



**AUSVET**

# Lumpy Skin Disease

**A literature review**

Department of Agriculture, Water and  
the Environment  
March, 2022

Emma Zalcman and Brendan Cowled

## Disclaimer

This report is for the use of the client only and is confidential information. If you have received a copy of this report in error, please delete it and notify the sender. Ausvet gives no warranty that the information contained in this report is correct or complete and shall not be liable for any loss howsoever caused, whether due to negligence or other circumstances, arising from use of or reliance on this information.

© 2022 Ausvet

This work is copyright and, apart from any fair use as permitted under the *Copyright Act 1968*, no part may be reproduced without written permission from the publishers, Ausvet. Requests and inquiries concerning reproduction and rights should be addressed to Ausvet at the address below.

Ausvet

Level 1, 34 Thynne St, Bruce, ACT 2617 Australia

[www.ausvet.com.au](http://www.ausvet.com.au)

ABN: 64 613 142 9

Contact: Emma Zalcman

[emma@ausvet.com.au](mailto:emma@ausvet.com.au)

# Contents

---

Abbreviations and acronyms .....	v
<b>1 Introduction.....</b>	<b>1</b>
<b>2 Methods .....</b>	<b>3</b>
<b>3 Epidemiology of Lumpy skin disease .....</b>	<b>5</b>
3.1 Hosts.....	5
3.2 Strains .....	5
3.3 Transmission.....	6
3.3.1 Routes of transmission.....	6
3.3.2 Estimating the basic reproduction number.....	7
3.3.3 Specific vectors .....	8
3.3.4 Wind-assisted transmission.....	12
<b>4 Geographical distribution of Lumpy Skin Disease .....</b>	<b>14</b>
4.1 Geographical distribution to date .....	14
4.1.1 Spread to South-East Asia .....	15
4.2 Projected spread in the region.....	17
<b>5 Information relevant to assessing potential for spread to Australia .....</b>	<b>19</b>
5.1 Ecological conditions for spread.....	19
5.2 Distribution of vector species in Australia.....	20
5.2.1 Flies .....	20
5.2.2 Mosquitoes .....	21
5.2.3 Midges.....	22
5.2.4 <i>Tabanidae</i> .....	23
5.2.5 Hard ticks .....	24
5.3 Density and distribution of relevant livestock species in Australia .....	25
5.3.1 Domestic cattle .....	25
5.3.2 Feral species .....	25
5.4 Density and distribution of relevant livestock species in neighbouring countries .....	26
<b>6 The role of climate change in the spread of LSDV .....</b>	<b>27</b>
<b>7 Risk assessment related to Lumpy Skin Disease .....</b>	<b>29</b>
<b>8 Relevant research gaps .....</b>	<b>31</b>
<b>9 References.....</b>	<b>32</b>
<b>Appendix One.....</b>	<b>39</b>
Search terms.....	39
<b>Appendix Two .....</b>	<b>40</b>

Livestock movement report .....	40
<b>1.1.1 Tables</b>	
Table 1 Research gaps relevant to upcoming risk assessment .....	31
<b>1.1.2 Figures</b>	
Figure 1 Global spread of LSD. Figure extracted from (Kumar et al., 2021) .....	15
Figure 2 Spread of LSD in South east Asia (figure developed by Dr Michael Patching) .....	17
Figure 3 Historical (red dots) and contemporary (yellow dots) distribution records of <i>A. aegypti</i> in Australia 1887-2016 (Beebe et al., 2009; Trewin et al., 2017).....	22
Figure 4 Monsoonal weather patterns relevant to the movement of <i>A. aegypti</i> in Northern Australia.....	22
Figure 5 <i>Culicoides</i> trapping results from 03/03/2020 -03/03/2022 with cattle density (NAMP, 2022) .....	23
Figure 6 Monsoonal weather patterns relevant to the movement of <i>Culicoides spp.</i> in Northern Australia.....	23
Figure 7 Occurrence reports of <i>Tabanidae</i> spp. (Atlas of living Australia, 2022).....	24
Figure 8 Approximate of Australian ‘tick line’ (MLA, 2022) .....	25
Figure 9 Cattle density in Australia .....	25
Figure 10 Cattle density of Papua and West Papua Provinces of Indonesia .....	26

## Abbreviations and acronyms

---

Abbreviation	Definition
BTV	Bluetongue Virus
EFSA	European Food Safety Authority
ENM	Ecological Niche Models
EU	European Union
FAO	Food and Agricultural Organisation
IPPC	Intergovernmental Panel on Climate Change
IQR	Interquartile Range
LSD	Lumpy Skin Disease
LSDV	Lumpy Skin Disease Virus
MLA	Meat and Livestock Australia
NAMP	National Arbovirus Monitoring Program
OIE	World Organisation of Animal Health
PCR	Polymerase Chain Reaction
PNG	Papua New Guinea
$R_0$	The basic reproduction number
RPC	Representative Concentration Pathway
SSP	Shared Socioeconomic Pathways
The Department	The Department of Agriculture, Water and the Environment
UK	United Kingdom

# 1 Introduction

---

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* (Issimov et al., 2020; Tuppurainen et al., 2017). Clinically, it is characterised by multiple skin lesions, fever, lymph node enlargement, a drop in milk production and poor reproductive performance (Khan et al., 2021). Affected farmers experience severe economic loss from a sharp decline in milk yield, milk quality, hide damage, body weight reduction, abortion, infertility and in rare cases the death of animals (Babiuk et al., 2008). Typically, morbidity in diseased herds is low to moderate, ranging from 5-20%; however in rare outbreaks it can approach 100% (OIE, 2010; Tuppurainen and Oura, 2012; Woods, 1988). In countries where LSD becomes endemic, control through widespread vaccination with an effective vaccine is possible (EFSA et al., 2019).

LSD was first reported in Zambia in 1929 but spread quickly in the three years that followed to other African nations (Khan et al., 2021; Morris, 1930). Until 1984, LSD was contained within countries of sub-Saharan Africa (Tuppurainen and Oura, 2012). Unconfirmed cases of the disease were reported in Oman and Kuwait between 1984 and 1988 but the first confirmed case in the Middle East was reported in Egypt in 1988 (Ali et al., 1990; Davies, 1991; House et al., 1990). In 1989, the disease spread to Israel, interestingly by suspected windborne transmission of *Stomoxys calcitrans* flies from Egypt carrying the virus (Yeruham et al., 1995). In the coming years, the disease continued to spread across contiguous countries in several directions throughout the Middle East, moving westerly into Iran and easterly into other central Asian countries (EFSA AHAW Panel, 2016). In 2015, the disease emerged in eastern Europe and spread to several countries (EFSA, 2018). It was effectively controlled in Europe through vaccination and on that continent, it only persists in Russia (EFSA, 2018).

Global climate change and changes in the trading patterns of animals and animal products have resulted in LSD becoming an emerging disease threat (Azeem et al., 2022). Since 2019, the spread of LSD has gained pace in Asia with introductions and outbreaks reported in Hong Kong, mainland China, India, Bhutan, Myanmar, Nepal, Bangladesh, Thailand, Laos, Cambodia, Vietnam and Malaysia (Acharya and Subedi, 2020; Arjkumpa et al., 2021; Azeem et al., 2022; Flannery et al., 2021; Gupta et al., 2020). On March 2, 2022 the disease was reported for the first time in Indonesia (OIE, 2022). It is now firmly established in Asia and is becoming a threat to livestock health and food security there (Azeem et al., 2022).

With the rapid spread of the disease across South-east Asia and its ability for vector borne spread, there is now concern that the disease could enter Australia. Whilst the import of live animals and animal products is highly regulated, there are several non-regulated pathways that could theoretically result in the introduction of LSDV. The consequence of LSDV entering and establishing in Australia may be high, with severe production impacts, as well as the large economic consequences resulting from disruptions to trade and the cost of any eradication or control campaign.

