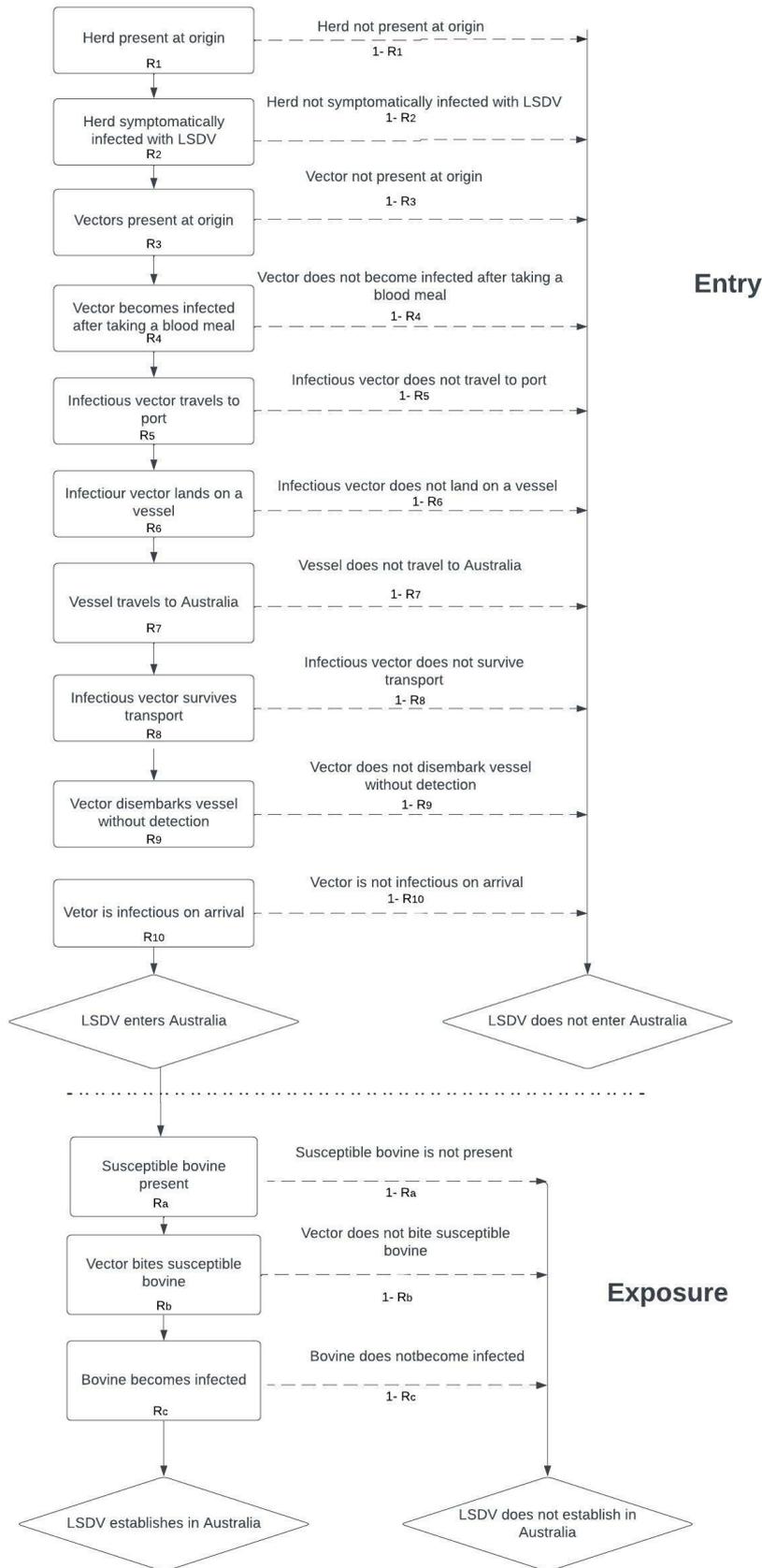


Figure 7 Scenario tree for transport of LSDV-carrying arthropods via commercial vessels (including returning live export ships)

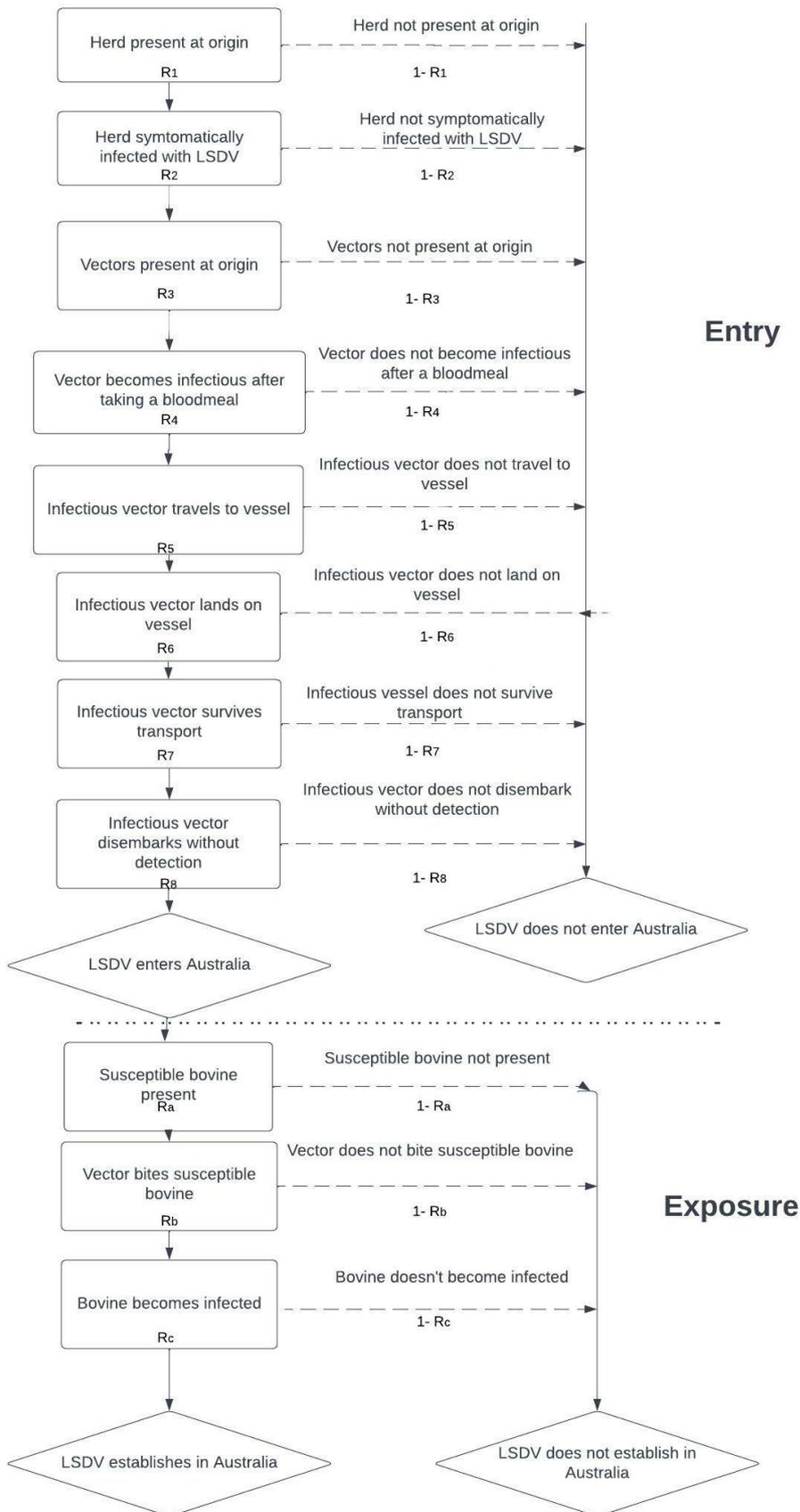


Figure 8 Scenario tree for transport of LSDV-carrying arthropods via Torres Strait Treaty movements

## 4.4 Data sources

We used a variety of data sources to inform the qualitative values assigned to each node. The reasoning and data source used for each assessment is described in Section 4.6.

## 4.5 Spatial analysis

### 4.5.1 Windborne dispersal

#### **R<sub>0</sub> Origin countries of interest**

*Countries included:* Indonesia, PNG and Timor-Leste

*Uncertainty:* Moderate

*Justification:* Our entomologists were asked to estimate the maximum distance arthropods from each vector category could travel over water, assuming wind assistance. They noted that maximum travel distances would vary between species within the broad vector categories. For example, *Culicoides brevitarsis* are known to travel over long distances, whereas other midge species, such as mangrove-breeding species, rarely travel far from their breeding sites. Thus, we asked our experts to consider the maximum travel distance for any species within the three vector categories, using the available literature. A realistic maximum dispersal distance for midges was estimated at 500 km. Mosquitoes and heavy fliers were estimated to have shorter maximum flight distances, at 180 km and 225 km, respectively (Hogsette and Ruff, 1985; Yeruham *et al.*, 1995; Showler and Osbrink, 2020). Importantly, evidence from the literature suggests that longer-distance dispersal is possible, particularly of *Culicoides* midges (Ducheyne *et al.*, 2007; Eagles *et al.*, 2014). However, our definition of eastern Indonesia included Lombok, which was previously reported to be the most westerly potential source location for *Culicoides* (Eagles *et al.*, 2014).

We considered all countries with a land border within 500 km of the Australian mainland to be potential points of origin for windborne transmission (Figure 9). Indonesia was subdivided into western, central and eastern regions for improved geographical resolution (Figure 10). Distances were calculated as straight-line distances based on the closest point between land borders. We cannot be certain that this distance encompasses all possible origin countries from which windborne travel is possible, so we estimated the uncertainty to be moderate. As noted in Section 2.3, we excluded countries with a land area of <3000 km<sup>2</sup>, with the exception of Singapore where LSDV has already been detected.

#### **R<sub>0</sub> Arrival destinations**

*Regions included:* N1a, N2a, N2b, N3, N4, N5, N6, N7, N8a, N8b, N9, N10, Q1a, Q1b, Q2, Q3, Q4a, Q4b, Q5a, Q6a, Q6b, Q6c, W3, W4 and W5

*Uncertainty:* Moderate

*Justification:* We considered all NAQS risk zones within a 500 km radius of the origin countries of interest as potential arrival destinations. We choose to use NAQS risk zones as these are most useful for planning surveillance efforts, compared to other geographical divisions such as Statistical Area 2 (SA2) or natural resource management regions. Importantly however, NAQS areas only extend for a relatively short distance beyond the coastline, whereas vectors may be deposited by wind further inland where the density of susceptible hosts and conditions for vector establishment may be different to that at the coastline. NAQS risk zones are shown in Figure 11.

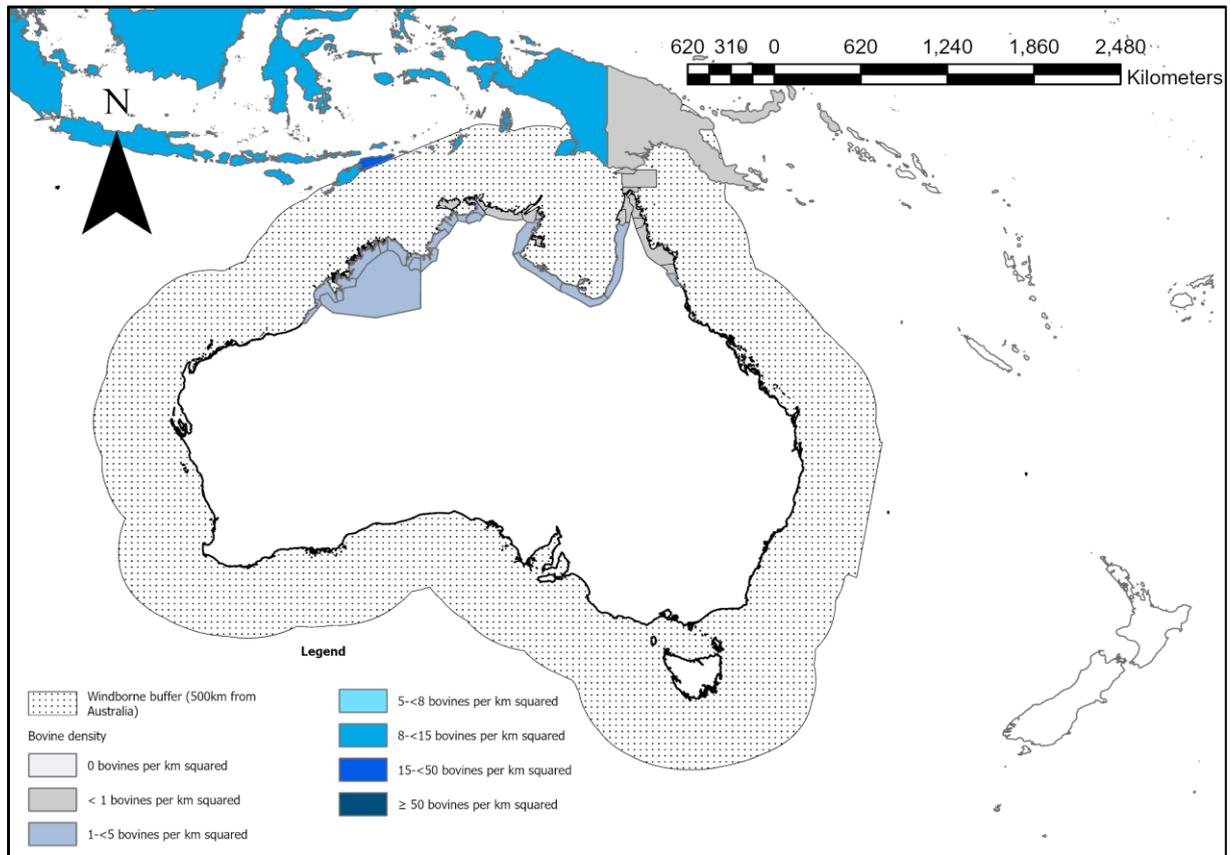


Figure 9 Bovine densities (per km<sup>2</sup>) in regions within 500 km of Australian land borders and within NAQS risk zones.

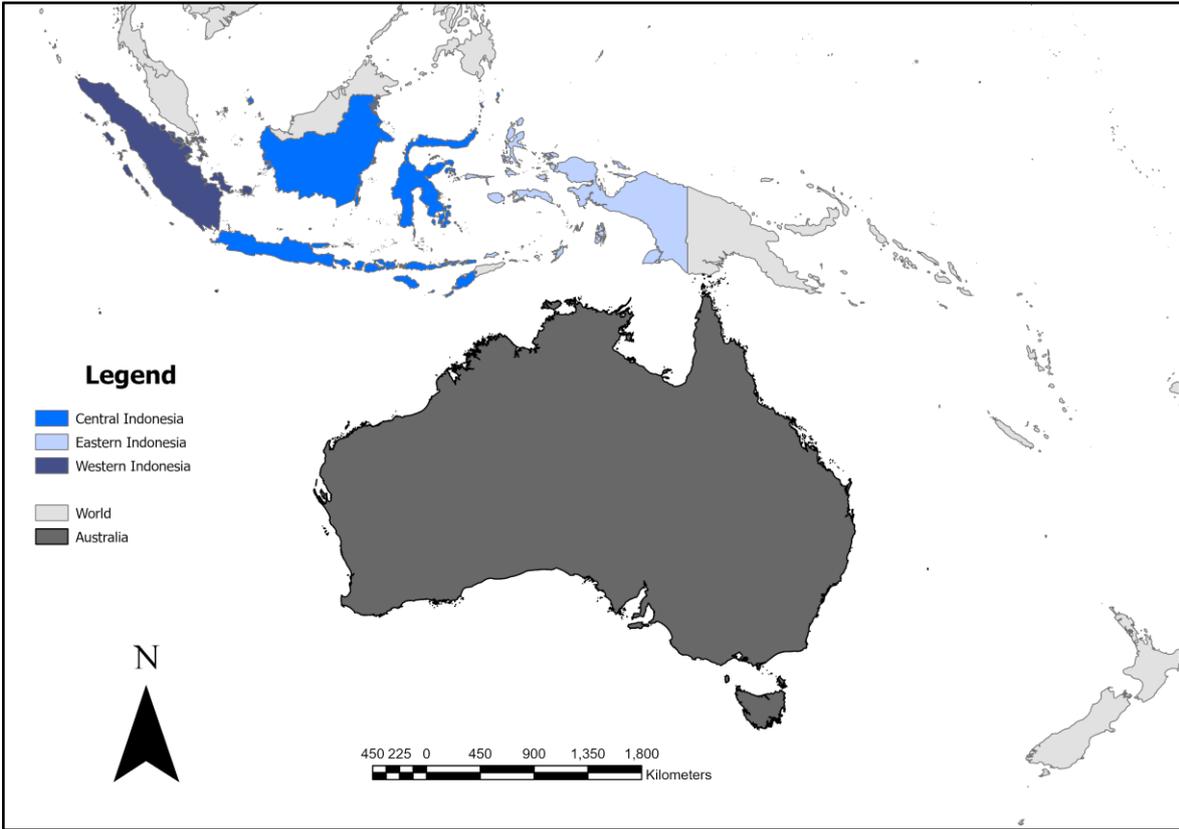


Figure 10 Map of Indonesian geographical subdivisions

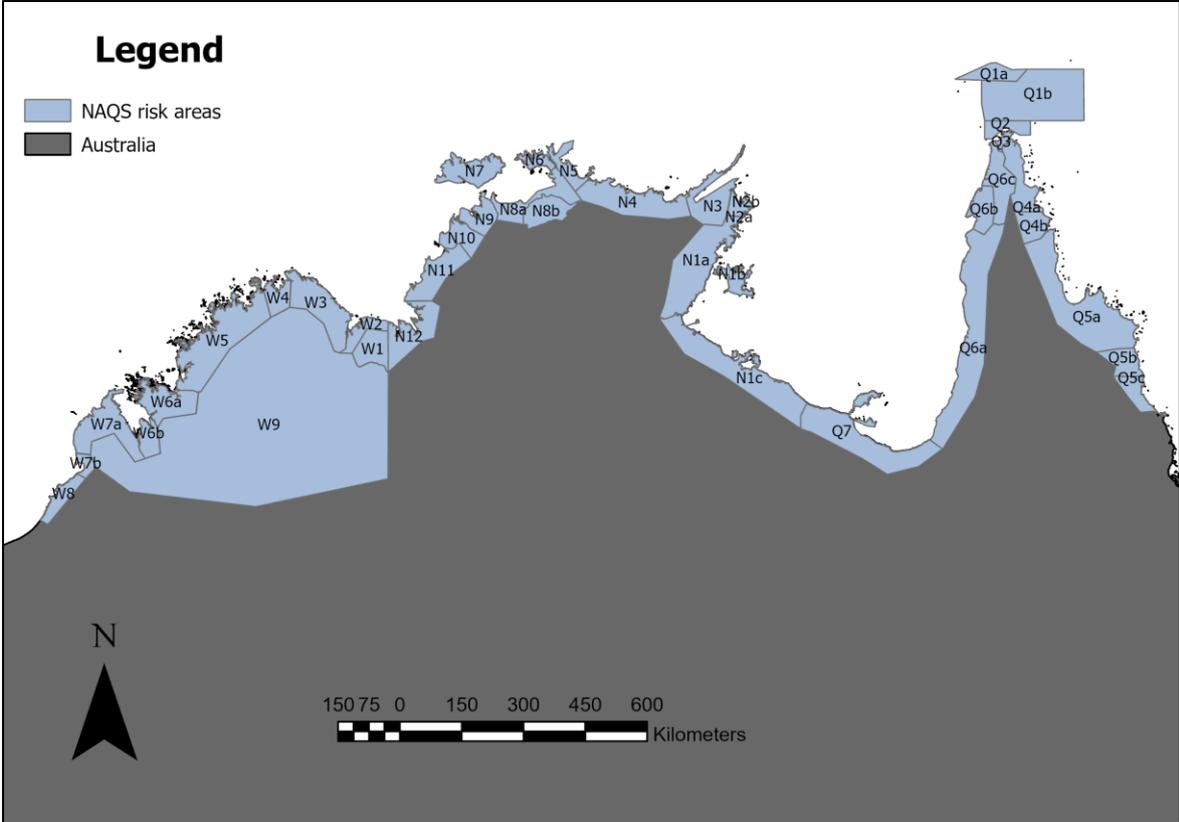


Figure 11 Map of NAQS risk zones

## 4.5.2 Commercial vessels (excluding live export vessels)

### **R<sub>0</sub> Origin countries of interest**

*Countries included:* Bangladesh, Brunei Darussalam, Cambodia, China and associated autonomous regions, India, Indonesia, Japan, Republic of Korea, Lao People's Democratic Republic, Malaysia, Myanmar, PNG, Philippines, Singapore, Sri Lanka, Thailand, Timor-Leste, Viet Nam