The Department of Agriculture, Water and the Environment (the Department) recognises the potential cost (both social and economic) of LSDV entering Australia and has consequently commissioned the development of a qualitative framework to evaluate the risk of LSDV entering Australia. The risk-assessment will be focused on non-regulated pathways into Australia, especially natural or windborne spread from neighbouring countries. The first step of developing this framework is a literature review to ensure the risk assessment framework is based on contemporary science and to enable the risk assessment to be evidence-based. The results of the literature review are summarised here. Note that this is a literature review and not a risk assessment. Therefore, risk pathways, risk assessment or complex analysis

on the potential for LSDV to enter Australia are not presented. Instead, relevant background scientific literature is collated and summarised.

## 2 Methods

---

The aim of the literature review was specifically to inform the risk assessment.

The review aimed to answer the following research questions:

1. What is the epidemiology of LSD? In particular, what are the hosts and relevant pathogenic strains of LSDV? How is it transmitted and in the case of vector-borne transport, is it mechanically or biologically transmitted?
2. In which countries and regions is LSDV present (with a focus on Australia's near neighbours) and what are the predicted future movements of the disease (including to Australia)?
3. What is the role of climate change in the future spread of LSDV and how will extreme climate change scenarios impact the potential entry and establishment of LSDV in Australia in 10 years' time?
4. Have there been risk assessments on LSDV in other countries and what can they tell us about appropriate frameworks for this risk assessment?

We used BIOSIS Previews on the Web of Science<sup>1</sup> to search the core collection for 'lumpy skin disease'. This database references back to 1926 and is the premier database for life science. It includes virtually all journal and non-journal (e.g., conference proceedings) globally. We then reviewed each title for relevance to answering the research questions. We excluded papers (based on title) focused on LSD in countries outside the region (except when relevant to vectors, climatic factors or risk analysis), vaccination, or specific clinical, pathological or diagnostic findings. We then exported the list of relevant titles and reviewed each paper individually. In some cases, review of a particular paper revealed an additional publication of relevance that did not appear on our original list of relevant titles. In this case, the paper was added to a secondary list and reviewed separately (snowballing). In total, over 100 original peer-reviewed publications relevant to the research questions were reviewed.

To pick up on preprint publications or work that hasn't yet been peer reviewed we entered a number of different relevant search terms into Google Scholar and examined the first 50 titles appearing for each search term (see Appendix One). Whilst the use of 'and' may have been restrictive, the use of 'or' generated an extremely high volume of irrelevant results.

Lastly, we also reviewed the following for completeness and consistency;

Importation of frozen bovine in vitro produced embryos from Canada and the United States – final review<sup>2</sup>

Inspector-General of Biosecurity Report 2017-2018/02: Hitchhiker pest and contaminant biosecurity risk management in Australia

Inspector-General of Biosecurity Report 2016-2017/01: Review of Department of Agriculture and Water Resources management of biosecurity risk posed by invasive vector mosquitoes.

---

<sup>1</sup> BIOSIS Previews - Web of Science Group (clarivate.com)

<sup>2</sup> This was reviewed as an example of a contemporary Import Risk Analysis and included LSDV as a hazard

The Australian Department of Agriculture, Environment and Water Resources Biosecurity Import Risk Analysis Guidelines 2016

Note that our methodology did not include review of LSD control or vaccination. These are complex and important issues but are beyond the scope of this work.

## 3 Epidemiology of Lumpy skin disease

---

The aim of this section is to answer the research questions - What is the epidemiology of LSDV? In particular, what are the hosts and relevant strains of LSDV? How is it transmitted and in the case of vector-borne transport, is it mechanically or biologically transmitted?

### 3.1 Hosts

LSDV can infect both cattle (*Bos taurus*) and water buffalo (*Bubalus bubalis*) (Tuppurainen et al., 2017). All ages and breeds of cattle are susceptible but young cattle and those at the peak of their lactation appear to be most vulnerable (Tuppurainen et al., 2011). Thin-skinned and high-producing dairy *Bos taurus* breeds are highly susceptible to LSDV, whereas *Bos indicus* may have some natural resistance to the virus (Gari et al., 2011). Banteng cattle (*Bos javanicus*) have been infected with LSDV in Asia, but whether they are more or less susceptible than other breeds is not known (OIE, 2022)

There is evidence of antibodies to LSDV in several wild African ruminant species including African buffalo, blue wildebeest, eland, giraffe, impala and great kudu but clinical disease has only been observed in captive oryx and experimentally infected giraffe and impala (Barnard, 1997; Fagbo et al., 2014; Greta et al., 1992; Young et al., 1970). LSDV may persist in susceptible wildlife, making it plausible to consider wild species as a source of recurrence or reservoir after seemingly successful eradication from domestic animals (Calistri et al., 2018; Gortazar et al., 2021). There is no evidence of clinical disease or seropositivity in wildlife outside the African continent, but there are also no studies that indicate work in this area.

### 3.2 Strains

There are several Polymerase Chain Reaction (PCR), real-time PCR and high-resolution melt qPCR based methods for the detection of the LSDV genome (Balinsky et al., 2008; Bowden et al., 2008; Gelaye et al., 2017, 2013; Haegeman et al., 2013; Heine et al., 1999; Ireland and Binepal, 1998; Lamien et al., 2011; Stram et al., 2008; Stubbs et al., 2012). Molecular epidemiological studies of LSDV rely on analysing particular regions; namely GPCR, the RPO30, the P32 and the EEV glycoprotein genes (Gelaye et al., 2015; Goff et al., 2009; Hosamani et al., 2004; Lamien et al., 2011; Menasherow et al., 2016, 2014). This is because the virus is large and has too many repeat regions to easily sequence or assemble.

For several years, the genome of LSDV appeared to be relatively stable, with isolates recovered over decades in Africa showing only minor genomic differences in the regions sequenced (Badhy et al., 2021; Goff et al., 2009; Kara et al., 2003; Lamien et al., 2011; Tulman et al., 2001). This trend continued as the disease spread into the Middle East and Europe (Abutarbush et al., 2016; Agianniotaki et al., 2017; Stram et al., 2008). For many years, LSDV therefore appeared to exist as two genetic lineages; field isolates and live attenuated vaccine strains (Calistri et al., 2018).

However, all this changed following the discovery of Neethling-vaccine-like viral genomic profiles in Russia in 2017 and 2019 (A. Kononov et al., 2019; Sprygin et al., 2020; A. Sprygin et al., 2018). The authors attributed these variants to recombination events between the Neethling vaccine strain and field isolates and this has prompted a rethink on the merits of categorizing LSDV into two broad lineages (Badhy et al., 2021; Sprygin et al., 2020). The impact of the recombination events on the virulence and transmission capacity of LSDV remains unclear and these events are the subject of ongoing work (Sprygin et al., 2018a)

Viral sequencing is highly recommended when investigating outbreaks, as it can give information on the possible source of disease introduction and will contribute to a better understanding of LSDV strain variability and dynamics (Flannery et al., 2021).

## 3.3 Transmission

### 3.3.1 Routes of transmission

Since the earliest outbreaks of LSD in Africa, the movement of infected cattle along roads, 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 occur in scattered herds in the absence of any movement, suggesting an alternative means of short distance spread (Tuppurainen and Oura, 2012). It is now understood that transmission between animals can occur through arthropods, contaminated feed and water, and direct routes such as saliva, secretions and semen (Namazi and Tafti, 2021). There is also limited evidence of intrauterine transmission (Rouby and Aboulsoud, 2016). The widespread consensus is that the main route of transmission is through arthropods and is most likely to be mechanical, with longer distance spread facilitated by the movement of animals (Chihota et al., 2001; Namazi and Tafti, 2021; Tuppurainen and Oura, 2012).