*Uncertainty:* Moderate

*Justification:* Our entomology experts were asked to estimate the maximum number of days that arthropods from each vector category could survive on a commercial vessel with limited access to a food source. We combined their maximum estimates with information from the literature on LSDV decay rates, concluding that the maximum reasonable duration for an insect to travel to Australia and retain LSDV infectivity is five days (Weiss, 1968; Chihota *et al.*, 2001, 2003; Issimov *et al.*, 2020; Sanz-Bernardo *et al.*, 2021). A recent publication, however, reported successful viral isolation of LSDV from laboratory-infected *Aedes japonicus* and *Culicoides nubeculosus* for up to 10 days post-infection (Paslaru *et al.*, 2022). In contrast, other publications have suggested that vectors must re-feed within 24 hours for transmission to be successful (Chihota *et al.*, 2003; Sohler *et al.*, 2019). While there are sporadic reports of living Australian *Culicoides* being detected in Chinese seaports, suggesting that longer duration travel is possible, the experts queried whether such aged insects would be in a condition to be able to seek and bite a susceptible host (Nie *et al.*, 2005).

For commercial vessels excluding live export vessels we calculated that the maximum distance that could be covered in five days is 5,555 km, using a travel speed of 25 knots. We therefore considered all countries within 5,555 km of an Australian port to be potential origins (Figure 12, Figure 13). As noted in Section 2.3, we excluded countries with a land area of <3000 km<sup>2</sup>, with the exception of Singapore where LSDV has already been detected. Distances were calculated as straight-line distances based on the closest point to any land border (not to specific seaports in origin countries) and did not account for shipping routes or intervening land masses or other obstacles, so real travel distances are probably greater than estimated. Therefore, distances estimated could be considered a worst-case scenario (i.e. faster transit of vectors than what actually occurs).

It is not possible to exclude the possibility of travel from greater distances, so we estimated the uncertainty to be moderate.

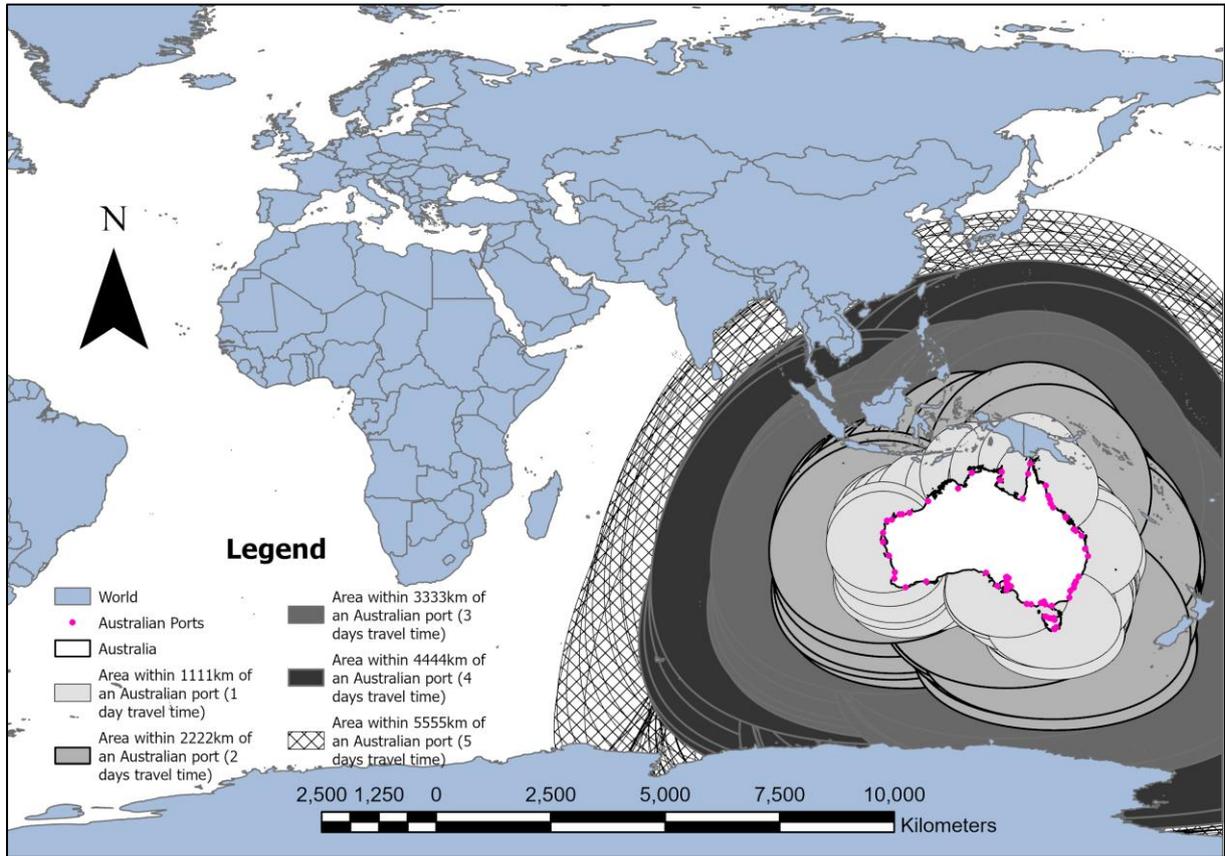
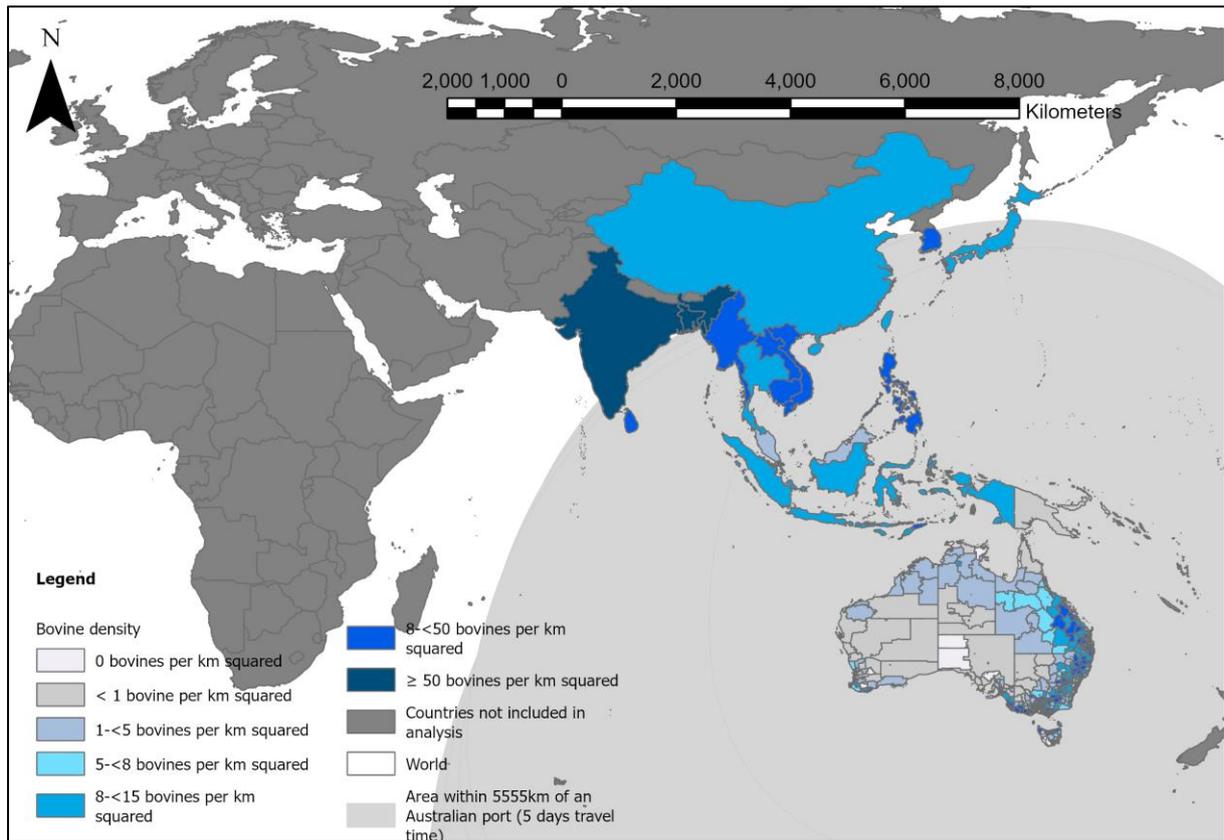


Figure 12 Map of Australian seaports showing areas within 1 to 5 days' travel time for commercial ships (excluding live export vessels)



**Figure 13 Bovine density (per km<sup>2</sup>) in countries within 5 days' travel distance for commercial vessels (excluding live export ships) and in Australian Statistical Area 2 regions.** Grey shading indicates countries outside 5 day's travel or those excluded from the analysis such as New Zealand

### **R<sub>0</sub> Arrival destinations**

*Ports included* (Figure 14): Albany, Ardrossan, Ballina, Batemans Bay, Beauty Point, Botany Bay, Brisbane, Broome, Bunbury, Bundaberg, Burnie, Cairns, Cape Cuvier, Cape Flattery Harbor, Dampier, Darwin, Devonport, Dover, Eden, Esperance, Fremantle, Geelong, Geraldton, Gladstone, Gove, Hay Point, Hobart, Jervis Bay, Karumba, Kingscote, Klein Point, Launceston, Lucinda, Mackay, Melbourne, Milner Bay, Mourilyan Harbour, Newcastle, Onslow, Point Murat, Port Adelaide, Port Alma, Port Bonython, Port Giles, Port Hedland, Port Huon, Port Kembla, Port Latta, Port Lincoln, Port Pirie, Port Walcott, Portland, Stanley, Sydney, Thevenard, Thursday Island, Townsville, Useless Loop, Wallaroo, Warrnambool, Weipa, Welshpool, Western Port, Whyalla, Wyndham

*Uncertainty:* Moderate

*Justification:* See reasoning above. We included all Australian seaports that were within 5,555 km of another country (except where that country was excluded based on criteria discussed above) (Figure 14). We obtained our list of Australian seaports and their point location from the World Port Index (National Geospatial-Intelligence Agency, 2019).



It is not possible to exclude the possibility of travel from greater distances, so we estimated uncertainty to be moderate.

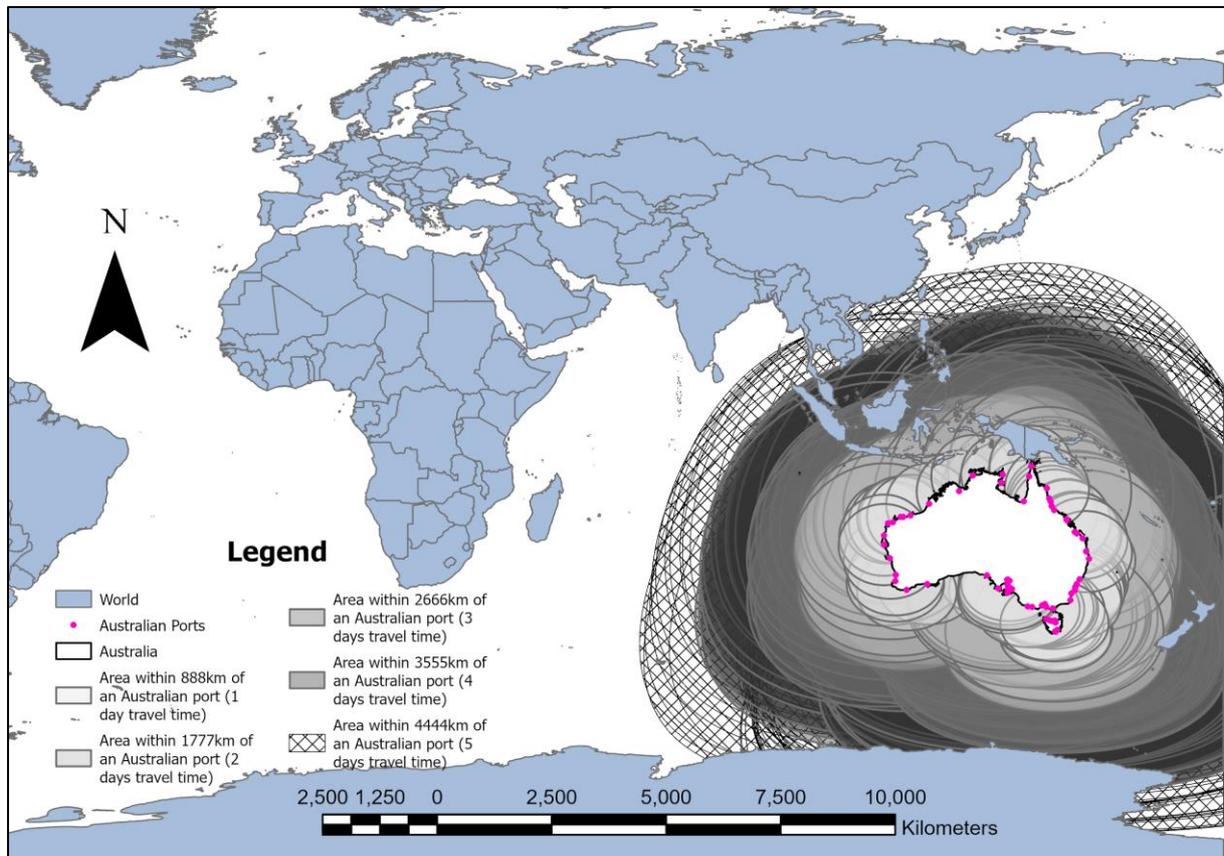


Figure 15 Map of Australian seaports showing areas within 1 to 5 days' travel time for live export vessels

### R<sub>0</sub> Arrival destinations

*Ports included:* Albany, Ardrossan, Ballina, Batemans Bay, Beauty Point, Botany Bay, Brisbane, Broome, Bunbury, Bundaberg, Burnie, Cairns, Cape Cuvier, Cape Flattery Harbour, Dampier, Darwin, Devonport, Dover, Eden, Esperance, Fremantle, Geelong, Geraldton, Gladstone, Gove, Hay Point, Hobart, Jervis Bay, Karumba, Kingscote, Klein Point, Launceston, Lucinda, Mackay, Melbourne, Milner Bay, Mourilyan Harbour, Newcastle, Onslow, Point Murat, Port Adelaide, Port Alma, Port Bonython, Port Giles, Port Hedland, Port Huon, Port Kembla, Port Latta, Port Lincoln, Port Pirie, Port Walcott, Portland, Stanley, Sydney, Thevenard, Thursday Island, Townsville, Useless Loop, Wallaroo, Warrnambool, Weipa, Welshpool, Western Port, Whyalla, Wyndham

*Uncertainty:* Moderate

*Justification:* See reasoning above. We included all Australian seaports that were within 4,445 km of another country (except where that country was excluded based on criteria discussed above). A list of all Australian seaports and their point locations was obtained from the World Port Index (National Geospatial-Intelligence Agency, 2019) (Figure 14).

#### 4.5.4 Torres Strait Treaty movements

##### **R<sub>0</sub> Origin countries of interest**

*Countries included:* PNG

*Uncertainty:* Negligible

*Justification:* Treaty villages are only located in PNG

##### **R<sub>0</sub> Arrival destinations**

*Regions included* (Figure 11): Q1a, Q1b and Q2

*Uncertainty:* Low

*Justification:* During normal periods of traditional movements, the majority (98% in 2016–2017) of traditional visitors visit the top western islands of Boigu, Dauan and Saibai (T. Kerlin, NAQS, pers. comm.). Other traditional visitors will only travel to other islands in the Torres Strait Protected Zone but are not permitted under the Treaty to travel further south. There is some potential that illegal travel could extend beyond these destinations.

### 4.6 Qualitative values for each node

#### 4.6.1 Windborne dispersal

##### **R<sub>1</sub> Herd present at origin**

*Qualitative assessment:*

PNG: Negligible

Indonesia: Low

Timor-Leste: Moderate

*Uncertainty:* Moderate

*Justification:* We used livestock count data from FAOSTAT (the FAO database on food and agriculture statistics) and divided the number of cattle and buffalo by area for each country to estimate density in individuals per km<sup>2</sup> (FAO, 2022) (Figure 9). For Indonesia, we calculated the density at a country level and assigned this uniform density for western, central, and eastern areas. Densities were divided into six classes (<1; >=1–5; >=5–8; >= 8–15; >= 15–50; >= 50 cattle per km<sup>2</sup>), which were then assigned to qualitative likelihood categories (i.e. negligible, extremely low, very low, low, moderate and high, respectively).

We considered uncertainty to be moderate for these estimates, since they are geographically coarse and official livestock counts do not always reflect the true value.

##### **R<sub>2</sub> Herd symptomatically infected with LSDV**

*Qualitative assessment:*

PNG: Low

Timor-Leste: Low

Indonesia: Low

*Uncertainty:* High

*Justification:* Current evidence suggests that asymptomatic animals contribute minimally to vector-borne transmission of LSDV due to low titres of virus in the blood and skin (Sanz-Bernardo *et al.*, 2021). Therefore, we considered only symptomatically infected individuals to be infectious. Typically, only 20–60% of infected animals develop clinical disease (Magori-Cohen *et al.*, 2012).

No data are available on either the point prevalence of symptomatic LSDV infection in endemic regions or the incidence of disease. But we considered that this would be no more than 30% of animals at any single point in time, in countries where no effective control measures were in place (i.e. low likelihood).

Thus, we coarsely classified countries based on their anticipated LSDV incidence at endemicity, using the human development index (HDI) (United Nations Development Programme, 2020) as a proxy for the availability of veterinary services and consequent ability to implement control measures in the different regions. Countries with a HDI >0.9 were considered to have a theoretical very low LSDV prevalence at endemicity (0.1–5%), while countries with a HDI <0.9 were classified as low (5–30% incidence at endemicity).

Critically, seroprevalence estimates alone do not reflect the proportion of actively symptomatic animals. One solution has been to multiply the mean duration of infectiousness by the seroprevalence and divide this by the mean duration of immunity to estimate the proportion of active infections (Berg *et al.*, 2015). Immunity to natural LSDV infection is widely considered to be lifelong (Kitching, 2003; European Food Safety, 2018; Namazi and Tafti, 2021).

Because of the use of HDI as a proxy to estimate the capacity of a country to control disease, we estimated this assessment to have a high level of uncertainty.

### **R<sub>3</sub> Vectors present at origin**

*Qualitative assessment:* High

*Uncertainty:* Low

*Justification:* We asked our entomology experts to estimate the probability of vectors from each category being present in agricultural settings in the origin countries. All three experts concluded that species from these groups were likely to be present.

We considered the uncertainty around this parameter to be low given the consistency of the expert opinion and concordance with earlier conclusions in risk assessments that vectors are likely to be present in most areas (Horigan *et al.*, 2018).

### **R<sub>4</sub> Vector becomes infectious after taking a protein meal**

*Qualitative assessment:*

Mosquitoes: Low

Midges: Low

Heavy fliers: Moderate

*Uncertainty:* Moderate

*Justification:* We asked our entomology experts to estimate the probability of arthropods from each group becoming infectious with LSDV after taking a protein meal. Our experts consulted peer-reviewed transmission studies and concluded that this likelihood was low to moderate, depending on vector category (Carn and Kitching, 1995a; Chihota *et al.*, 2001, 2003; Sohier *et al.*, 2019; Issimov *et al.*, 2020; Sanz-Bernardo *et al.*, 2021). Where expert opinion diverged, we used the highest likelihood category. Of note, only female mosquitoes and midges take protein meals.

We estimated the uncertainty around these values to be moderate. Whilst estimates were based on both expert opinion and published literature, transmission studies typically involved small numbers of animals and artificial conditions, and the opinion between our entomology experts varied.

### **R<sub>5</sub> Infectious vector successfully travels via wind**

#### *Qualitative assessment:*

Distances of 0–100 km (Mosquitoes, Midges, Heavy fliers): High, High, High

Distances of 101–200 km (Mosquitoes, Midges, Heavy fliers): High, High, Moderate

Distances of 201–400 km (Mosquitoes, Midges, Heavy fliers): Low, Moderate, Low

Distances of 401–500 km (Mosquitoes, Midges, Heavy fliers): Low, Moderate, Extremely Low

*Uncertainty:* High

*Justification:* We asked our entomology experts to estimate the probability of arthropods from the different vector categories travelling defined ranges. Literature relevant to flight distances is discussed earlier under origin countries of interest. For this parameter, we found a high level of discrepancy between the estimates provided. We chose to consider the highest likelihoods for inclusion in our analysis and noted the level of uncertainty to be high.

### **R<sub>6</sub> Vector is infectious when entering Australia**

#### *Qualitative assessment:*

Midges: Moderate

Mosquitoes: High

Heavy flier: High

*Uncertainty:* High

*Justification:* We consulted our entomology experts to estimate the probability of arthropods from the different vector categories still being infectious with LSDV when entering Australia. Our experts noted that a parcel of air (representative of an insect) could reportedly cover 500 km in about 30 hours (Daly and Tran-Nguyen, 2008). Combined with knowledge of LSDV decay rates described in the literature, they provided numerical estimates of the probability of a vector still being infectious after one or two days of windborne travel (Weiss, 1968; Chihota *et al.*, 2001, 2003; Issimov *et al.*, 2020, 2021; Sanz-Bernardo *et al.*, 2021). We used the most likely probability provided by the experts and took the highest probability where opinions diverged. We used the estimates for one day of travel for distances up to 500 km.

### **R<sub>a</sub> Susceptible bovine present**

#### *Qualitative assessment:*

N2a, N2b, N3, N4, N5, N6, N7, Q1a, Q1b, Q2, Q3, Q4a, Q4b, Q5a, Q6b, Q6c: Negligible

N1a, N8a, N8b, N9, N10, Q6a, W3, W4 and W5: Extremely low

*Uncertainty:* Moderate

*Justification:* We used cattle numbers from the ABS 2016 livestock census defined at the SA2 level (Australian Bureau of Statistics, 2017). Absolute numbers were converted to densities (cattle per km<sup>2</sup>) by dividing by the area of each SA2 region. Densities were divided into six classes (<1; >=1–5; >=5–8; >=8–15; >=15–50; >=50 cattle per km<sup>2</sup>), which were then assigned to qualitative likelihood categories (i.e. negligible, extremely low, very low, low, moderate and high, respectively) (Figure 9). NAQS risk zones

and SA2 regions were overlaid and NAQS risk zones were assigned the highest cattle density within the superimposed area.

Buffalo and feral cattle numbers were not included due to lack of explicit data. Data on buffalo numbers per SA2 or NAQS risk zone are not available. Feral cattle occur around most pastoral areas, but at lower densities than commercial cattle; these are likely to be counted as domestic cattle during the livestock census (Woolnough *et al.*, 2005; Reid *et al.*, 2020).

### **R<sub>b</sub> Vector bites susceptible bovine**

*Qualitative assessment:*

Mosquitoes: Moderate

Midges: Moderate

Heavy fliers: High

*Uncertainty:* High

*Justification:* We asked our entomology experts to estimate the likelihood of arthropods from each group biting a bovine, if available. Importantly, only female mosquitoes and midges seek protein meals, giving a maximum likelihood of ‘moderate’ for these groups, although we recognise that the sex ratio may not be equal in these species. We used the maximum value from expert opinion to assign a qualitative likelihood and, where opinions diverged, we used the highest likelihood category.

Expert opinion varied and all noted that this was species dependant. For example, *Aedes aegypti* are anthropophilic, so may be less likely to bite a bovine than other mosquito species. One expert also noted that the lifecycle of several arthropod species involves a gonotrophic cycle, where females are not seeking protein meals at all times. For these reasons, we allocated a high level of uncertainty to this parameter.

### **R<sub>c</sub> Bovine becomes infected**

*Qualitative assessment:*

Mosquitoes: Very low

Midges: Low

Heavy fliers: Low

*Uncertainty:* Moderate

*Justification:* We reviewed the literature to estimate the likelihood that a bovine host would become infected after being bitten by an infectious vector. Notably, LSDV transmission experiments have all used large batches of insects (50–300 insects per batch) (Weiss, 1968; Chihota *et al.*, 2001, 2003; Magori-Cohen *et al.*, 2012; Sohier *et al.*, 2019; Issimov *et al.*, 2020; Sanz-Bernardo *et al.*, 2021). The minimum infectious dose for LSDV has been estimated at  $>10^1$  50% tissue culture infectious dose (TCID<sub>50</sub>) (Carn and Kitching, 1995b), and it was calculated that an individual *Stomoxys calcitrans* could only transfer  $10^{-0.8}$  TCID<sub>50</sub> (Sohier *et al.*, 2019). Given the smaller proboscises of midges and mosquitoes, presumably they would be unable to transfer more virus than *S. calcitrans*. It has therefore been concluded by some that one single insect cannot transmit sufficient virus to induce disease (Sohier *et al.*, 2019).

We used the lowest likelihood category identified in the literature for each vector category based on these batch transmission experiments. This is still likely to overestimate the actual risk, since the likelihood that multiple infectious insects would arrive simultaneously through any of the pathways and would then feed on the same host would seem to be extremely low. Because we have some limited data on which to base our assessment, we allocated an uncertainty of moderate to this estimate.

## 4.6.2 Commercial vessels (excluding live export vessels)

### **R<sub>1</sub> Herd present at origin**

*Qualitative assessment:*

Brunei Darussalam, PNG, Singapore: Negligible

Malaysia: Extremely low

China and associated autonomous regions, Indonesia, Japan, Thailand: Low

Cambodia, Lao People's Democratic Republic, Myanmar, Philippines, Republic of Korea, Sri Lanka, Timor-Leste, Viet Nam: Moderate

Bangladesh, India: High

*Justification:* See Justification for R<sub>1</sub> in windborne dispersal.

### **R<sub>2</sub> Herd symptomatically infected with LSDV**

*Qualitative assessment:*

Japan, Republic of Korea, Singapore: Very low

Bangladesh, Brunei Darussalam, Cambodia, China and associated autonomous regions, India, Indonesia, Lao People's Democratic Republic, Malaysia, Myanmar, Philippines, PNG, Sri Lanka, Thailand, Timor-Leste, Viet Nam: Low

*Uncertainty:* High

*Justification:* See Justification for R<sub>2</sub> in windborne dispersal.

### **R<sub>3</sub> Vectors present at origin**

*Qualitative assessment:* High

*Uncertainty:* Low

*Justification:* See Justification for R<sub>3</sub> in windborne dispersal.

### **R<sub>4</sub> Vector becomes infectious after taking a protein meal**

*Qualitative assessment:*

Mosquitoes: Low

Midges: Low

Heavy fliers: Moderate

*Uncertainty:* Moderate

*Justification:* See Justification for R<sub>4</sub> in windborne dispersal.

### **R<sub>5</sub> Infectious vector travels to port**

*Qualitative assessment:*

Brunei Darussalam, Japan, Malaysia, Republic of Korea, Singapore: Negligible

China and associated autonomous regions, Indonesia: Extremely low

Bangladesh, Philippines, Thailand, Viet Nam: Low

India, Lao People's Democratic Republic, Myanmar, Timor-Leste: Moderate

Cambodia, PNG, Sri Lanka: High

*Uncertainty:* High

*Justification:* We used urbanisation index as a proxy for the likelihood that an infectious vector would travel to a seaport in the country of origin. We considered it more likely that a vector would reach a port in less urbanised countries, principally due to the shorter distances between agricultural activities and seaports. The percent urban population was sourced from the 2020 Central Intelligence Agency World Factbook (Central Intelligence Agency, 2020). We used a relative ranking of origin countries, whereby we subdivided the percent urban population into six even quantiles and these were assigned to the six likelihood categories (i.e. negligible, extremely low, very low, low, moderate, high). Urbanisation index at a country level may be a poor proxy for distance between ports and agricultural activities, which is likely to vary for each individual port. For this reason, we assigned an uncertainty of high.

## **R<sub>6</sub> Infectious vector lands on the vessel**

*Qualitative assessment:*

Mosquitoes: Low

Midges: Low

Heavy fliers: Low

*Uncertainty:* High

*Justification:* The likelihood that an infectious vector lands on a vessel bound for Australia was estimated as low based on expert opinion from the Department's Animal Biosecurity branch. Insects, particularly adult mosquitoes, are attracted by carbon dioxide emitted by both people and livestock and by the lights of the vessel at night, depending on species-specific behaviour. Whilst arthropods are regularly found in insectocutors on ships arriving in Australian ports, it is thought that these are frequently of Australian origin and are attracted to the ships upon docking, rather than from the countries of origin (M. Gorton, NAQS; J. Early, A. Robinson, DAWE, pers. comm.). No origin ports or countries were specifically identified as particularly high risk on a routine basis.

We considered the likelihood to be lower for cargo ships compared to returning live export vessels, since insects may be more attracted to livestock ships. However, given the qualitative nature of this assessment both pathways were ranked as low. Because of the lack of data for this parameter, the uncertainty was considered to be high.

## **R<sub>7</sub> Vessel travels to Australia**

*Qualitative assessment:*

Bangladesh, Brunei Darussalam, Cambodia, Lao People's Democratic Republic, Myanmar, Philippines, PNG, Singapore, Sri Lanka, Timor-Leste: Very low

China and associated autonomous regions, India, Indonesia, Japan, Malaysia, Republic of Korea, Thailand, Viet Nam: Low

*Uncertainty:* Low

*Justification:* We used data from the Department of Infrastructure, Transport, Regional Development and Communications on 2018–2019 Australian sea freight volumes (Table 1.10) (Bureau of Infrastructure and Transport Research Economics, 2021) to estimate the likelihood of commercial ships arriving from each country. The 10 countries that traded the largest weight of sea freight with Australia were classified as low risk, while other countries were classified as very low risk. As this assessment was based on official data,

we considered the uncertainty to be low. However, this may not be the ideal proxy for this parameter, since we are actually interested in the proportion of ships from each country that travel to Australia.

### **R<sub>8</sub> Infectious vector survives transport**

*Qualitative assessment:* This was parameterised depending on the interaction between vector category and travel time, generating many potential combinations. Specifically, travel times were estimated for every combination of origin country and destination port based on the speed calculations discussed in 4.5.2. Then for each of these journeys, the likelihood of each of the three vector groups surviving the journey was estimated from expert entomology opinion. For example, if the travel time between Timor-Leste and Darwin was estimated to be less than one day, our estimate for mosquito survival was based on entomology expert opinion on how likely a mosquito was to survive a one-day journey on a commercial ship. For full results, see Appendix 4.

*Uncertainty:* High

*Justification:* Our entomology experts were asked to estimate the probability of each vector category surviving one, two, three, four or five days on a commercial vessel without ready access to a food source, considering prior knowledge and published literature on vector survival. This was combined with the time required to travel from the origin to the destination (calculated using maximum travel speeds as described earlier under R<sub>0</sub>).

We used the most likely likelihood provided by the experts and took the highest likelihood category where opinions diverged.

### **R<sub>9</sub> Vector disembarks vessel without detection**

*Qualitative assessment:*

Mosquitoes: Very low

Midges: Very low

Heavy fliers: Very low

*Uncertainty:* Moderate

*Justification:* The likelihood that an infectious vector on a commercial vessel (not including returning live export vessels) would disembark without detection was estimated as very low based on a combination of expert opinion from the Biosecurity Operations Division within the Department's Animal Biosecurity branch and review of a report from the Inspector-General of Biosecurity (Inspector-General of Biosecurity, 2018). Commercial vessels biosecurity risks are managed through the Maritime Arrivals Reporting System (MARS) and detailed risk mitigation measures are in place. MARS uses a risk engine to support decisions prioritising assessment and inspection activities. In 2017, 75 percent of vessel voyages were subject to at least one inspection by a biosecurity officer (leaving 25 percent that were not) (Inspector-General of Biosecurity, 2018). The Vessel Compliance Scheme (VCS) uses the MARS risk engine to reduce inspection rates of vessels that have a history of compliance (Inspector-General of Biosecurity, 2018). The Inspector-General of Biosecurity report shows the failure rate of different types of vessels on the VCS. For the vessels considered in this pathway, failure rates ranged from less than 1 percent to around 3 percent in 2017 (Inspector-General of Biosecurity, 2018). Importantly, not all vessels that fail to comply will contain vectors from our groups of interest. Failure implies a lack of mitigation strategies such as fogging etc.

### **R<sub>10</sub> Vector is infectious on arrival**

*Qualitative assessment:* This was parameterised depending on the interaction between vector category and travel time, generating many potential combinations, using the same principle as discussed in R<sub>s</sub>. For full results, see Appendix 4.

*Uncertainty:* High

*Justification:* We consulted our entomology experts to estimate the probability that arthropods from the different vector categories would still be infectious with LSDV when entering Australia after one, two, three, four and five days on a commercial vessel considering prior knowledge and published literature on viral decay (Weiss, 1968; Chihota *et al.*, 2001, 2003; Issimov *et al.*, 2021; Sanz-Bernardo *et al.*, 2021). This was combined with the time required to travel from the origin to the destination (calculated using maximum travel speeds as described earlier under R<sub>0</sub>).

We used the most likely likelihood provided by the experts and took the highest likelihood category where opinions diverged.