The transmission of LSDV through arthropod vectors has been demonstrated in a series of experimental studies where potential vectors were permitted to feed on diseased animals and then tested for the presence of the virus and their capacity to transmit the virus to healthy animals (Chihota et al., 2003, 2001; Issimov et al., 2020). The varied success of transmission seen in this work is discussed in the vector section of this report, as it differs depending on the vector species involved. It is worth noting that because only approximately one third of experimental animals exhibit severe clinical disease after direct inoculation with virulent LSDV, smaller studies should be interpreted with caution because their size may limit their potential to detect transmission via the specific vector, even if it does occur in field settings (Sprygin et al., 2019).

In a field setting, vector transmission is further supported by observations that most LSD outbreaks have occurred in the summer when arthropods are at the peak of their activity and in some regions, outdoor herds have been found to be at higher risk of infection than indoor herds (EFSA, 2018; Kahana-Sutin et al., 2017; Namazi and Tafti, 2021).

No studies to date have demonstrated evidence of anything other than mechanical transmission (i.e., no evidence of biological transmission) of LSDV by vectors, with the exception of the transstadial and transovarial transmission described in hard ticks and one study involving *Culicoides punctatus* (see Specific vectors). The amount of LSDV in vectors during experimental studies appears to decline over a period of 1–7 days following exposure, with no evidence of increases in viral load (Chihota et al., 2003, 2001; Issimov et al., 2020; Paslaru et al., 2021). Further to this, in proof of concept work, LSDV was injected into the thorax of three different fly species in an attempt to bypass the midgut (where virus is often killed before it can replicate) (Issimov et al., 2021). Viral DNA was detected up to seven days after inoculation but the virus failed to replicate (Issimov et al., 2021). These studies suggest that biological transmission or replication of the virus within the vector does not occur, at least not in the vector species' studied.

Lastly, one study demonstrated that experimental infection into the conjunctival sac or intradermally results in lower infection than intravenous inoculation; the typical route seen when insects feed from the lumen of blood vessels, further suggesting that vector-borne transmission is the most efficient means of LSDV spread (Carn and Kitching, 1995).

Direct transmission through contact between infected animals is thought to be of little importance. This theory was first proposed following a small study where healthy animals were kept in close contact with diseased animals for one month; they developed no clinical signs of disease and were later challenged and found to be susceptible, indicating that direct transmission had not occurred (Carn and Kitching, 1995). Again, it is worth noting that small studies may fail to detect transmission even if it does occur in a natural field setting because only one third of animals contract the disease even following direct inoculation (Sprygin et al., 2019). Later, modelling that used data from a large outbreak in Israel to compare three different contact models found that indirect transmission was the only parameter that could solely explain all the outbreak dynamics and that cattle density was not a risk factor for disease (Magori-Cohen et al., 2012). However, in other modelling using European data, animal density was found to be a risk factor (EFSA, 2018). Some strains may be more capable of direct transmission than others (Aleksandr et al., 2020).

Skin lesions and scabs of infected animals are considered to be the main source of infection (for vectors), as the virus persists in these for long periods (Namazi and Tafti, 2021). It can remain viable for long periods in the environment within dried up scabs (up to 33 days in necrotic skin nodules, 35 days in desiccated crusts and at least 18 days in air-dried hides) (Namazi and Tafti, 2021). The virus is also excreted in blood, nasal secretions, saliva, semen and milk (Namazi and Tafti, 2021). The virus can reside in lymph nodes and testes but tends not to be present in deep skeletal meat or traditional offal products, making the risk of transmission through meat very low (Kononov et al., 2019).

### 3.3.2 Estimating the basic reproduction number

Some studies have estimated the basic reproduction number ( $R_0$ ) of LSDV, both independently of the vector and in relation to specific vectors. Magori-Cohen et al (2012) used a dataset from a large outbreak in a dairy farm in Israel in 2006 to estimate the  $R_0$  induced by direct transmission versus indirect transmission, without regard for the specific vector. They found  $R_0$  induced by indirect transmission in the presence of an infectious cow for one day in the herd was 15.7, compared to 0.36 for direct transmission (Magori-Cohen et al., 2012). This was useful in providing further evidence that indirect transmission is likely to be far more important than direct transmission. EFSA (2019) used a dataset collected during outbreaks in Albania in 2016 to estimate  $R_0$  within a village. They found it varied considerably between villages from 0.03 to 3.58 with a median of 0.87 (EFSA et al., 2019). The  $R_0$  (or in this case  $R_e$ ) declined during the outbreak, potentially due to the effect of seasonality (and therefore vector presence) on transmission rate and this in part may explain the variation between villages (EFSA et al., 2019). Molla et al (2017) used a susceptible-infectious-recovered (SIR) epidemic model to estimate the  $R_0$  using data from outbreaks in Ethiopia. They estimated an  $R_0$  of 1.07 for crop-livestock production systems and 1.09 for intensive production systems (Molla et al., 2017).

Gubbins et al (2019) went onto to estimate the  $R_0$  for transmission of LSDV by five species of biting insects. They derived an expression for  $R_0$  using a transmission model that considered the underlying process involved in vector to cattle transmission (Gubbins, 2019). The parameters in the expression were then estimated using data from published transmission studies (see details of transmission studies under individual vector species). The data from these studies were reanalysed using Bayesian methods to quantify uncertainty (Gubbins, 2019). Latent and infectious periods for LSDV were estimated, again using the outcome of challenge experiments and Bayesian methods (Gubbins, 2019). Uncertainty and sensitivity analysis were used to calculate  $R_0$  and determine the parameters that had the greatest influence (Gubbins, 2019). Their results are discussed below as they relate to individual vector species.

Sanz-Bernardo et al (2021) used the data obtained in their transmission study, combined with data from earlier transmission studies and previously determined vector life history parameters (those used in Gubbins et al 2019), to recalculate  $R_0$  values for four vector species (Sanz-Bernardo et al., 2021). The

derived expression they used for  $R_0$  was different to that used by Gubbins et al (2019), although a lot of the parameters and data used were similar. Their results are discussed below in relation to individual vector species.

Regardless of the study, the  $R_0$  reported by different authors varies and confidence intervals are wide. This potentially reflects the complex nature of transmission and the difficulty of performing such calculations in multifaceted management situations (EFSA et al., 2019; Magori-Cohen et al., 2012; Molla et al., 2017).

### 3.3.3 Specific vectors

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 blood-feeding arthropod species could play a role (Berg et al., 2015). The probability of vectors acquiring LSDV from subclinical animals appears to be very low when compared with that from clinical animals (Sanz-Bernardo et al., 2021). Whilst most studies suggest the virus is likely to survive in vectors for 2–6 days (on mouthparts or within the animal themselves), the possibility of longer-term survival cannot be ruled out (Chihota et al., 2003, 2001; FAO, 2016; Horigan et al., 2018).

Evidence on potential vectors of LSDV is summarised below.

#### *Flies*

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 is commonly used for 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, midges and *Tabanidae* are all part of the order *Diptera* and are therefore considered flies. However, in this section, we look at insects that are more commonly referred to as flies; those species from the *Muscidae* family.

*Stomoxys calcitrans* or the stable fly is one of the most commonly suspected vector species for LSDV (Sprygin et al., 2019). Of all the species investigated as potential vectors, *S. calcitrans* has been the subject of the most studies. The combination of results from experimental transmission studies, field epidemiological studies and work relating to the estimation of  $R_0$  suggest that *S. calcitrans* is capable of mechanical transmission of LSDV in field settings and is likely to be an effective vector (Chihota et al., 2003; Gubbins, 2019; Issimov et al., 2020; Kahana-Sutin et al., 2017; Paslaru et al., 2021; Sanz-Bernardo et al., 2021; Sohler et al., 2019; Yeruham et al., 1995). What is unclear is whether *S. calcitrans* is usually the only vector in a field setting, and if not, how much *S. calcitrans* contributes to transmission versus other vector species.