### **R<sub>a</sub> Susceptible bovine present**

*Qualitative assessment:*

Ballina, Botany Bay, Brisbane, Broome, Bunbury, Cairns, Cape Cuvier, Cape Flattery Harbor, Darwin, Eden, Geelong, Gladstone, Gove, Jervis Bay, Mackay, Melbourne, Milner Bay, Newcastle, Point Murat, Port Adelaide, Port Bonython, Port Hedland, Port Kembla, Sydney, Thevenard, Thursday Island, Townsville, Thursday Island, Useless Loop, Wallaroo, Weipa, Whyalla: Negligible

Ardrossan, Batemans Bay, Dampier, Dover, Karumba, Kingscote, Klein Point, Lucinda, Onslow, Port Giles, Port Huon, Port Lincoln, Port Pirie, Port Walcott, Wyndham: Extremely low

Bundaberg, Mourilyan Harbour, Western Port: Very low

Port Alma, Port Dalrymple: Low

Beauty Point, Burnie, Devonport, Esperance, Hay Point, Port Latta, Portland, Stanley: Moderate

Albany, Fremantle, Geraldton, Hobart, Launceston, Warrnambool, Welshpool: High

*Uncertainty:* Moderate

*Justification:* Data on Australian livestock numbers are available through the ABS livestock census and are aggregated at the Statistical Area Level 4 (SA4) and natural resource management levels, and intermittently at the SA2 level. We used SA2 data (the most recent aggregation is from 2016) because of the higher spatial resolution. We calculated cattle density per km<sup>2</sup> for each SA2 and assigned qualitative likelihood categories, as described above. We then used the cattle density in the SA2 region where each seaport was located to estimate the likelihood that a susceptible host would be present at the arrival destination. Densities were divided into six qualitative categories as described in R<sub>a</sub> of the windborne pathway (Figure 13). As discussed further in the Limitations and assumptions section, we note that SA2 level aggregation (based on human population) does not necessarily correlate well with free-ranging livestock populations, particularly around live export ports (e.g., Townsville, Fremantle, Launceston, Hobart). We did not include buffalo in our density calculations, since buffalo are absent from the SA2 regions where seaports are located (Department of Sustainability, Environment, Water, Population and Communities, 2011; Saalfeld, 2014). We also did not consider whether environmental conditions at individual seaports would be conducive to vector establishment and spread.

### **R<sub>b</sub> Vector bites susceptible bovine**

*Qualitative assessment:*

Mosquitoes: Moderate

Midges: Moderate

Heavy fliers: High

*Uncertainty:* High

*Justification:* See Justification for  $R_b$  in windborne dispersal.

#### **$R_c$ Bovine becomes infected**

*Qualitative assessment:*

Mosquitoes: Very low

Midges: Low

Heavy fliers: Low

*Uncertainty:* Moderate

*Justification:* See Justification for  $R_c$  in windborne dispersal.

### **4.6.3 Returning live export vessels**

#### **$R_1$ Herd present at origin**

*Qualitative assessment:*

Brunei Darussalam, PNG, Singapore: Negligible

Malaysia: Extremely low

China and associated autonomous regions, Indonesia, Japan, Thailand: Low

Cambodia, Lao People's Democratic Republic, Myanmar, Philippines, Sri Lanka, Timor-Leste, Viet Nam: Moderate

India: High

*Justification:* See Justification for  $R_1$  in windborne dispersal.

#### **$R_2$ Herd symptomatically infected with LSDV**

*Qualitative assessment:*

Japan, Singapore: Very low

Brunei Darussalam, Cambodia, China and associated autonomous regions, India, Indonesia, Lao People's Democratic Republic, Malaysia, Myanmar, Philippines, PNG, Sri Lanka, Thailand, Timor-Leste, Viet Nam: Low

*Uncertainty:* High

*Justification:* See Justification for  $R_2$  in windborne dispersal.

#### **$R_3$ Vectors present at origin**

*Qualitative assessment:* High

*Uncertainty:* Low

*Justification:* See Justification for  $R_3$  in windborne dispersal.

#### **$R_4$ Vector becomes infectious after taking a protein meal**

*Qualitative assessment:*

Mosquitoes: Low

Midges: Low

Heavy fliers: Moderate

*Uncertainty:* Moderate

*Justification:* See Justification for R<sub>4</sub> in windborne dispersal.

### **R<sub>5</sub> Infectious vector travels to port**

*Qualitative assessment:*

Brunei Darussalam, Japan, Malaysia, Singapore: Negligible

China and associated autonomous regions, Indonesia: Extremely low

Philippines, Thailand, Viet Nam: Low

India, Lao People's Democratic Republic, Myanmar, Timor-Leste: Moderate

Cambodia, PNG, Sri Lanka: High

*Uncertainty:* High

*Justification:* See Justification of R<sub>5</sub> in commercial vessels.

### **R<sub>6</sub> Infectious vector lands on the vessel**

*Qualitative assessment:*

Mosquitoes: Low

Midges: Low

Heavy fliers: Low

*Uncertainty:* High

*Justification:* See Justification for R<sub>6</sub> in commercial vessels. We considered the likelihood to be lower for other commercial vessels compared to returning live export vessels, since insects may be more attracted to livestock ships. However, given the qualitative nature of this assessment both pathways were ranked as low.

### **R<sub>7</sub> Vessel travels to Australia**

*Qualitative assessment:*

Cambodia, India, Lao People's Democratic Republic, Myanmar, PNG, Singapore, Timor-Leste, Viet Nam: Negligible

Brunei Darussalam, Japan, Malaysia, Philippines, Thailand: Very low

China and associated autonomous regions: Low

Indonesia: Moderate

*Uncertainty:* Moderate

*Justification:* We used data on all Australian livestock exports from the Department limited to 2021 and 'sea' mode to assess the likelihood of a returning ship being from a specific country (Australian Government Department of Agriculture, Water and the Environment, 2022). We calculated the relative proportion of animals exported to each country to estimate the proportion of ships returning from each country. This proportion was converted to a qualitative likelihood category using the table described in

Section 3.6. Note that this calculation was performed on total animal numbers, not number of ships, and would not account for differences in vessel size/capacity or loading density. This may not be the ideal proxy for this parameter, since we are specifically interested in the proportion of ships from each country that travel to Australia.

### **R<sub>8</sub> Infectious vector survives transport**

*Qualitative assessment:* This was parameterised depending on the interaction between vector category and travel time, generating many potential combinations. For full results, see Appendix 4.

*Uncertainty:* High

*Justification:* See Justification for R<sub>8</sub> in commercial vessels.

### **R<sub>9</sub> Vector disembarks vessel without detection**

*Qualitative assessment:*

Mosquitoes: Extremely low

Midges: Extremely low

Heavy fliers: Extremely low

*Uncertainty:* Moderate

*Justification:* The likelihood that an infectious vector on a ship is not detected was estimated as extremely low based on expert opinion from the Biosecurity Operations Division within the Department's Animal Biosecurity branch and considering the current risk mitigation procedures in place. Notably, every returning livestock vessel is inspected on arrival at its first port. Pre-arrival, livestock ships are thoroughly cleaned, disinfected with soda ash, and receive two insecticide treatments, although the effectiveness of these treatments may not be uniform across decks (J. Early, A. Robinson, DAWE, pers. comm.). While treatments are ineffective against larvae, pupae and eggs, there is no evidence of biological transmission of LSDV, and transstadial and transovarial transmission have only been reported for ixodid ticks (Tuppurainen *et al.*, 2011). Insectocutors are located on board, although these preferentially attract heavy fliers since mosquitoes and midges are not attracted by the ultraviolet light used in these devices.

### **R<sub>10</sub> Vector is infectious on arrival**

*Qualitative assessment:* This was parameterised depending on the interaction between vector category and travel time, generating many potential combinations. For full results, see Appendix 4.

*Uncertainty:* High

*Justification:* See Justification for R<sub>10</sub> in commercial vessels.

### **R<sub>a</sub> Susceptible bovine present**

*Qualitative assessment:*

Ballina, Botany Bay, Brisbane, Broome, Bunbury, Cairns, Cape Cuvier, Cape Flattery Harbor, Darwin, Eden, Geelong, Gladstone, Gove, Jervis Bay, Mackay, Melbourne, Milner Bay, Newcastle, Point Murat, Port Adelaide, Port Bonython, Port Hedland, Port Kembla, Sydney, Thevenard, Thursday Island, Townsville, Thursday Island, Useless Loop, Wallaroo, Weipa, Whyalla: Negligible

Ardrrossan, Batemans Bay, Dampier, Dover, Karumba, Kingscote, Klein Point, Lucinda, Onslow, Port Giles, Port Huon, Port Lincoln, Port Pirie, Port Walcott, Wyndham: Extremely low

Bundaberg, Mourilyan Harbour, Western Port: Very low

Port Alma, Port Dalrymple: Low

Beauty Point, Burnie, Devonport, Esperance, Hay Point, Port Latta, Portland, Stanley: Moderate  
Albany, Fremantle, Geraldton, Hobart, Launceston, Warrnambool, Welshpool: High

*Uncertainty:* Moderate

*Justification:* See Justification for  $R_a$  in commercial vessels.

#### **$R_b$ Vector bites susceptible bovine**

*Qualitative assessment:*

Mosquitoes: Moderate

Midges: Moderate

Heavy fliers: High

*Uncertainty:* High

*Justification:* See Justification for  $R_b$  in windborne dispersal.

#### **$R_c$ Bovine becomes infected**

*Qualitative assessment:*

Mosquitoes: Very low

Midges: Low

Heavy fliers: Low

*Uncertainty:* Moderate

*Justification:* See Justification for  $R_c$  in windborne dispersal.

### **4.6.4 Torres Strait Treaty movements**

#### **$R_1$ Herd present at origin**

*Qualitative assessment:* Negligible

*Uncertainty:* Low

*Justification:* See Justification for  $R_1$  in windborne dispersal.

#### **$R_2$ Herd symptomatically infected with LSDV**

*Qualitative assessment:* Low

*Uncertainty:* High

*Justification:* See Justification for  $R_2$  in windborne dispersal.

#### **$R_3$ Vectors present at origin**

*Qualitative assessment:* High

*Uncertainty:* Low

*Justification:* See Justification for  $R_3$  in windborne dispersal.

#### **$R_4$ Vector becomes infectious after taking a protein meal**

*Qualitative assessment:*

Mosquitoes: Low

Midges: Low

Heavy fliers: Moderate

*Uncertainty:* Moderate

*Justification:* See Justification for R<sub>4</sub> in windborne dispersal.

#### **R<sub>5</sub> Infectious vector travels to vessel**

*Qualitative assessment:* High

*Uncertainty:* High

*Justification:* See Justification for R<sub>5</sub> in commercial vessels. PNG has a low urban population.

#### **R<sub>6</sub> Infectious vector lands on vessel**

*Qualitative assessment:*

Mosquitoes: Low

Midges: Low

Heavy fliers: Low

*Uncertainty:* High

*Justification:* See Justification for R<sub>6</sub> in commercial vessels.

#### **R<sub>7</sub> Infectious vector survives transport**

*Qualitative assessment:* Low

*Uncertainty:* Moderate

*Justification:* Whilst travel times are short, most vessels making this journey are open (T. Kerlin, NAQS, pers. comm.). Hence, we assume that insects would likely be blown out whilst vessels are motoring. We assumed that if an infectious vector did survive this journey, it would still be infectious on arrival, as travel times are short.

#### **R<sub>8</sub> Infectious vector disembarks without detection**

*Qualitative assessment:*

Mosquitoes: Very low

Midges: Very low

Heavy fliers: Very low

*Uncertainty:* Moderate

*Justification:* All goods brought ashore from these vessels are inspected. Occasionally, inspections occur whilst goods are still within vessels; however, generally there is limited surveillance of vessels for arthropods in the Torres Strait (M. Gorton, NAQS, pers. comm.). It is possible that vectors could escape these vessels, but we considered this unlikely. Furthermore, currently a cordon sanitaire is in place around Thursday Island and Horn Island to prevent dispersal of *Aedes albopictus* to mainland Australia (M. Gorton, NAQS, pers. comm.). While other insect species are not monitored specifically, the interventions in place will likely also impact other vectors, at least mosquitoes, to some extent.

#### **R<sub>a</sub> Susceptible bovine present**

*Qualitative assessment:* Negligible

*Uncertainty:* Low

*Justification:* There are no known bovines in Torres Strait. The most recent report describes a lone bull on Prince of Wales Island (next to Thursday Island) from 2006 (T. Kerlin, NAQS, pers. comm.).

#### **R<sub>b</sub> Vector bites susceptible bovine**

*Qualitative assessment:*

Mosquitoes: Moderate

Midges: Moderate

Heavy fliers: High

*Uncertainty:* High

*Justification:* See Justification for R<sub>b</sub> in windborne dispersal.

#### **R<sub>c</sub> Bovine becomes infected**

*Qualitative assessment:*

Mosquitoes: Very low

Midges: Low

Heavy fliers: Low

*Uncertainty:* Moderate

*Justification:* See Justification for R<sub>c</sub> in windborne dispersal.

### **4.6.5 Summary of qualitative values for each node**

A summary of the range of values at each node for each pathway is shown in Figure 16. This demonstrates the relative importance of each node and identifies the nodes with increased variability within each pathway.

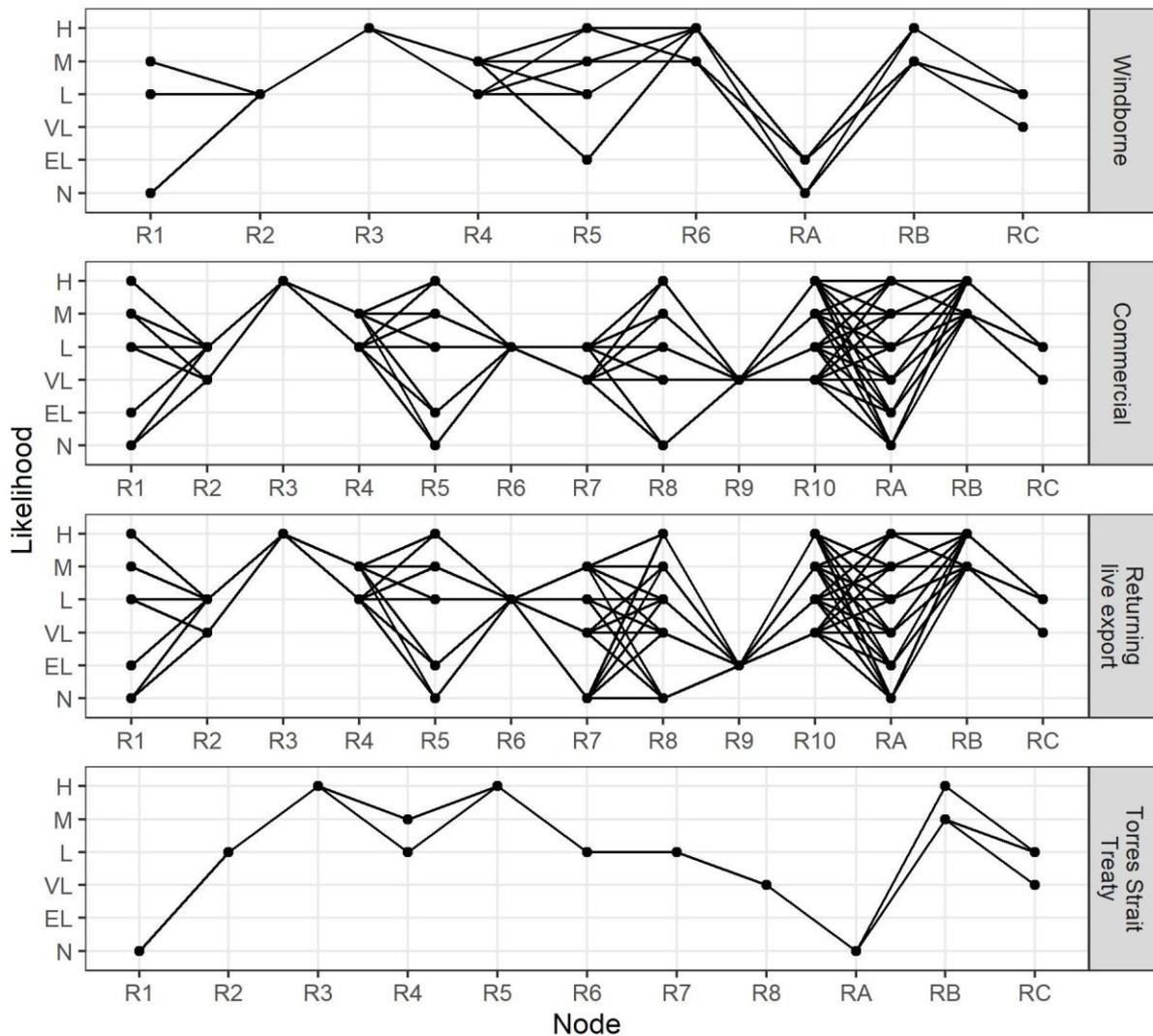


Figure 16 Qualitative likelihood at each node, by pathway<sup>3</sup>

## 4.7 Overall qualitative risk of each pathway

### 4.7.1 Qualitative analysis

There were 108 unique combinations of origin country, arrival destination and vector category for the windborne dispersal pathway, 2,139 combinations for the commercial shipping (excluding live exports) pathway, 1,428 combinations for the returning live export vessels pathway and nine combinations for entry of insects via the Torres Strait Treaty pathway.

<sup>3</sup> The range of qualitative likelihood values at each node for each pathway is shown. N negligible; EL extremely low; VL very low; L low; M moderate; H high. Nodes R<sub>7</sub> to R<sub>10</sub> and R<sub>9</sub> to R<sub>10</sub> are absent from the windborne dispersal pathway and Torres Strait Treaty pathway, respectively.

### *Windborne dispersal*

All combinations for the windborne dispersal pathway were considered negligible. The combination of two 'low' nodes or a 'moderate' and a 'low' node at R<sub>1</sub> and R<sub>2</sub> generated a cumulative likelihood of 'very low', which was subsequently combined with a 'low' node at R<sub>4</sub> or R<sub>5</sub> and a 'very low' or 'negligible' node at R<sub>a</sub> resulting in all combinations being negative by R<sub>b</sub> (see Figure 17).

### *Commercial shipping (excluding live export)*

All combinations for introduction of infectious vectors via commercial ships (excluding live export vessels) were considered negligible. The 'negligible' likelihood at R<sub>1</sub> eliminated 447 combinations, while the 'negligible' or 'extremely low' likelihood at node R<sub>5</sub> eliminated a further 867, with all remaining cumulative combinations being 'very low' or 'extremely low' (see Figure 17). When combined with the 'low' likelihood at R<sub>6</sub> and the 'very low' likelihood at node R<sub>9</sub>, all remaining combinations became 'negligible' by node R<sub>10</sub>.

### *Returning live export vessels*

All combinations for introduction of vectors via returning live export vessels were considered negligible. As for commercial shipping, the 'negligible' likelihood at R<sub>1</sub> eliminated 327 combinations, while the 'negligible' or 'extremely low' likelihood at node R<sub>5</sub> eliminated a further 600 (see Figure 17). When combined with the 'very low' likelihood at node R<sub>6</sub>, all remaining combinations became 'extremely low' or 'negligible' by node R<sub>7</sub> and 'negligible' by node R<sub>8</sub>.