Weiss et al (date?) reported isolating the virus from *S. calcitrans* and *Biomya fasciata* in the 1960s. Furthermore, stable flies are aggressive and persistent feeders with painful bites leading to interrupted feeding on multiple hosts in quick succession (Sprygin et al., 2019; Weiss, 1968)<sup>3</sup>.

---

<sup>3</sup> The text where Weiss reported his findings could not be retrieved as it has not been published electronically.

Chihota et al (2003) attempted to use *S. calcitrans* to experimentally transmit the virus from infected to healthy cattle, however none of the susceptible animals seroconverted or showed any reaction to exposure and the virus only persisted for 24 hours post-feeding in the flies (Chihota et al., 2003). Nonetheless, in this work, no attempt was made to infect cattle immediately after *S. calcitrans* fed, which is probably what would occur in a field setting.

In later work, Issimov et al (2020) attempted a similar experiment with three different species of *Stomoxys*, including *S. calcitrans* (Issimov et al., 2020). In their work, flies were not allowed to feed to engorgement on the infected animals and instead were moved immediately onto recipient animals to complete their feed (Issimov et al., 2020). Large numbers of flies were used and five out of the six recipient animals consequently tested positive for LSDV on PCR (Issimov et al., 2020). Also in this study, flies were tested by PCR for the virus at 0 hours, 6 hours and then daily after engorgement (Issimov et al., 2020). Viral DNA was not detected in any of the flies beyond 48 hours after their feed and the majority of flies were positive for less than 24 hours, adding to the body of evidence suggesting that transmission is mechanical and explaining why transmission attempts in earlier studies failed (Chihota et al., 2003; Issimov et al., 2020).

Sohier et al (2019) also demonstrated LSDV transmission (most likely to be mechanical) by *S. calcitrans* through three independent experiments (Sohier et al., 2019). Interestingly only 5/14 of the recipient animals presented with clinical signs; starkly different from that reported by Issimov et al (2020). One potential explanation is that the number of flies that continued feeding on recipient animals could not be estimated, so some animals may have been bitten by infected flies twice in Issimov's work (Paslaru et al., 2021). Another potential explanation is that higher infection doses could be inoculated by some flies through regurgitation during blood feeding (Paslaru et al., 2021).

Paslaru et al (2021) investigated the presence of viral DNA on regurgitated blood by allowing flies that were exposed to LSDV to feed on small cotton pads soaked with blood (stimulating a blood meal from an animal) (Paslaru et al., 2021). LSDV DNA could be retrieved from the cotton pads up until three days after the flies had fed but no attempt was made to check if this was infectious. It remains to be confirmed if virus on mouth parts alone is enough to trigger an infection as recovered viral loads appear low (Paslaru et al., 2021). LSDV DNA was also detected in the bodies and heads of flies up to three days after their feed (Paslaru et al., 2021). Interestingly, faecal samples from *S. calcitrans* were also tested for LSDV in Paslaru et al's (2021) work. LSDV DNA was detected in faeces for up to two days post feed (Paslaru et al., 2021).

Similar work by Sanz-Bernardo et al (2021) (and likely occurring concurrently to Paslaru et al 2021) demonstrated retention of LSDV DNA (detected by PCR) in *S. calcitrans* for up to 8 days post feed (Sanz-Bernardo et al., 2021). In this study, a greater number of flies were used and the proportion that retained the virus over time declined, indicating that small fly numbers might explain the lack of retention in earlier work (Sanz-Bernardo et al., 2021). The authors estimated the mean virus retention of LSDV in *S. calcitrans* to be 5.5 days with a 95% credible interval of 3.2–12.3 days. Flies were not tested for the virus beyond 8 days.

In field settings, *S. calcitrans* was suspected to be responsible for the first known LSD outbreak outside of Africa, which occurred in Israel in 1989 (Yeruham et al., 1995). This was speculative and based on the fact that no new animals had been introduced, LSDV has been previously isolated from *S. calcitrans*, there were adequate winds to carry infected *S. calcitrans* from neighbouring Egypt and these flies predominated over other blood-feeding insects in the region (Yeruham et al., 1995).

Later work in Israel modelled the association between vector abundance and LSD outbreaks in dairy farms (Kahana-Sutin et al., 2017). This work found a significant association between *S. calcitrans* abundance and LSD outbreaks (Kahana-Sutin et al., 2017). The authors of this study suggested that the

competence of *S. calcitrans* as a vector should be re-examined using shorter periods between feeding on an infected host and feeding on a healthy animal to more accurately represent field conditions (Kahana-Sutin et al., 2017). This work was completed before the transmission studies conducted by Sohler et al (2019) and Issimov et al (2020). The horn fly, *Haematobia irritans*, was also highly abundant on beef cattle during the 2012–2013 outbreaks in northern Israel but its role in LSDV transmission has not been investigated (Berg et al., 2015).

Sanz-Bernardo et al (2021) estimated the  $R_0$  of *S. calcitrans* to be 19.1 (see 3.3.2). This was relatively consistent with Gubbins (2019) who found *S. calcitrans* to be among the most efficient of vectors, with an approximate  $R_0$  of 15.5 (95% prediction interval of 1.4–81.9). The wide prediction intervals of this study should be noted.

The common housefly, *Musca domestica*, may also be capable of transmitting LSDV, as large number of these flies were trapped near an outbreak of LSD in Russia and subsequently tested positive to the virus (Sprygin et al., 2018b). *M. domestica* and *M. stabulans* also tested positive for LSDV when collected from traps placed near farms where LSD first appeared in China (Wang et al., 2021)

### *Mosquitoes*

As discussed above, mosquitoes are part of the order *Diptera* (true flies) and fall into the family *Culicidae*. There are approximately 3,500 species of mosquitoes and several that transmit pathogens such as Zika virus, *Plasmodium* (which cause malaria) and dengue virus. Mosquitoes live in most parts of the world and are particularly attracted to areas with still water because their larvae and pupae need 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). Experimental transmission studies have indicated that some species of mosquitoes may be theoretically capable of carrying LSDV, but only *Aedes aegypti* has been shown to transmit the virus to recipient animals (Chihota et al., 2003, 2001; Sanz-Bernardo et al., 2021). *A. aegypti* may be theoretically capable of transmitting the disease in an experimental setting, but traditionally favours human hosts so the importance of its role in field settings is unclear.

In early work by Chihota et al (2003) *Culex* spp. were shown to feed multiple times on different hosts and LSDV DNA was detected in *Culex quinquefasciatus* several days after feeding on infected cattle (Chihota et al., 2003; Sprygin et al., 2019). Despite this, in the same study very few of the mosquitoes actually took a bloodmeal from the infected animals, and none of the susceptible animals (that were later exposed to the mosquitoes) became diseased (Chihota et al., 2003). In later work, *C. quinquefasciatus* was again exposed to experimentally infected animals and tested positive for viral DNA up to two days after exposure (Sanz-Bernardo et al., 2021). This study did not include experimental transmission to healthy animals. Gubbins (2019) estimated the  $R_0$  of *C. quinquefasciatus* in theoretical transmission of LSDV would sit at around 0.8 (95% predictive interval of 0.9–3.5) and Sanz-Bernardo et al (2021) estimated it to be around 0.55 (95% credible interval of 0.06–2.37). This suggests that even if transmission with *C. quinquefasciatus* was possible, it may be an ineffective means of transmission.

The early transmission experiments also used *Anopheles stephensi* (Chihota et al., 2003). Infectious virus could be detected for up to four days post feeding by viral isolation (and eight days via PCR) (Chihota et al., 2003). *A. stephensi* mosquitoes more readily took a bloodmeal, however no virus was isolated from these recipient animals and they also tested negative on PCR (Chihota et al., 2003). Further, Gubbins (2019) estimated that the  $R_0$  for transmission via *A. stephensi* would sit around 1.6 (95% predictive interval of 0.2–6.0), potentially also making it an inefficient vector (keeping in mind the wide predictive intervals).