### *Torres Strait Treaty*

All combinations for the Torres Strait Treaty pathway were considered negligible. This is primarily due to the 'negligible' classification at R<sub>1</sub> because of low cattle density in PNG (low uncertainty) (Figure 9). Further, for all destination regions, bovine density at arrival destination (R<sub>a</sub>) was also 'negligible' (low uncertainty) (Figure 9). In other words, due to the low bovine density around PNG Treaty villages and the lack of cattle in the Torres Strait regions, all combinations are negligible with low uncertainty.

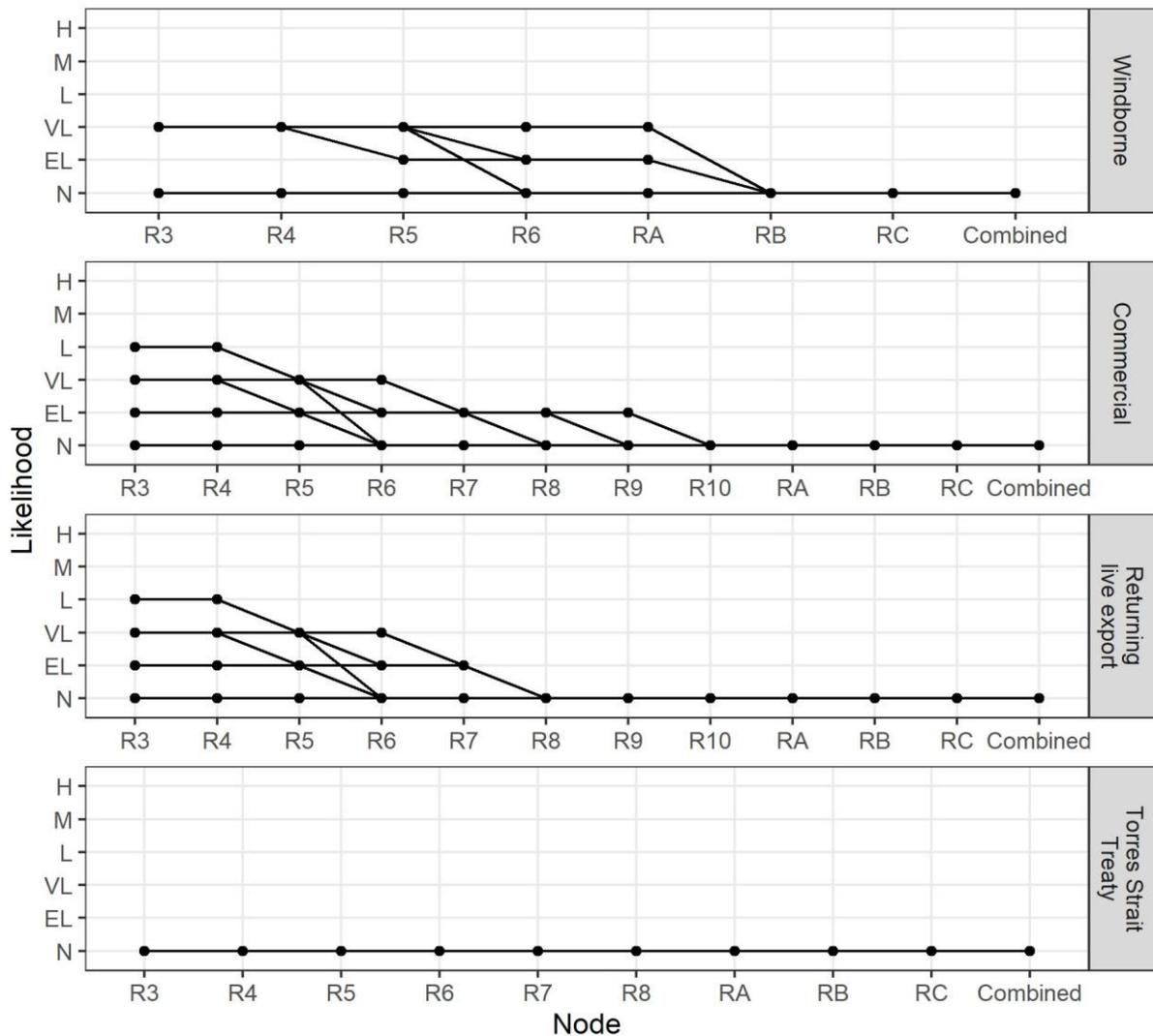


Figure 17 Cumulative qualitative likelihood at each node, by pathway<sup>4</sup>

#### 4.7.2 Semi-quantitative analysis

Because of the poor resolution from the qualitative assessment (that is, all pathways being negligible) we also conducted a semi-quantitative risk assessment. It is important to note that the final semi-quantitative probability for each combination of variables (i.e. origin, destination, vector category) within each pathway is unitless. Our semi-quantitative analysis provides a summary measure of the proportion of higher risk nodes present for each specific combination of variables, relative to other combinations within

<sup>4</sup> Qualitative likelihoods were iteratively combined over each node using the matrix described in the Methodology. The combined likelihood going into each node is shown. N negligible; EL extremely low; VL very low; L low; M moderate; H high. Nodes R7 to R10 and R9 and R10 are absent from the windborne dispersal pathway and Torres Strait Treaty pathway, respectively.

that pathway. Results between pathways cannot be compared due to differences in the length of pathways resulting in smaller numbers for longer pathways.

#### *Windborne dispersal*

The semi-quantitative likelihood for the windborne dispersal pathway was assessed as higher for midges, relative to mosquitoes and heavy fliers (Figure 18). This was due to midges being assessed as more likely to be transported via wind ( $R_5$ ). NAQS risk zones (Figure 11) W3, W4, W5, N10, N1a, N8a and b, N9 and Q6a were found to be the destinations at highest risk. This was driven by the higher cattle densities within these NAQS risk zones, parameterised in node  $R_a$  (Figure 9). Additionally, Q1a, Q1b and Q2 were identified as destinations of higher risk for heavy fliers only, due to the ‘moderate’ and ‘high’ likelihoods at  $R_4$  (bovine-vector transmission) and  $R_B$  (vector bites bovine), respectively. There were more NAQS risk zones within a 500 km radius of eastern Indonesia than for the other regions assessed.

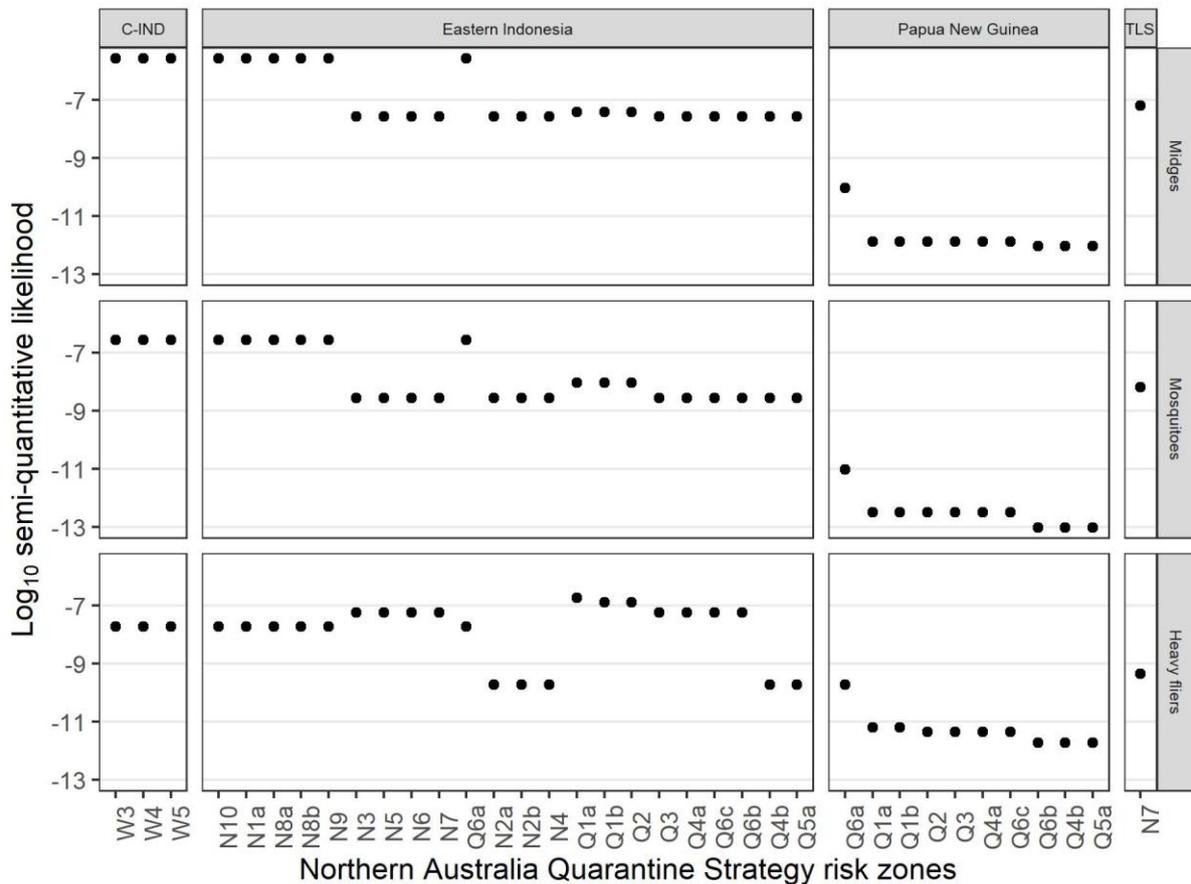


Figure 18 Semi-quantitative analysis of possible scenario trees within the windborne dispersal pathway<sup>5</sup>

*Commercial shipping (excluding live export)*

We found that the semi-quantitative likelihood estimates of LSDV incursion via commercial ships (excluding live export vessels) was broadly similar across all vector categories but varied depending on country of origin (Figure 19). Timor-Leste, India, Viet Nam, Thailand, Cambodia, the Philippines, Myanmar, Laos, Indonesia and Sri Lanka generally were found to have an elevated likelihood of importation of LSDV-infected vectors via commercial ships (excluding live export vessels) (Figure 19). These are the closer countries to Australia with the exception of PNG, which has a negligible cattle population (Figure 20). When looking at destination seaports, the risk ranking did not account for the volume of shipping traffic between origin country and destination or environmental conditions conducive to vector survival, so must be interpreted cautiously (Appendix 4). For example, Launceston and Hobart were among the higher risk seaports, due to the relatively high cattle density within the SA2 area in which

<sup>5</sup> Qualitative categories were converted to maximum probabilities based on Table 1 and nodes within a pathway were multiplied together to derive a semi-quantitative likelihood value for each combination of origin country, vector category, and destination (n = 108). Plots are faceted by country of origin and vector category. Destinations (NAQS risk zones) that were >500 km from the country of origin were not assessed (see section 3.6). C-IND central Indonesia, TLS Timor-Leste. W Western Australia, N Northern Territory, Q Queensland.

these ports are located (Figure 13). However, most tropical insect species would be unlikely to survive well in these environmental conditions.

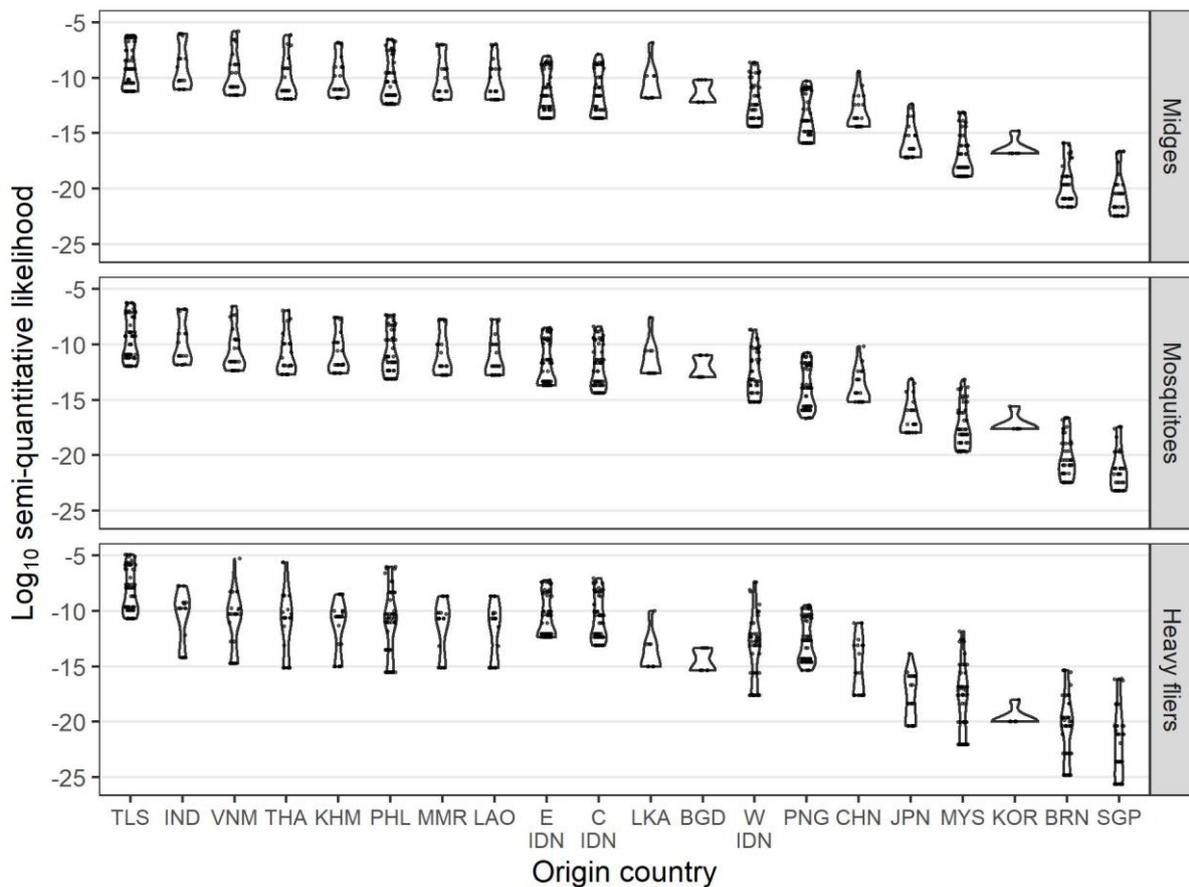


Figure 19 Semi-quantitative analysis of possible scenario trees within the commercial shipping (excluding live export vessels) pathway<sup>6</sup>

<sup>6</sup> Qualitative categories were converted to maximum probabilities based on Table 1 and nodes within a pathway were multiplied together to derive a semi-quantitative likelihood value for each combination of origin country, vector category and destination (n = 2,139). Violin plots show the distribution of log10-transformed semi-quantitative likelihood values by origin country, faceted by vector category. Individual points within each violin plot represent a different Australian seaport destination. TLS Timor-Leste, IND India, VNM Viet Nam, THA Thailand, KHM Cambodia, PHL Philippines, MMR Myanmar, LAO Lao People’s Democratic Republic, E eastern, IDN Indonesia, C central, LKA Sri Lanka, BGD Bangladesh, W western, PNG Papua New Guinea, CHN China and associated autonomous regions, JPN Japan, MYS Malaysia, KOR Republic of Korea, BRN Brunei Darussalam, SGP Singapore.

### Returning live export vessels

As for commercial ships (excluding live export vessels), semi-quantitative likelihoods were found to vary by origin country rather than vector category (Figure 20). The highest-risk origin countries were the Philippines, Indonesia, Thailand, Timor-Leste, and Viet Nam – generally the closer countries to Australia with the exception of PNG, which has a negligible cattle population (Figure 20). Again, the risk ranking of destination seaports did not account for the volume of shipping traffic between origin country and destination port, and so should be interpreted cautiously (Appendix 4). Overall, the semi-quantitative likelihoods for the returning live export vessels pathway were generally slightly lower than those estimated for the commercial shipping (excluding live export vessels) pathway. This was primarily driven by node R<sub>9</sub> (vector disembarks ship undetected) being higher (‘very low’) for the commercial shipping pathway than for the live export pathway (‘extremely low’), due to the extensive disinfection and inspection procedures in place for returning live export vessels.

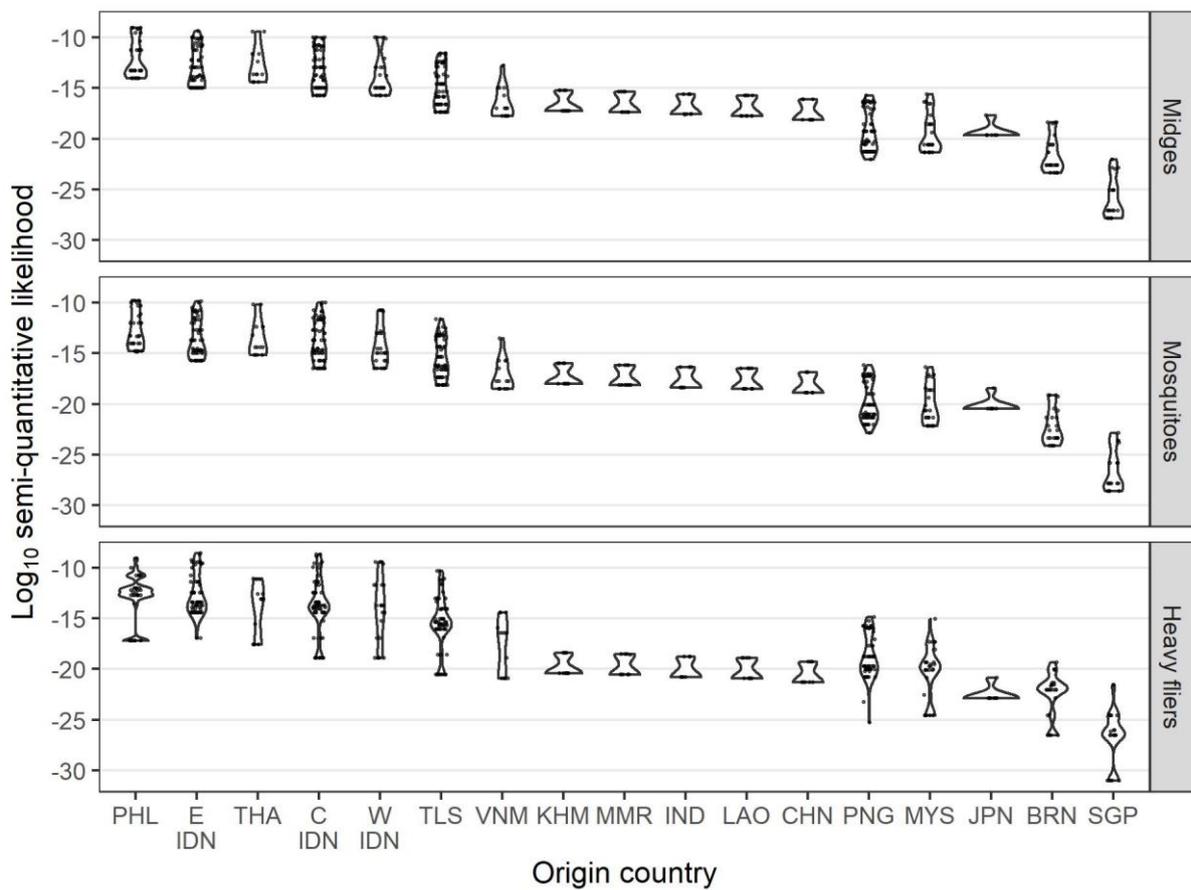


Figure 20 Semi-quantitative analysis of possible scenario trees within the returning live export vessel pathway<sup>7</sup>

### Torres Strait Treaty

The highest likelihoods were associated with heavy fliers, followed by midges and then mosquitoes (Figure 21). All NAQS risk zones assessed returned the same likelihoods, since cattle densities are negligible in all three zones.