Lastly, in Chihota et al's (2001) work, *A. aegypti* was shown to be fully capable of mechanical transmission of LSDV from infected to susceptible cattle for at least six days after feeding on infected

cattle. There was no significant loss in viral DNA load at six days and susceptible animals became diseased (Chihota et al., 2001). An additional later study further confirmed *A. aegypti* could acquire LSDV from feeding on diseased animals, and in this work viral DNA was retained for up to eight days in some insects (Sanz-Bernardo et al., 2021). Gubbins et al (2019) estimated the  $R_0$  for LSDV when transmitted by *A. aegypti* to be 7.4 (95% prediction interval of 1.3–17.6). Sanz-Bernardo et al (date) estimated it to be 2.41 (95% credible interval of 0.50–5.22). As discussed earlier, wide intervals and variation between studies demonstrates the uncertainty associated with these estimates. Some have suggested that the role of *A. aegypti* in LSDV transmission in field conditions may be limited by its preference for human hosts (Berg et al., 2015; Schaffner et al., 2013). Nonetheless, we know that the range of *A. aegypti* is expanding geographically, so it is an important vector to monitor (Kraemer et al., 2019).

### *Midges*

Midges are also part of the order *Diptera* and are therefore classified as flies. There are several families commonly referred to as midges but the most relevance to LSDV transmission is the family *Ceratopogonidae*. This family contains more than 5,000 species, including several *Culicoides* spp. Species from the family *Ceratopogonidae* are distributed worldwide on every continent except Antarctica (Boorman, 1993).

Experimental transmission studies, estimates of  $R_0$  and a small field trapping study suggest that species of the family *Ceratopogonidae* could well be involved in the transmission of LSDV. Which species and how much they contribute to transmission is unclear.

Chihota et al (2003) conducted experiments with donor and recipient animals using *Culicoides nubeculosus*. In this work, virus was detected by virus isolation and PCR only immediately post feeding (Chihota et al., 2003). None of the susceptible animals seroconverted after being fed upon by the infected midges (Chihota et al., 2003). In a later study, LSDV was demonstrated in *C. nubeculosus* up to four days post feeding, but this work did not look at capacity for the vector to go on to infect recipient cattle (Sanz-Bernardo et al., 2021). Gubbins et al (2019) estimated the  $R_0$  for LSDV when transmitted by *C. nubeculosus* to be 1.8 (95% prediction interval of 0.06–13.5). Sanz-Bernardo et al estimated it to be 7.09 (95% credible interval of 0.24–37.10). As discussed earlier, wide intervals and variation between studies demonstrates the uncertainty associated with these estimates.

In outbreaks in Turkey, LSDV was detected in *C. punctatus* trapped around infected farms (Şevik and Doğan, 2017). Further, ruminant beta-actin mRNA was not detected in these same midges, indicating that a recent bloodmeal hadn't taken place and replication may be occurring within *C. punctatus* (Şevik and Doğan, 2017). This is the only evidence suggestive of anything beyond mechanical transmission.

### *Tabanidae (horse flies)*

The family *Tabanidae* are also in the order *Diptera*. They are a cosmopolitan family with over 4000 species (Lessard, 2013). In Australia, these flies are referred to as 'March flies' but they are more commonly known as 'horse flies' in other regions.

The role of the tabanids in the transmission of LSDV had been speculated mostly because they are able to mechanically transmit a wide range of other disease agents such as *Trypanosoma evansi*, *Besnoitia besnoiti*, *Loa loa* and equine infectious anaemia virus and are found around cattle (Baldacchino et al., 2014). Evidence of their role to date is limited and largely restricted to work by Sohler et al (2019) who demonstrated transmission of LSDV by *Haematopota* spp. from donor animals to a single recipient animal.

### *Hard ticks*

Ticks are parasitic arachnids that fall into two major families: the *Ixodidae* or hard ticks and the *Argasidae* or soft ticks. There are over 800 tick species world-wide (Dehghani et al., 2019). Ticks require vertebrate

hosts to feed but spend most of their lives off their hosts digesting their meals and developing through juvenile stages into adults (Anderson and Magnarelli, 2008). Only hard ticks have been associated with LSDV transmission.

Several studies have suggested that hard ticks such as *Rhipicephalus appendiculatus* are capable of LSDV transmission (Lubinga et al., 2014b, 2014a, 2015; Tuppurainen et al., 2011, 2013a). However, the prolonged attachment of ticks to the host makes it unlikely that they could be solely responsible for rapidly spreading epidemics (Namazi and Tafti, 2021). It is more likely that, if ticks are involved in the epidemiology of the disease, then they are acting as reservoirs for the virus (Kahana-Sutin et al., 2017).

The passage of LSDV from engorged *Amblyomma hebraeum* nymphs to adults and from engorged female *Rhipicephalus decoloratus* to larvae after exposure to cold temperatures has been demonstrated, indicating possible over-wintering of the virus in these tick species (Lubinga et al., 2015). Transovarial passage of LSDV has been shown in *A. hebraeum*, *R. decoloratus* and *R. appendiculatus*, and in some studies recipient animals became infected after being exposed to the resultant adult ticks (Lubinga et al., 2014b; Tuppurainen et al., 2013b). In addition, the virus appears to be capable of crossing the midgut wall in ticks, indicating a potential for biological transmission (Lubinga et al., 2014a). Vertical transmission of LSDV in ticks may contribute to environmental maintenance, explaining the capacity of the virus to continue to survive over winter, in the absence of abundant arthropods (Berg et al., 2015).

Lastly, it has recently been proposed that migratory wild birds infested with LSDV-infected ticks may be responsible for the spread of LSDV from Russia or Kazakhstan to Bangladesh (Azeem et al., 2022). Whilst some migratory birds spend their summer in Russia or Siberia, they fly southwards in the winter and Bangladesh provides a potential habitat (Azeem et al., 2022). Phylogenetic analysis found a close association between the recent Indian/Bangladeshi LSDV isolates with the 2019 isolates from Russia and Kazakhstan (Azeem et al., 2022).

### 3.3.4 Wind-assisted transmission

LSD outbreaks that occurred in Israel in 1989 and 2006 appear to contradict the theory that arthropod spread is predominately short distance (Klausner et al., 2017; Magori-Cohen et al., 2012; Yeruham et al., 1995). In both these outbreaks, Egypt was suffering from exceptionally severe outbreaks at a similar time and there were no other outbreaks occurring in the region (Klausner et al., 2017). Most cattle herds in Israel are closed and the borders are tightly controlled, due to conflict in the region, so introduction of the disease through movement of infected cattle is highly unlikely (Klausner et al., 2017). Klausner et al (2017) suggested phylogenetic analysis demonstrated that the Israeli isolate from the 2006 outbreak was identical to an isolate analysed from the 1989 outbreak in Egypt. Although it seems unlikely that a large virus would remain genetically stable over such a longer 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 to the theory that these outbreaks occurred as a result of long-distance windborne spread of vectors (Klausner et al., 2017).

Klausner et al (2017) identified relevant synoptic systems that could have allowed long-distance dispersal of infected vectors by wind from Egypt to Israel in the months preceding the 1989 and 2006 outbreaks (Klausner et al., 2017). They then used backward Lagrangian trajectories (using the HYSPLIT model) from the receptor sites in Israel for each relevant synoptic system (Klausner et al., 2017). Their analysis identified several atmospheric routes that could have connected potential points of disease origin in Egypt to the areas where outbreaks occurred in Israel (Klausner et al., 2017). Results from the 2006 outbreak don't indicate a particular location as the likely source, but results from 1989 indicate that windborne transport was most likely to have occurred from Damietta or Port Said in Egypt to Pedium in Israel (Klausner et al., 2017). These locations are 266 and 221 km, respectively, from the point of

outbreak in Israel (Klausner et al., 2017). The analysis indicated a travel time of around one day, which is consistent with previous work suggesting that mechanical transmission can occur for more than a day after feeding (Klausner et al., 2017). In the context of this study, it is worth noting that whilst Indonesia and Timor Leste are over 1000 km from the Australian mainland, Papua New Guinea (PNG) is only 4 km from Sabai Island (an Australian island in the Torres Strait) and less than 200 km from the Australian mainland.