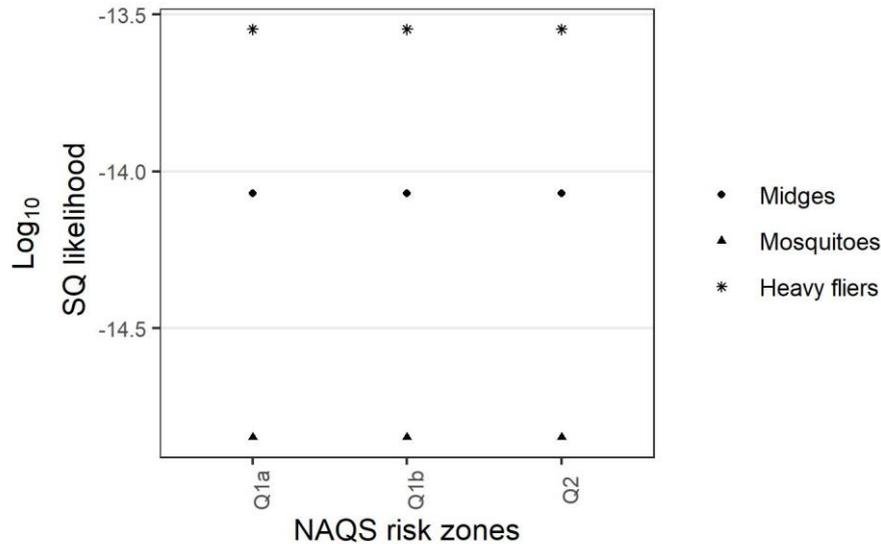


Figure 21 Semi-quantitative analysis of possible scenario trees within the Torres Strait Treaty pathway<sup>8</sup>

## 4.8 Sensitivity analysis

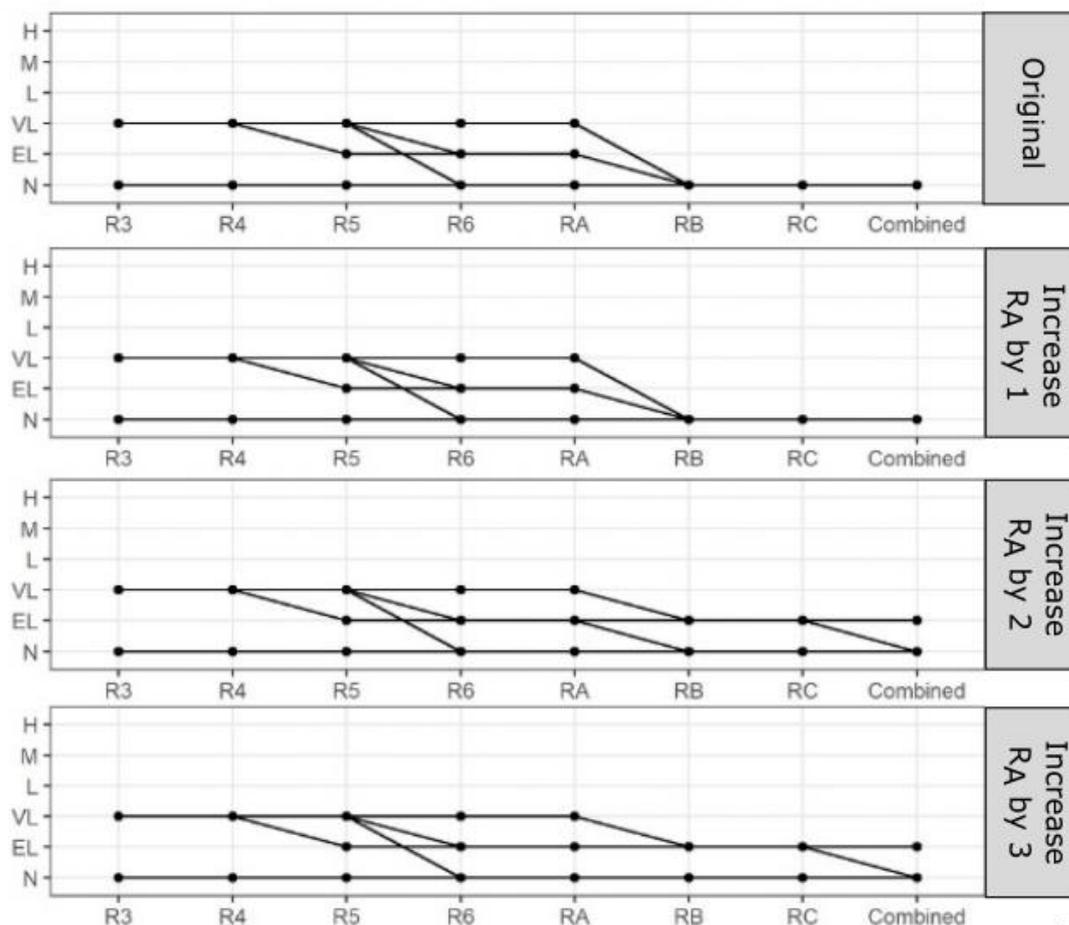
To assess the sensitivity of our results, we modified parameters at key nodes and re-evaluated the resulting qualitative likelihood outcomes.

Only for the windborne dispersal pathway did the final cumulative likelihood of LSDV importation change under our alternative scenarios (Figure 22). We explored the impacts of increasing cattle densities in the destination NAQS risk zones ( $R_a$ ) to simulate local heterogeneities in cattle populations in these regions. A survey of individual pastoral lease managers in the Western Kimberley region conducted in 2008 identified that mean stocking rates of these leases were 0.07 cattle per hectare, or seven cattle per km<sup>2</sup> (Cowled *et al.*, 2008), corresponding to the ‘very low’ category in our assessment. In contrast, using the ABS livestock census data, the cattle densities in these regions were classified as ‘extremely low’ (1–5 per km<sup>2</sup>). As this is a key node at which many pathways combined to negligible and there is clearly uncertainty at this node, we increased the likelihood categories at  $R_a$  for each NAQS risk zone by one, two, and three increments. All combinations remained negligible with an increase in cattle density by one

<sup>7</sup> Qualitative categories were converted to maximum probabilities based on Table 1 and nodes within a pathway were multiplied together to derive a semi-quantitative likelihood value for each combination of origin country, vector category and destination (n = 1,428). Violin plots show the distribution of log<sub>10</sub>-transformed semi-quantitative likelihood values by origin country, faceted by vector category. Individual points within each violin plot represent a different Australian seaport destination. PHL Philippines, E eastern, IDN Indonesia, THA Thailand, C central, W western, TLS Timor-Leste, VNM Viet Nam, KHM Cambodia, MMR Myanmar, IND India, LAO Lao People’s Democratic Republic, CHN China and associated autonomous regions, PNG Papua New Guinea, MYS Malaysia, JPN Japan, BRN Brunei Darussalam, SGP Singapore.

<sup>8</sup> Qualitative categories were converted to maximum probabilities based on Table 1 and nodes within a pathway were multiplied together to derive a semi-quantitative likelihood value for each combination vector category and destination (n = 24). Plots are faceted by vector category. Q Queensland.

category. However, after increasing livestock densities by two categories, the following combinations yielded a cumulative qualitative likelihood of LSDV incursion of ‘extremely low’: midges from central Indonesia to W3, W4, W5; midges from eastern Indonesia to N10, N1a, N8a, N8b, N9, Q6a; heavy fliers from eastern Indonesia to Q1a, Q1b, Q2. Increasing  $R_a$  by three categories identified the following combinations as extremely low, in addition to those just described: midges from eastern Indonesia to N2a, N2b, N3, N4, N5, N6, N7, Q1a, Q1b, Q2, Q3, Q4a, Q4b, Q5a, Q6b, Q6c; midges from Timor-Leste to N7; heavy fliers from eastern Indonesia to N3, N5, N6, N7, Q3, Q4a, Q6b, Q6c. Even increasing  $R_a$  by three likelihood categories, the LSDV incursion risk by windborne dispersal did not exceed ‘extremely low’.



**Figure 22 Sensitivity analysis for the windborne dispersal pathway.** The cumulative qualitative likelihood at each node is shown, after adjusting  $R_a$ , the livestock density at arrival destinations (NAQS risk zones).

For both shipping pathways, we systematically increased nodes  $R_4$ ,  $R_5$ ,  $R_6$ ,  $R_7$  and  $R_8$  by one likelihood category. Node  $R_3$  was not modified because vector presence was already considered to be high in all origin countries. Node  $R_9$  was not modified because there was low uncertainty around the likelihood of an insect disembarking a ship in Australia. Under all alternative scenarios, the likelihood of LSDV importation via hitchhiker arthropods on commercial ships (Figure 23) and returning live export vessels (Figure 24) remained negligible. This highlights the importance of the biosecurity measures already in place to control arthropod pests, i.e. node  $R_{10}$ .

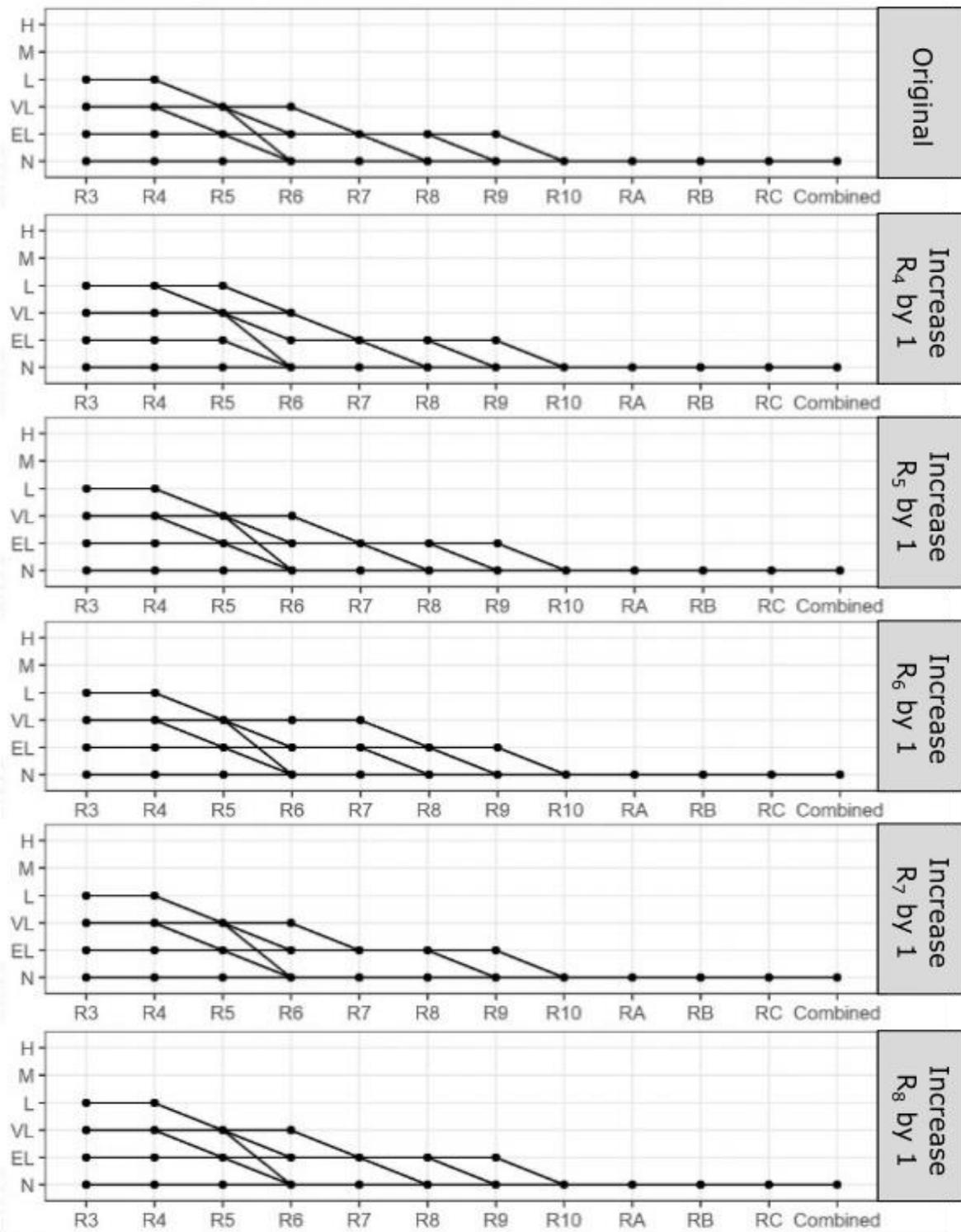


Figure 23 Sensitivity analysis for the commercial shipping (excluding live export) pathway. The cumulative qualitative likelihood at each node is shown, after adjusting individual parameters.

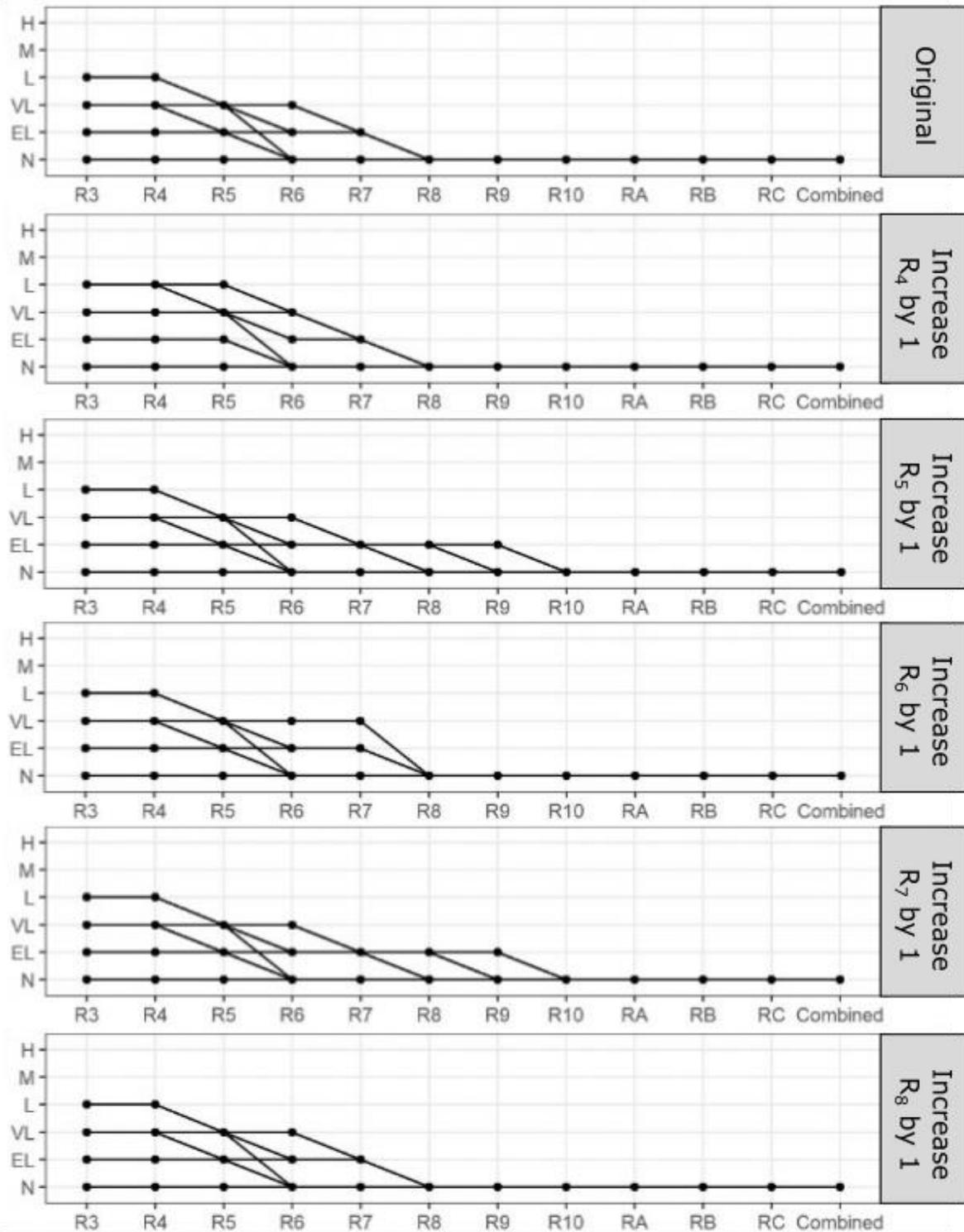


Figure 24 Sensitivity analysis for the live export vessels pathway. The cumulative qualitative likelihood at each node is shown, after adjusting individual parameters.

For the Torres Strait Treaty pathway, we used alternative scenarios whereby the cattle and buffalo density in PNG was increased to extremely low (1–5 per km<sup>2</sup>), very low (5–8 per km<sup>2</sup>), low (8–15 per km<sup>2</sup>) or moderate (15–50 per km<sup>2</sup>) densities. The cumulative likelihood of importation of LSDV via the Torres Strait Treaty pathway remained negligible under all alternative scenarios (Figure 25), principally because of the negligible cattle densities in the arrival destinations (R<sub>a</sub>) (Figure 9).