The potential for vector transport by wind associated with synoptic systems is influenced by the capacity of a vector to survive such a journey (Klausner et al., 2017). et al (2017) describe the humidity and temperature required for optimal survival of *Stomoxys calcitrans*. They conclude that atmospheric travel under the dry conditions seen in their proposed synoptic systems is possible, although not ideal for fly survival (Klausner et al., 2017).

There are several examples of possible transmission of other viruses through wind-assisted travel of vectors. Ritchie and Rochester et al (2001) proposed that Japanese encephalitis virus was introduced to Australia by wind-blown *Culex* spp. (Ritchie and Rochester, 2001). Others have suggested that bovine ephemeral fever spread from Korea to Japan via wind and that wind assisted in the spread of bluetongue virus (BTV) in Europe (Hendrickx et al., 2008; Shirakawa et al., 1994). Eagles et al (2014) looked for the potential source of exotic *Culicoides* species and isolates of novel BTV found in Australia. These specimens, collected as part of an active arbovirus surveillance program were used to assess the plausibility of dispersal from neighbouring countries (Eagles et al., 2014). A likely dispersal event was identified for five of the six cases examined with the source location varying from Lombok, to Timor-Leste and southern Papua PNG (Eagles et al., 2014).

Researchers in Spain recently developed a methodology for estimating the risk of wind-borne introduction of flying insects into a country (Fernández-Carrión et al., 2018). Their model predicts the number density of insects introduced over space and time based on the advection of wind currents, the deposition on the ground and the survival of the insect in the climatic conditions of the day (Fernández-Carrión et al., 2018). They compared their model outputs to actual field data on BTV outbreaks in Spain during the study period and found the risk period and region identified by the model matched the field data, validating the model (Fernández-Carrión et al., 2018).

## 4 Geographical distribution of Lumpy Skin Disease

---

The aim of this section is to answer the research question - In which countries and regions is LSD present (with a focus on the Australia's near neighbours) and what are the predicted future movements of the disease (including risk to Australia)?

### 4.1 Geographical distribution to date

As described earlier, LSD was first reported in Zambia in 1929 but spread quickly within Africa (Khan et al., 2021; Morris, 1930). LSD was largely contained in the African continent until 1984 when it moved into the Middle East (Davies, 1991; House et al., 1990; Tuppurainen and Oura, 2012). In 1989, the virus spread to Israel and in the following years, the virus continued to spread across contiguous countries in several directions throughout the Middle East, moving westerly into Iran and into other central Asian countries (EFSA AHAW Panel, 2016; Yeruham et al., 1995).

In 2015, the disease first emerged in Europe and spread to several countries but was effectively controlled through mass vaccination (EFSA, 2018). Since 2017, Russia is the only country on the European continent to report outbreaks of LSD (OIE, 2022).

Since 2019, the spread of LSDV has increased in Asia. China reported its first outbreak of LSD in August 2019, with the virus later spreading to Taiwan (Gupta et al., 2020; Lu et al., 2021). Outbreaks occurred in feral cattle in Hong Kong in October 2020 (Flannery et al., 2021).

In South 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 first reported outbreaks in September 2020 (Azeem et al., 2022).

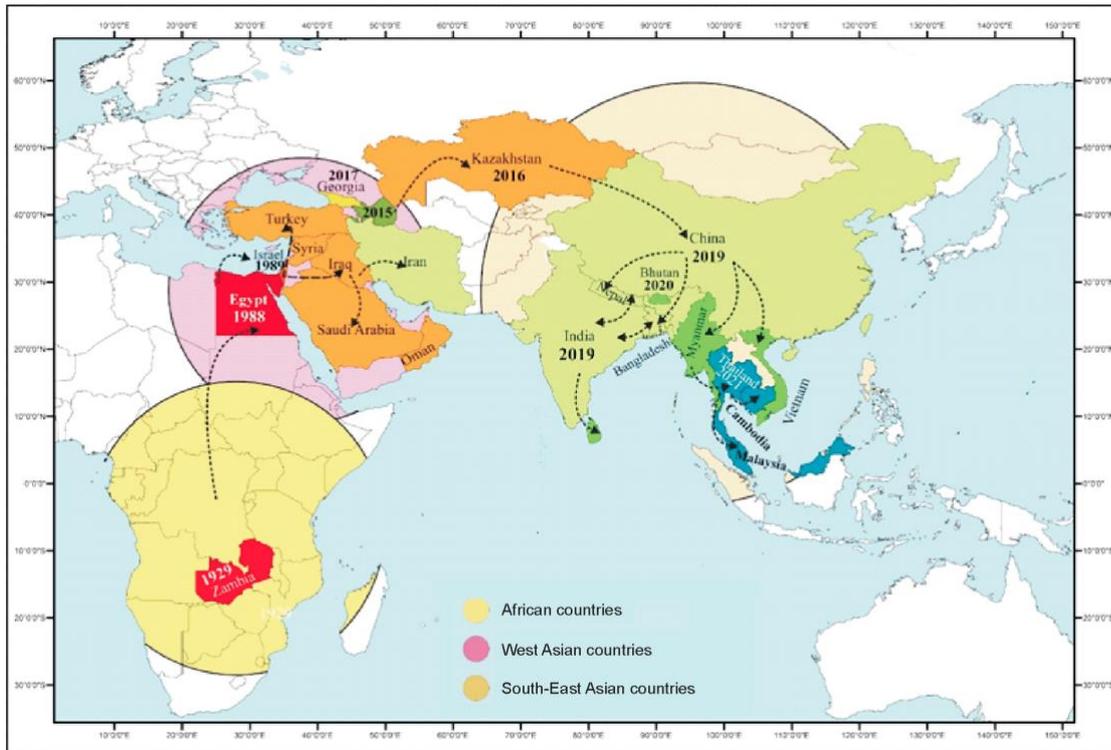


Figure 1 Global spread of LSD<sup>4</sup> (Kumar et al., 2021).

#### 4.1.1 Spread to South-East Asia

In South East Asia, the disease was reported for the first time in Laos, Thailand, Cambodia, Vietnam and Malaysia in 2021 (OIE, 2022). Indonesia reported the disease for the first time on March 2, 2022 (OIE, 2022). Presumably, it spread across the narrow Malacca straight from Malaysia with the assistance of windborne vector dispersal. Singapore also reported the disease for the first time in 2022 (OIE, 2022). In most cases, anecdotal reports preceded official reports; a typical occurrence in the region (Smith et al., 2015).

Even with known models for the movement of livestock through Asia there remain challenges in accurately modelling the direction of movement of any disease through the region. Each country maintains a record of official trade, however, it is widely accepted that these numbers are a poor indicator of true volume and movement as it is not in the interests of traders to go through official channels (Roche et al., 2021). For this reason, we consulted Singapore veterinarian and regional livestock movement expert, Dr Michael Patching. We summarise several of his observations here (for full report, see Appendix Two).

It is likely that the virus moved south from China into Vietnam from an outbreak in Eastern China in July 2020 (Patching, 2022). This goes against the normal flow of livestock movements from Vietnam and South East Asia north into China (Smith et al., 2015). The LSDV isolates from early outbreaks in Vietnam showed a close molecular relationship with those in China (Azeem et al., 2022). By the end of

<sup>4</sup> This map was developed in 2021. Since the map was developed, LSD has also spread into Laos, Vietnam and Indonesia.

the year there was clinical disease in Myanmar (OIE, 2022). It is unclear if this originated from northern or eastern China, or from some other origin to the west (Patching, 2022).

Clinical disease continued down the coast of Vietnam throughout 2020 and by the middle of 2021 it was being reported in Ha Tinh Province (OIE, 2022). Anecdotally, there was a widespread outbreak of the disease in feedlots in northern and central Vietnam during the first half of 2021 (Patching, 2022). One feedlot owner with large numbers of Australian cattle reported to be suffering significant production losses in some lines of cattle, and there was communication between Vietnamese cattle farmers about purchase and use of the LSD vaccine (Patching, 2022). The feedlots were also known to be trying to sell infected cattle into abattoirs without reporting, but in some cases clinical signs meant that the hides had lost value (Patching, 2022).

The first clinical signs of the disease were observed in eastern Thailand in April 2021, and it is likely that the virus movement was related to the trucking of cattle back across the border from Vietnam (Arjkumpa et al., 2021). It has been claimed by some traders that infected cattle from Vietnam were being moved into Vietnamese provinces and into Laos and Cambodia because they could not be sold in Vietnamese abattoirs (Patching, 2022).

It is also possible that the virus in cattle in Thailand originated from the movement of cattle from China or Myanmar (Patching, 2022). Thailand commonly feeds cattle from Myanmar and this movement often facilitates the spread of foot and mouth disease into Thailand and the region (Smith et al., 2015). The main cattle production region in Thailand is in the north-east, where the outbreak was first observed (Bunmee et al., 2018). This area is an important transition hub for cattle movement throughout the region.

The movement of the virus then likely followed traditional trading routes; south into Malaysia and circulating east back through Cambodia and Laos into Vietnam (Smith et al., 2015). It is also possible that there were cattle traded from Vietnam into Laos and Cambodia against historical trading routes due to the price signalling brought about by inability to sell these infected cattle to Vietnamese abattoirs (Patching, 2022).

Interestingly, there have been no significant official or unofficial reports of LSD in southern Vietnam, at least in Australian cattle feedlots (OIE, 2022). The feedlots in southern Vietnam have greater biosecurity and less movement of local cattle into them (Patching, 2022). They also had more time to vaccinate their cattle against the disease or slaughter early.



Figure 2 Spread of LSD in South-East Asia (figure developed by Dr Michael Patching)

## 4.2 Projected spread in the region

Figure 1 and Figure 2 demonstrate the spread of LSDV in South-East Asia that has been seen so far. Critical to Australia is the projected spread of LSDV beyond Sumatra and into nearer neighbours, such as closer regions of Indonesia, Timor Leste and PNG. Indonesia, Timor Leste and PNG will become the early warning system for vector movement into northern Australia. There are no official movements of cattle into the Indonesia archipelago from mainland South-East Asia, although there are movements from Indonesia and East Malaysia into Malaysia (Patching, 2022). Unofficial movement of livestock from the mainland to the islands is unlikely because..., although not impossible.

With the price of Australian cattle likely to remain high until 2023, Indonesia continues to look to South America and Mexico to decrease reliance on Australia as a sole trading partner. Importers are actively exploring the possibility of importing cattle from Brazil, however, previous attempts to import cattle from Mexico have failed (Answorth, 2021). The risk of transmission of diseases including, but not limited to, LSD from imported cattle needs to be considered, although the disease is not currently in South America (Patching, 2022).

Cattle are also transported between Indonesian islands (Patching, 2022). The Indonesian Government has supported the construction of a livestock carrier to operate between the island of Nusa Tenggara (NTT) into Jakarta ([www.pelni.co.id](http://www.pelni.co.id)). The KM Camara Nusantara is managed by PELNI and delivered a total of 7,899 head in 2019 (Patching, 2022). It takes a route of Kupang - Waingapu - Tg. Priok - Cirebon - Kupang (Patching, 2022). There are also known informal movements of cattle between Indonesia and Timor Leste, including an estimated 5,000 head annually in 2015 from Timor Leste into Indonesia

(Patching, 2022; Waldron et al., 2018). Movement from Timor Leste to Indonesia is of little consequence to the spread of LSD, as Indonesia is more likely to become infected before Timor Leste.

Timor Leste and PNG both have ambitions to increase national cattle herd numbers, but low consumer demand (due to lack of wealth) will mean that importing livestock will not be a reality unless it is government-supported. Even if unofficial trade occurred, the low volume of this trade channel would limit the probability of transmission between the nations (Patching, 2022). This is compared to the high volume of land-based trade that exists in mainland Asia (Smith et al., 2015).

In summary, the rapid spread of LSDV through South-East Asia is not surprising, given what is understood about the high volume of unofficial trade that occurs across national borders on a daily basis in the region. The spread of LSDV to Indonesia is of great concern to Australia, however, movement south-easterly (and towards Australia) is likely to occur more slowly (if at all) due to the geographical restrictions on livestock movement posed by the island composition of Indonesia.

## 5 Information relevant to assessing potential for spread to Australia

---

The potential for LSDV to enter and establish in Australia is dependent on the probability of entry, combined with environmental conditions and agricultural and landscape factors conducive to establishment at the point of entry (including livestock density). There is no published risk assessment for the entry of LSDV in Australia (hence the reason for this review). Methodical risk assessment of entry of LSDV into Australia requires comprehensive mapping of risk pathways. This will be completed as part of the risk assessment. Literature that may inform the probability of establishment is reviewed here.

### 5.1 Ecological conditions for spread

Some authors have modelled the ecological conditions that favour the spread of LSDV in other regions using data available from previous outbreaks (Alkhamis and VanderWaal, 2016; Allepuz et al., 2019; Machado et al., 2019). Because of the critical role of blood-feeding arthropods in LSDV transmission, it is no surprise that the distribution and spread of LSDV are heavily influenced by environmental conditions and landscape (Abera et al., 2015; Alkhamis and VanderWaal, 2016; Lubinga et al., 2015; Tuppurainen et al., 2013b).

Allepuz et al (2019) used logistic regression modelling and data from the Balkans, Caucasus and the Middle East to identify factors associated with occurrence of LSD (Allepuz et al., 2019). They found increased odds of LSD were associated with cropland, grassland or shrubland (as opposed to forest), high cattle densities, higher annual mean temperature and higher diurnal temperature (Allepuz et al., 2019). Optimal quantitative values were not calculated, but we know Australia has croplands, grasslands and shrublands, as well as areas of high cattle density, high temperature and moderate-high diurnal temperatures.

Alkhamis and VanderWaal (2016) used data on outbreaks in the Middle East and the maximum entropy ecological niche modelling technique (Maxent) to build ecological niche models (ENM) for LSD. Maxent builds models by extracting associations between the presence of LSD outbreaks with environmental variables to characterise the environmental requirements for a disease agent (Alkhamis and VanderWaal, 2016). Their final Maxent model indicated that only six of the selected environmental variables were needed to predict disease in the Middle East; annual precipitation, mean diurnal temperature range, livestock production type, mean diurnal range, land cover and goat, sheep and buffalo densities (Alkhamis and VanderWaal, 2016). They found that geographical regions with an annual precipitation between 50 and 100 mm and a diurnal temperature range of approximately 12 °C were the most suitable for LSD (Alkhamis and VanderWaal, 2016). Geographical regions with croplands, urban and mixed rain-fed arid livestock production areas were also found to be most suitable (Alkhamis and VanderWaal, 2016), as were regions with low goat density (Alkhamis and VanderWaal, 2016). However, there were discrepancies in the relative contribution of each variable across different models (Alkhamis and VanderWaal, 2016). Mean annual precipitation of 50 to 100 mm is only seen in central desert parts of Australia, whereas diurnal ranges of around 12 °C are seen in most parts of the country (Australian Bureau of Meteorology, 2022). However, it is important to note that the range of mean annual precipitation used in this modelling was low because all data were from the Middle East, a region dominated by desert. Therefore, the favoured annual precipitation for LSDV spread determined by this study could never have been a globally high value.