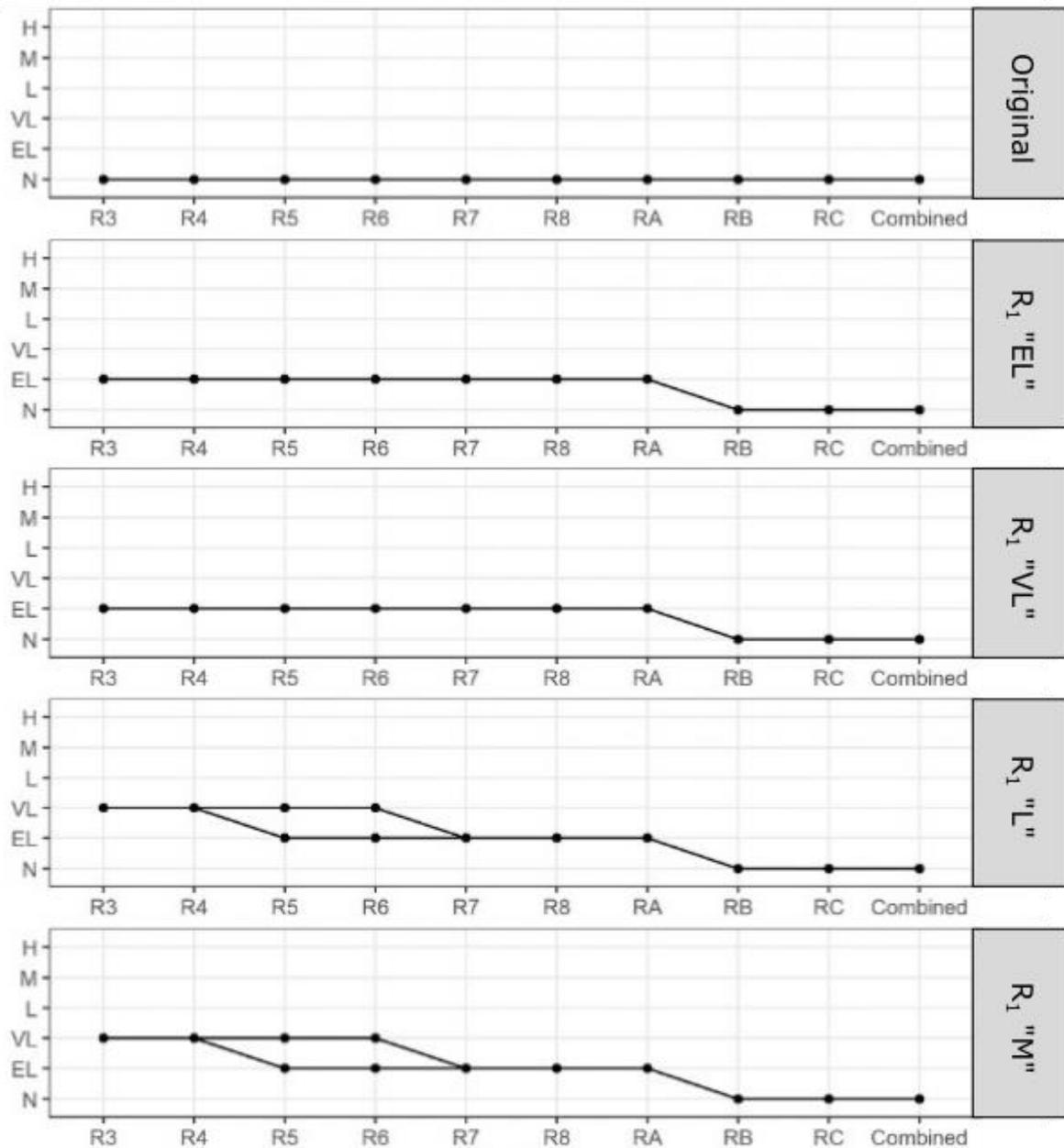


Figure 25 Sensitivity analysis for the Torres Strait Treaty pathway. The cumulative qualitative likelihood at each node is shown, after adjusting  $R_1$ , the livestock density in PNG.

## 4.9 Potential impacts of climate change

Climate change through human-induced greenhouse gas emissions has resulted in marked warming since the mid-20th century (IPCC, 2021). Australia has already experienced increasing temperatures, shifting rainfall patterns and rising oceans, presenting considerable challenges to humans, animals and the environment (Moise *et al.*, 2015). Much attention has been focussed on the impacts of climate change on vector-borne diseases, although not necessarily specifically in the Australian context (reviewed in Rocklöv and Dubrow, 2020). A major threat to Australia is the introduction and establishment or range expansion of important vector species such as *Aedes albopictus* or *Aedes aegypti*, respectively (Hall *et al.*, 2021).

Therefore, it is reasonable to consider the impacts of climate change on the risk of LSDV incursion into Australia.

Global climate modelling projections are generally divided into 20-year time periods, representing different emission scenarios (Moise *et al.*, 2015). Here we consider only near future (i.e. 2020–2039) projections, as approaches to disease control and agricultural practices are likely to change markedly by the end of this century, limiting the usefulness of any further projections.

Substantial future warming is projected with very high confidence for northern Australia, including the Torres Strait. Mean warming is predicted to increase by 0.5–1.3°C above 1986–2005 levels, and maximum and minimum temperatures are also projected to increase (Suppiah *et al.*, 2011; Moise *et al.*, 2015). Northern Australia is expected to experience an increase in the frequency of hot days and a longer duration of warm spells (Moise *et al.*, 2015). While warmer climates are generally conducive to insect survival, optimal temperatures for survival and development of mosquitoes, midges and heavy fliers are typically between 20–25°C (Gilles, David and Duvall, 2005; Hendrickx *et al.*, 2008; Venter, Boikanyo and de Beer, 2019; Rocklöv and Dubrow, 2020; Tugwell *et al.*, 2021). Therefore, increased temperatures may inhibit LSDV vector survival to some extent, particularly during the high-risk monsoon season (December to April) for windborne dispersal.

Through the 20th century there was a trend towards slightly increased rainfall, particularly across the north-western regions (Moise *et al.*, 2015). However, natural variability, including prolonged periods of drought as well as above average rainfall driven in part by the El Niño Southern Oscillation, has dominated these longer-term trends. Natural climate variability is expected to continue to be the major driver of annual mean rainfall in northern Australia, although substantial changes to wet-season rainfall cannot be ruled out (based on conflicting results from different models) (Moise *et al.*, 2015). The Torres Strait is perhaps projected to experience less change in rainfall than other parts of northern Australia (Suppiah *et al.*, 2011). The intensity of heavy rainfall events is projected to increase, with high confidence, while changes to drought frequency are less clear (Moise *et al.*, 2015). Changes in relative humidity are projected to be minimal (Suppiah *et al.*, 2011; Moise *et al.*, 2015). Moderate to heavy rainfall is known to impede flight of *Culicoides* (Burgin *et al.*, 2013; Eagles *et al.*, 2014). However, vector abundance is widely known to be associated with wet areas, with LSDV outbreaks typically coinciding with the onset of the rainy season in endemic regions (Tuppurainen and Oura, 2012). Overall, rainfall changes due specifically to climate change are unlikely to be major drivers of LSDV dynamics in northern Australia.

Only small changes in mean surface wind speed (i.e. -4 to +3% for northern Australia and -1.12 to 2.47% for the Torres Strait) are projected for northern Australia under near-future climate models (Suppiah *et al.*, 2011; Moise *et al.*, 2015). Tropical cyclones are projected, with medium confidence, to increase in intensity (by 2–11%) but are anticipated to occur less frequently (Suppiah *et al.*, 2011; Moise *et al.*, 2015). While these cyclone events may be more likely to transport vectors from our near neighbours, strong winds are known to inhibit flight activity and reduce insect survival, particularly for fragile species like mosquitoes (Hendrickx *et al.*, 2008; Agren *et al.*, 2010; Boyle *et al.*, 2012; Sanders *et al.*, 2012; Sedda *et al.*, 2012; Chen *et al.*, 2020).

The potential impacts of climate change on international shipping were also investigated. Overall, the demand for international shipping is expected to continue to grow into the future, independent of the impacts of climate change (Kuhn and Beaufoy, 2009). This will likely increase the volume of shipping travel to Australia; however, the volume of shipping was not considered in our assessment and therefore this would not affect our results. Importantly, shipping is also likely to become more expensive until a workable global solution to reducing carbon emissions is established (Kuhn and Beaufoy, 2009). This could lead to reduced demand for international freight if local alternatives are available. The direct impacts of climate change on international shipping are likely to be related to an increased frequency and intensity of extreme weather events. This could lead to damage to ships, cargo and ports, changes in

shipping routes, and perhaps higher fuel consumption by ships due to changes in wind velocity and patterns (Kuhn and Beaufoy, 2009). All of these are likely to lead to increased travel times, thereby reducing the risk of importing life and infectious vectors in the context of LSDV transmission.

Overall, we determined that climate change projections were not likely to unequivocally increase any of the parameter estimates in our qualitative model. Thus, we did not re-evaluate our assessment for future climate scenarios.

## 5 Discussion and conclusions

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We undertook a qualitative risk assessment for the entry of LSDV into Australia via four unregulated pathways. For each pathway we defined a scenario tree comprising successive nodes, each of which must occur for the incursion of LSDV into Australia. We did not assess the consequences of entry, as we assumed it to be extreme. Each pathway comprised different combinations of origin country and arrival destination, and all combinations were assessed separately for three separate vector categories: midges, mosquitoes and heavy fliers. Overall, there were 3,684 individual combinations assessed across the four pathways.

We parameterised each node within each scenario tree conditionally for origin country, destination and/or vector category where relevant, using data sourced from the peer-reviewed literature, grey literature and expert opinion from various reputable sources. Parameters were converted to qualitative likelihood categories and these categories were combined across all nodes within a pathway using a matrix approach to generate a cumulative qualitative likelihood for each combination.

Based on our qualitative risk assessment methodology, the risk of LSDV entry into Australia via all pathways was negligible. Critically, this assessment is unitless and does not account for the absolute number of vector arrivals. Since an LSDV incursion is a binomial process, even an event with a negligible likelihood of occurrence may come to pass if the volume of arthropods arriving in Australia is high. Based on Table 1, the maximum probability corresponding to the negligible qualitative likelihood category was  $10^{-5}$ . Hence, for every one million arthropods that arrive in Australia we could anticipate a median of 10 LSDV incursions, even with a negligible likelihood categorisation. For example, a recent risk assessment of LSDV spread in South, East and Southeast Asia returned a negligible risk of incursion with low uncertainty for Singapore, which then experienced an outbreak (in highly susceptible dairy breeds) within two years (Roche *et al.*, 2020). Nevertheless, it is unlikely that the introduction of one infectious vector will result in LSDV establishing in Australia, as a swarm of insects is widely considered to be necessary to initiate a bovine infection (Yeruham *et al.*, 1995; Chihota *et al.*, 2003; Kahana-Sutin *et al.*, 2017; Sohler *et al.*, 2019; Issimov *et al.*, 2020; Sanz-Bernardo *et al.*, 2021). In this context and taken together with likely BTV incursion scenarios, this is likely to be a cluster of midges (or other insects) that are taken up during a weather event and deposited at a reasonably discrete location where there is a cluster of cattle on arrival in the risk zone in Australia. This limits the application of deterministic and average density approaches. Furthermore, given the low cattle densities in northern Australia, the infection of one animal may not necessarily result in disease establishment and spread. Thus, the term ‘negligible’ should be interpreted in the broader context of Australia’s biosecurity systems, taking into account the absolute frequency of arthropod incursions via the pathways analysed here.

To better assess the relative risk of the different pathways and combinations within each pathway, we also conducted a semi-quantitative analysis. While semi-quantitative analysis has several limitations (Krisper, 2021), it may avoid some of the ambiguities and range compression of a qualitative risk assessment and is often considered to be very useful by risk managers (De Vos *et al.*, 2019; European Food Safety Authority *et al.*, 2020).

Within each pathway, we were able to identify certain vector categories, origin countries and/or destinations that were associated with higher likelihoods of LSDV entry and exposure. For windborne dispersal, midges returned the highest likelihood values for LSDV incursion. It is well-known that midges in particular, but also mosquitoes and other haematophagus insects, can be dispersed over long distances via weather events (Muller *et al.*, 2001; Johansen *et al.*, 2003, 2004, 2005; Hemmerter *et al.*, 2007; Hendrickx *et al.*, 2008; Agren *et al.*, 2010; Boyle *et al.*, 2012; Sedda *et al.*, 2012; Beebe *et al.*, 2013; Burgin *et*

*al.*, 2013; Eagles *et al.*, 2014; Lessard *et al.*, 2021). By origin country, central and eastern Indonesia were associated with the highest likelihood values, although the only other countries evaluated for windborne dispersal were Timor-Leste, which was only within 500 km of NAQS risk zone N7, and PNG, for which the livestock density was considered negligible. By arrival destination, Western Australian regions W3, W4 and W5, the Northern Territory regions N10, N1a, N8a and b, N9, and the Queensland regions Q6a, Q1a, Q1b and Q2 had higher likelihood values than other risk zones. The Northern Territory in particular, but also Western Australia, have previously been identified as high-risk regions for wind-assisted dispersal of *Culicoides* from Timor-Leste and parts of Indonesia (Eagles *et al.*, 2012). Further studies also revealed that dispersal was possible to the northern parts of Queensland from eastern Indonesia and PNG (Eagles *et al.*, 2013).

For the shipping pathways, high-risk origin countries included the Philippines, Timor-Leste, Indonesia, India, Thailand, Viet Nam, Cambodia, Myanmar, Laos and Sri Lanka, depending on vessel type. Notably, one key parameter, the prevalence of actively infected and symptomatic animals in these countries, is highly uncertain. Even when endemic, LSDV incidence will not be homogeneous, either geographically or temporally (Tuppurainen and Oura, 2012). Likewise, vector abundances will also vary considerably by season. Therefore, the inferences gained from ranking countries without accounting for temporal and spatial variation in disease incidence and vector abundance are likely to be limited. The semi-quantitative likelihood of LSDV incursion did not vary appreciably between vector categories for the shipping pathways. Ranking of destinations was problematic because we did not account for the volume of shipping traffic into each destination seaport. For example, the ports of Hobart and Launceston were associated with higher likelihood values due to the relatively high density of cattle within these SA2 regions. Yet one would presume Tasmanian ports would be at considerably lower risk than highly trafficked mainland ports. Furthermore, environmental conditions at these ports are not conducive to establishment and spread of vectors, a fact that was not accounted for in this analysis. These limitations should be taken into consideration when interpreting the outputs of this assessment.

Heavy fliers were associated with the highest likelihoods of LSDV incursion for the Torres Strait Treaty pathway, while mosquitoes were ranked lowest. However, because of the very low numbers of cattle in PNG and the Torres Strait islands this route was considered highly unlikely overall. Heavy fliers such as stable flies are aggressive feeders, biting repeatedly and irritating the host, which leads to frequent host switching (Scoles *et al.*, 2005; Baldacchino *et al.*, 2013). Many species do not have the classical gonotrophic cycle typical of mosquitoes and midges and therefore feed constantly, and generally both the males and females take protein meals. Thus, transmission of LSDV both from bovine to arthropod and from arthropod to bovine were considered highest with heavy fliers.

## 5.1 Limitations and assumptions

The conclusions that could be drawn from the qualitative risk analysis were limited because of the negligible outcome for all pathways assessed. Therefore, we also elected to undertake a semi-quantitative risk assessment to better assess the relative rankings of different scenarios within a pathway. Semi-quantitative approaches may offer a more consistent approach to evaluating risks compared to a qualitative approach, avoiding some of the ambiguities and range compression without requiring the detailed data or mathematical skills for a quantitative approach (European Food Safety Authority *et al.*, 2020).

We elected to convert the qualitative likelihood categories to maximum probabilities based on a previously described methodology (Biosecurity Australia, 2004) (Table 1). We then multiplied these discrete probabilities together in a deterministic approach, based on a previous semi-quantitative analysis methodology for the introduction of African swine fever virus into Belgium (Mauroy *et al.*, 2021). We

chose to use probability values, rather than a Likert scale as previously reported, because of the known limitations to combining ordinal values (Krisper, 2021). However, we note that the distribution of probability ranges that we used (Table 1) is arbitrary and applied equally to all parameters, which may not represent the underlying processes appropriately (Krisper, 2021).

In addition, this semi-quantitative approach also does not account for ‘the weakest link’ concept. Practically speaking, an event at a specific node is contingent on outcome of the previous nodes. However, in this semi-quantitative analysis the nodes are simply multiplied together. Therefore, if the likelihood of one event in the chain is negligible but the likelihood of other events in the chain are high, the overall likelihood score may be overestimated, when in reality the pathway is negligible because the ‘weakest link’ in the pathway has a negligible likelihood of occurring.

It is critical to note that, due to the different number of nodes in the scenario trees, we were not able to directly compare the four pathways. This is because, when multiplying numbers less than one, more multiplications will always lead to smaller numbers. The final semi-quantitative likelihood values are unitless and should simply be used to rank combinations within pathways.

The inclusion of additional categories in our qualitative analysis may have reduced the observed range compression; however, given the uncertainty around many of the parameter estimates, this would likely have introduced further quantification errors (Krisper, 2021). Indeed, the inclusion of additional categories has been suggested to avoid the well-established observation that extreme positions tend to be avoided during expert elicitation (Vose, 2000; Krisper, 2021). A quantitative risk assessment would avoid this range compression.

For both qualitative and semi-quantitative assessments, the choice of categories and cut-offs will directly influence the outcomes of the analysis. For example, we subdivided livestock densities into six categories: <1; >=1–5; >=5–8; >= 8–15; >= 15–50; >= 50 cattle per km<sup>2</sup>. It is not known what minimum cattle density is required to sustain an epizootic of LSDV. Therefore, practically, higher densities could have been more appropriately categorised as negligible; alternatively, perhaps we should have reserved the negligible category for areas where bovines were completely absent. Also, cattle are not randomly distributed; there is considerable clustering of livestock, particularly around watering points, which are also ideal habitats for vector establishment. This could increase the risk of transmission in certain locations. Similarly, the division of urbanisation index into six even quantiles may not be appropriate as risk may not scale linearly. Again, a quantitative approach would avoid the requirement for categorisation of variables that was necessary for our qualitative and semi-quantitative analysis.

Importantly, all forms of risk assessment depend on the quality of the underlying input parameters. These are subject to not only variability (the intrinsic distribution of values that a parameter can take) but also uncertainty, which depends on the level of knowledge about a parameter. Many parameters used in our analysis were associated with a high level of uncertainty, and many of the virological parameters are inherently variable. However, we did not explicitly incorporate uncertainty into our overall analysis, beyond assigning an uncertainty level to each individual parameter. Further research should be directed to addressing these uncertainties to improve our understanding of the risk of LSDV entry into Australia. A quantitative analysis would facilitate incorporation of uncertainty and variability into the assessment.

We defined countries of interest based on the distance from Australia, given expected vector survival times either on a ship or in wind currents. Insect survival time is highly uncertain, and therefore we may have excluded relevant origin countries if survival was longer than expected or if the distribution of insect survival time had an extended tail. For example, living Australian *Culicoides* have been detected in Chinese seaports, suggesting that longer duration travel is possible (Nie *et al.*, 2005). Windborne dispersal was implicated in the 1999 outbreak of BTV-16 in Rhodes, Greece, with Israel (over 700 km away) suggested as the source of the incursion (Ducheyne *et al.*, 2007). The mosquito *Culex tritaeniorhynchus* was reportedly

detected flying up to 500 km over ocean in the Northwest Pacific (Asahina, 1970). Therefore, the 500 km radius for windborne dispersal may not have been appropriate. The next closest origin countries (Philippines, Malaysia and western Indonesia) are all over 2000 km away from any NAQS risk zones. Critically, unlike BTV there is no evidence for active replication of LSDV in the arthropod vector, so it is problematic to extrapolate based on experiences with BTV. It is important to continue to bear in mind the biological differences between these virus families when comparisons are made.

We also did not incorporate directionality of airflow in this assessment. Previous research identified that the highest risk for incursion of exotic arthropod vectors was from December to April, during the tropical monsoon season (Eagles *et al.*, 2012). During this time, westerly to north-westerly winds flow from the Indian Ocean and southern Asian waters towards Australia (Moise *et al.*, 2015). In contrast, east to south-easterly trade winds dominate in northern Australian and Southeast Asia outside of the monsoon season (Moise *et al.*, 2015). El Niño events are associated with decreased strength of easterly trade winds and decreased convection over tropical regions, while La Niña events generally correspond to an increase in rainfall events, tropical cyclones and increased strength of the trade winds (Moise *et al.*, 2015). If ship or wind speed was faster than anticipated, the risks determined in this assessment would also have been underestimated, although the ship speeds used were maximum speeds. Further input from expert marine engineers and meteorologists may help to reduce this uncertainty. However, our distance calculations were based on straight-line distances to the closest land border, not accounting for circuitous shipping routes or obstacles such as land masses. Therefore, we assume that our travel times for shipping are probably underestimated. For example, our shipping time from China to Dampier was estimated at four days, while online reports suggest a travel duration of at least nine days (VesselFinder, no date).

We classified points of origin at the country level, which arguably does not provide adequate geographic resolution. Parameters such as livestock density at the country of origin ( $R_1$ ), LSDV incidence ( $R_2$ ), vector abundance ( $R_3$ ), likelihood that vectors will disperse to ports ( $R_5$ ), likelihood of vectors landing on the ship ( $R_6$ ) and likelihood of the ship travelling to Australia ( $R_7$ ) will vary considerably within a country. For example, some ports are likely to be in closer proximity to cattle and therefore are likely to have a higher vector abundance; ports with fewer ships may have a higher likelihood of vectors landing on that specific ship; transport to Australia will be more likely from certain ports. Similarly, for windborne dispersal, the risk from more distant regions within an origin country may be lower than from the closest land border, although this depends too on the distribution of hosts and vectors. Airflow is also known to be more turbulent over land (Gloster *et al.*, 2008). More detailed analyses at higher spatial resolution should be conducted for specific origin countries of interest.

For our windborne dispersal pathway, we used NAQS risk zones as our arrival destinations. This was consciously chosen in consultation with the Department and NAQS staff because of the utility of NAQS risk zones for animal biosecurity. However, our analysis did not account for the different sizes of the various NAQS areas. Logically, larger NAQS areas will be at overall higher absolute risk of vector incursions by wind. Furthermore, NAQS areas only extend for a relatively short distance beyond the coastline, whereas vectors may be deposited by wind further inland, where the density of susceptible hosts and conditions for vector establishment may be different to that at the coastline. For example, the detection of two exotic *Culicoides* species from Douglas Daly shows that dispersal beyond the NAQS risk zones is possible. However, no origin source outside Australia could be identified for this incursion, raising the possibility of onwards spread from an initial undetected incursion site within Australia. This highlights a need for enhanced surveillance for midges and other vector species relevant to LSDV transmission beyond the current NAQS risk zones. Notably, based on 2016 ABS livestock census data the cattle densities remain negligible or extremely low across most of northern Australia, somewhat mitigating this concern (Figure 13). Alternative classifications of arrival destinations that were considered included SA2, SA4 and natural resource management regions. The latter two systems span very large areas

in northern Australia with limited geographical resolution and thus were not considered to be appropriate. SA2 regions are based on human population density and also covered large spatial scales in parts of northern Australia, as well as not being particularly relevant to animal surveillance efforts. For these reasons, NAQS risk zones were chosen despite the noted limitations. Unfortunately, livestock densities based specifically on NAQS risk zones are not available. Therefore, we extrapolated based on livestock density at the SA2 level. More detailed information on livestock densities in at-risk areas of northern Australia would be extremely valuable. Alternatively, information on total cattle numbers and station areas could be obtained directly from individual stations in the relevant risk areas.

Critically, many of the parameters used in our risk assessment will vary over time. For example, the incidence of LSDV is highly likely to increase in the future in our near neighbours. Immediately following a novel incursion, when a population is maximally susceptible and prior to mitigation strategies being implemented, it is expected that there will be local peaks with extremely high disease incidence occurring in a series of waves, as is typical for emerging pathogens. The spread of LSDV will also depend on the response mounted by animal health authorities, which depends on the capacity of veterinary services at both national and local levels. Once endemic, incidence will likely also fluctuate in seasonal and cyclic patterns. Typically, LSD outbreaks occur in cycles over several years, coinciding with environmental conditions that favour high vector abundance (Tuppurainen and Oura, 2012). Therefore, the incorporation of spatial and temporal disease incidence is necessary to fully understand the incursion risk to Australia from LSDV.

Cattle densities, both in the country of origin and at the arrival destination, will also change over time. Our Australian livestock densities were derived from the 2016 ABS livestock census data; an updated dataset is likely to be released this year but was not available for this assessment. Livestock densities for origin countries were derived from FAOSTAT (FAO, 2022). Data obtained through sources such as this are likely to vary in quality depending on the primary source.

Vector abundance, too, will vary considerably on both seasonal and cyclic patterns. Furthermore, it is widely acknowledged that climate change is impacting vector abundance and distribution, although the interactions between climate and arthropod populations and disease transmission are complex and often unpredictable (Beebe *et al.*, 2013; Rocklöv and Dubrow, 2020). Here, we parameterised node  $R_3$  as either vectors present or vectors absent, without attempting to classify relative abundance between origin countries. Since this node was classified as high for all combinations, this may have overestimated the risk from some origin countries and contributed to the difficulties in ranking risks between countries. A better understanding of differences in vector abundances across countries would be useful to incorporate into future analyses.

We elected to group vectors into three categories: midges, mosquitoes and heavy fliers. Importantly, there is considerable species variation within these categories. For example, anthropophilic species of mosquito are of much less relevance to this assessment than zoophilic species. Yet many of the experimental studies on vector-borne transmission of LSDV have utilised *Aedes aegypti*, which is known to be anthropophilic but is readily available in laboratory settings due to its importance in the transmission of *Plasmodium* (which causes malaria), dengue virus and other pathogens (Chihota *et al.*, 2001; Sanz-Bernardo *et al.*, 2021). In contrast, there is no peer-reviewed literature on the role of calliphorids or *Musca* species beyond the *Stomoxys* genus in LSDV transmission, although these are known to be very effective mechanical vectors for diseases such as rabbit calicivirus and many human pathogens (Asgari *et al.*, 1998; Khamesipour *et al.*, 2018). Our entomology experts expressed concern about grouping so many species together; however, given the lack of species-specific vector information in the literature, further breakdown by vector category is unlikely to be useful.

For many nodes, specific data on the parameter of interest were not available and so proxy measures were used. Perhaps the most contentious of these were HDI in lieu of LSDV incidence and urbanisation index

in lieu of data on the spread on insects from livestock production areas to seaports. We readily acknowledge that both these proxies are far from ideal. Future assessments should focus on identifying more informative data sources to parameterise these nodes. Likewise, for the commercial shipping pathway we used the relative weight of trade to estimate the likelihood that a ship travels to Australia ( $R_7$ ). In fact, what we actually want to measure is both the probability that a ship in a port at an origin country is a commercial ship, and the probability that that ship will travel to Australia rather than to another country. For example, in the hypothetical situation where Australia received 100% of trade weight from country X we would have parameterised  $R_7$  as 100%. Yet country X may trade mostly (90%) with country Y and only 10% with Australia, and 50% of ships in port may be domestic ships. Thus, the actual probability of any given ship travelling to Australia from country X would only be 5%. Similarly, for node  $R_6$  for both shipping pathways, if only 1% of vessels in a port are commercial ships or returning live export vessels, then despite what the probability is of a vector landing on a ship, the chance that it is a ship of relevance to the LSDV assessment would be much lower. For both scenarios, our assessment would have further overestimated the cumulative risk of LSDV entry.

When analysing the outputs of our semi-qualitative assessment, we observed that the ranking of destination seaports for both shipping pathways was unexpected. For example, Launceston and Hobart were among the highest likelihood seaports for incursion of LSDV, while Darwin, Broome, Wyndham and Cairns were ranked comparatively low. This was because we did not account for differences in shipping traffic to different arrival ports, nor did we consider whether the environmental conditions at each port were conducive to vector spread and establishment. These data should be incorporated into future assessments.

There was considerable uncertainty around whether incursion of a single infectious vector could lead to an outbreak, given there is no evidence for viral replication within arthropod vectors (unlike for BTV). The current available literature discusses LSDV transmission always in the context of vector swarms. For example, field outbreaks of LSDV are strongly correlated with periods of high vector abundance, rather than simply the presence of individual vectors (Yeruham *et al.*, 1995; Kahana-Sutin *et al.*, 2017). Experimental transmission studies on LSDV have all used batches of insects (50–300 insects per batch) (Weiss, 1968; Chihota *et al.*, 2001, 2003; Magori-Cohen *et al.*, 2012; Sohier *et al.*, 2019; Issimov *et al.*, 2020; Sanz-Bernardo *et al.*, 2021). One study calculated that an individual *Stomoxys calcitrans* could only transfer  $10^{-0.8}$  TCID<sub>50</sub> of LSDV (Sohier *et al.*, 2019), while the minimum infectious dose was estimated at  $>10^1$  TCID<sub>50</sub> (Carn and Kitching, 1995b). The authors therefore concluded that it seemed improbable that one stable fly could transmit sufficient virus to induce LSD (Sohier *et al.*, 2019). Notably, this calculation was based on recently fed flies, prior to any significant viral decay; the time required for windborne dispersal or transport on ships would likely reduce the viral load present in vectors. We did not explicitly incorporate into our analysis the probability of one versus multiple infectious vectors arriving together. This can more easily be incorporated into a detailed quantitative analysis, noting the considerable uncertainties involved. However, it is worth bearing in mind that multiple vectors may be required to initiate infection.

Furthermore, LSDV transmission studies have generally involved highly susceptible *Bos taurus* breeds (Weiss, 1968; Chihota *et al.*, 2001, 2003; Magori-Cohen *et al.*, 2012; Sohier *et al.*, 2019; Issimov *et al.*, 2020; Sanz-Bernardo *et al.*, 2021), while *Bos indicus* and buffalo are common in northern Australia. LSDV transmission is widely thought to be driven by symptomatic animals, as average viral titres in the blood and skin of asymptomatic animals are very low (Sanz-Bernardo *et al.*, 2021). Typically, only 20–60% of infected animals develop clinical disease (Magori-Cohen *et al.*, 2012), and this may be further reduced in more resistant breeds. Further research should be directed towards investigating breed-specific differences in LSDV pathogenesis and transmission parameters.

## 5.2 Recommendations

Given the significant and increasing threat posed to Australia's livestock industries by LSDV, it is critical to maintain preparedness work to ensure that risks are appropriately managed. We propose several key recommendations in response to various challenges encountered in our analysis. Firstly, while there is considerable uncertainty associated with many of the required parameters, a quantitative analysis would provide further detailed insights into the risk of LSDV incursion via the chosen pathways, accounting for the absolute number of arthropod incursions. A quantitative approach would also allow for the incorporation of uncertainty and variability into the outputs and facilitate more detailed sensitivity analyses.

Secondly, we identified several key nodes that would benefit from additional research to refine highly uncertain input parameters. Arguably the most critical parameter in our analysis is the number of vectors required to initiate an infection. Typically, where exotic *Culicoides* have been detected in Australia, only single specimens have been recovered per sampling occasion (Eagles *et al.*, 2014). However, current evidence suggests that a swarm of vectors is required to transmit a minimum infectious dose of LSDV (Sohier *et al.*, 2019). We strongly suggest that future research is directed towards examining the role of single insects in LSDV transmission.

Additionally, understanding the true incidence of LSD, both in endemic regions and over the course of an epizootic, would help to define how many insects are likely to be infectious over a given time period. As the incidence of symptomatic disease may vary between cattle breeds, detailed pathogenesis and transmission studies should be conducted on *Bos indicus* and other cattle breeds relevant to the northern Australian context. Likewise, vector feeding behaviour and viral loads may vary between cattle breeds, which could be addressed by these studies.

Another poorly understood parameter is vector dispersal, either via wind or through self-directed flight. While several studies have investigated long-distance windborne dispersal of *Culicoides* midges to Australia, information for other vector species is underrepresented (Boyle *et al.*, 2012; Eagles *et al.*, 2012, 2013, 2014). Furthermore, the likelihood of vector survival after long-distance transportation is not known. Similarly, the frequency with which arthropods of different species disperse to ports and land on ships is not well described. For example, it would be beneficial for information on arthropod detections via vessel inspections, insectocutor trapping and post-insecticide treatments to be made publicly available to better inform some of these parameters. While these issues are being addressed, an extension of the National Arbovirus Monitoring Program to cover the relevant vectors and geographical areas of concern for LSDV, that is, beyond the current NAQS risk areas, would be highly beneficial.

We also encountered challenges when parameterising the susceptible livestock population within each NAQS risk zone. While national livestock census results are available, these are published at the SA4 and natural resource management geographic levels, and intermittently at the SA2 level. Yet these geographical subdivisions are not particularly useful for disease surveillance and animal management purposes. Having specific information about maximum livestock densities and distributions within and between NAQS risk zones would have utility beyond simply this LSDV risk assessment. These could perhaps be obtained through a combination of information from individual stations and the National Livestock Identification Scheme.

Finally, as discussed elsewhere there is no clear definition or best-practice methodologies for conducting semi-quantitative risk assessments, despite their reported utility to risk assessors (European Food Safety Authority *et al.*, 2020). While the use of semi-quantitative analyses is discouraged by the WOA (Murray and World Organisation for Animal Health, 2010), this assessment clearly highlights some of the limitations of a purely qualitative approach. Having expert consensus on appropriate (and inappropriate)

methodologies for semi-quantitative analyses, as well as a published comparison between all three methods, would have been useful when performing this assessment.

While the risk of LSDV incursion into Australia through the pathways assessed appears to be limited, especially in the context of current disease levels in neighbouring countries, it is imperative to keep in mind that the parameters used in this assessment are subject to change. Current mitigation measures, such as insecticide treatments of incoming vessels, must be maintained and adapted as the disease situation changes in potential origin countries. Periodic re-evaluations of this assessment and/or more quantitative approaches are strongly recommended to maintain our understanding of the risk of LSDV incursion via unregulated pathways.

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# Appendix 1

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## Consultation meeting participants

The following participants attended the consultation meeting on 25 March.

NAQS: Dr Skye Fruean, Dr Charlotte Burgoyne, Dr Michele Byers, Dr Tiffanie Huynh, Mr Tim Kerlin, Dr Josef Schmidt, Mr Matt Shields, Dr Guy Weerasinghe, Dr Cassandra Wittwer

The Department: Dr Jenny Baird, Dr Erin Davis, Dr Janene Kingston

Ausvet Pty Ltd: Dr Emma Zalcmán, Dr Brendan Cowled

## Appendix 2

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### Questions for entomology consultation

#### General

1. Are you aware of any evidence of biological transmission of LSDV in the arthropods from each group?
2. What is the likelihood of arthropods from each group becoming infected or capable of transmission (assuming mechanical transmission only) with LSDV after taking a protein meal? (Consider suggested readings below.)
3. What is the likelihood of arthropods from each group being present in agricultural settings in a country in Asia or PNG?
4. What is the maximum distance arthropods from each group would be able to fly over land assuming no host animal is present, wind assistance is available and the arthropod survives the travel?
5. What is the likelihood that arthropods from each group bite a bovine if they come into contact with one?

#### Cargo ship and Torres Strait

1. What is the longest arthropods from each group survive on a ship or vessel without a protein meal or food source?

Note: In the questions that follow, we've assumed a maximum of five days. If this maximum is less or more, adjust the next two questions as appropriate (e.g. if maximum survival is six days, also estimate the likelihood of each group surviving and being infectious after six days).

2. What is the likelihood of arthropods from each group surviving a journey of one, two, three, four or five days on a ship or vessel?
3. What is the likelihood that arthropods from each group would still be infectious with LSDV after one, two, three, four or five days aboard a ship or vessel?

#### Windborne

1. What is the maximum distance arthropods from each group would be able to fly over ocean, assuming wind assistance and survival at the end?
2. What conditions would be necessary for arthropods from each group to travel the maximum distance (and survive it)?
3. What is the likelihood of arthropods from each group being able to travel the maximum distance and distances less than that (over water), assuming optimal conditions?

Experts were asked to provide minimum, maximum and most likely values (along with confidence intervals) where likelihood values were requested.

## Appendix 3

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### R script

This script and accompanying data files are available at the Bitbucket repository <https://robynhall@bitbucket.org/robynhall/awe-1sd-21.git> upon request.

## Appendix 4

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Please see separate attachment for Appendix 4, Comprehensive results tables.