Machado et al (2019) used two modelling approaches to explore the distribution of LSDV in Eurasia with the aim of identifying environmental risk factors and determining the underlying risk of the disease spreading further in this region. Firstly, using ENM they identified risk factors and additional geographic areas in which, if introduced, LSDV would be likely to spread (Machado et al., 2019). Secondly, they used Bayesian hierarchical modelling to further refine risk factors and produce new estimates of risk (Machado et al., 2019). In the ENM, they found the most important variables with the highest contribution to the final model were annual mean solar radiation, annual mean wind speed and annual mean water vapor pressure (Machado et al., 2019). Their ENM suggested potentially suitable areas had monthly median wind speeds of 2.4 m s<sup>-1</sup> (IQR 2.0–2.8 m s<sup>-1</sup>), precipitation of ~46.1 mm (IQR 31.5–65.6 mm), with median maximum temperatures of 15.9 °C (IQR 8.8–22.8 °C), solar radiation of 14633 kJ m<sup>-2</sup> day<sup>-1</sup> (IQR 8524–20979 kJ m<sup>-2</sup> day<sup>-1</sup>) and water vapor pressure of 0.8 kPa (IQR 0.6–1.2 kPa). The suitable areas were between 300 and 1300 meters above sea level (median 782 meters: IQR 299–1306), with sizeable populations of potential hosts such as cattle and sheep (cattle densities median number of 8.3 head per km<sup>2</sup> (IQR 4.8–14.78 head per km<sup>2</sup>) and sheep 17.1 head per km<sup>2</sup> (IQR 6.2–38.4 head per km<sup>2</sup>). When this was combined with the Bayesian modelling, maximum temperature, precipitation and wind were the strongest risk factors (Machado et al., 2019). In Australia, monthly mean wind speeds of 2.4 m s<sup>-1</sup> (or 8.4 km per hour) are feasible in many areas, as are monthly mean precipitations of 46 mm (Australian Bureau of Meteorology, 2022). Median maximum temperatures of 15.9 °C are regularly observed (Australian Bureau of Meteorology, 2022). As with the previous study, it is important to note that ranges are reflective of data inputs.

## 5.2 Distribution of vector species in Australia

There has been much work on the specific vectors capable of transmitting LSDV however it is most likely that the virus can be transmitted by several 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 UK 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 UK*'. Since this was written, the disease has also spread through Asia, further demonstrating that whilst identifying particular vectors has been considered highly relevant in the literature, in a practical sense, most countries (including Australia) are likely to have vector species capable of transmitting the disease. Despite this, we've reviewed the distribution of the main groups of vectors known to potentially be capable of transmitting LSDV in Australia.

### 5.2.1 Flies

Species such as *Stomoxys calcitrans* (the stable fly) are found throughout Australia, particularly near livestock (Telfer, 2018). The stable fly in particular has become an increasingly serious pest of beef cattle, and many cattle feedlot and dairy operators have reported problems with large fly populations (Hogsette et al., 2012; Telfer, 2018). One study in Queensland aimed to determine the seasonal population dynamics of *S. calcitrans* and two additional *Musca* spp. by monitoring feedlots over a period of seven years (Godwin et al., 2017). They trapped over a million flies, with *M. domestica* (housefly) being the most common (67% of trapped flies), followed by *M. vetustissima* (Australian bush fly; 21% of trapped flies) and *S. calcitrans* (12% of trapped flies) (Godwin et al., 2017). Another comparable study that also included feedlots in three different climatic zones in Queensland and New South Wales came up with a very similar distribution (Hogsette et al., 2012).

**The horn fly (more commonly known as the buffalo fly in Australia), *Haematobia irritans*, has been identified as a problem for cattle producers in Northern Australia. As discussed earlier**

(Section 3.3.4), *H. irritans* was highly abundant on beef cattle during the 2012–2013 outbreaks in northern Israel but its role or capacity to transmit LSDV has not been investigated (Berg et al., 2015).

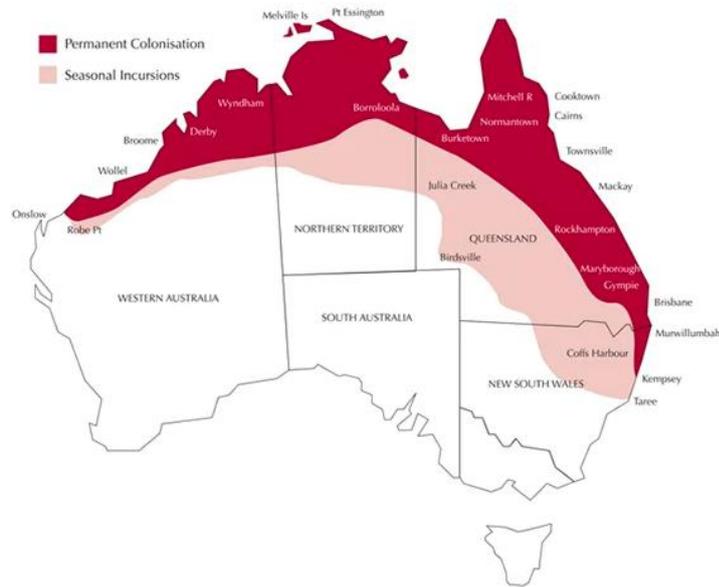


Figure 3 shows the distribution of buffalo fly in Australia.

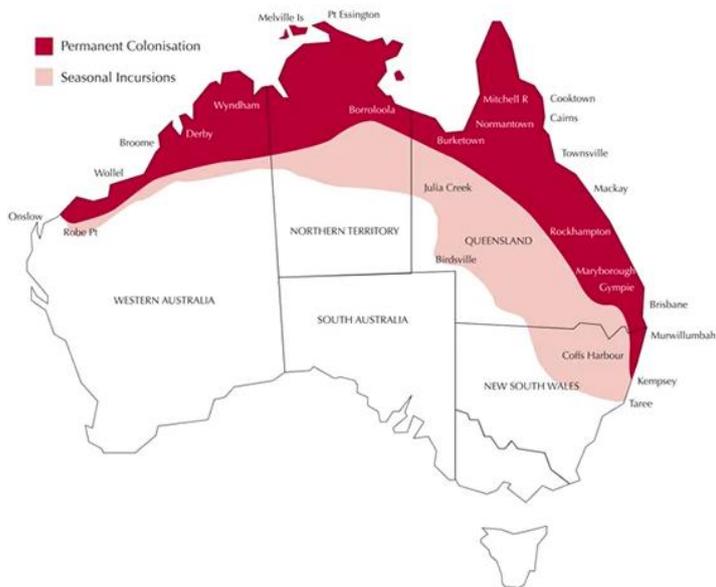


Figure 3 Distribution of buffalo fly (MLA, 2022a)

It can be assumed that common fly species will be present in any area with sufficient cattle density, particularly around feedlots and dairy enterprises.

### 5.2.2 Mosquitoes

Mosquitoes are present throughout Australia, but different species are found in different geographical regions. In total, there are more than 80 species of mosquito found in Australia (University of Sydney, 2022).

Most of the work on mosquito distribution in Australia is focused on *A. aegypti* because of its association with dengue virus and other human viruses. Australia is largely free of *A. aegypti*, with occasional

incursions detected through trapping (Inspector General of Biosecurity, 2017). Efforts to stop *A. aegypti* from establishing are expensive and disruptive but necessary (Inspector General of Biosecurity, 2017). Incursions of *A. aegypti* in Australia are relevant to potential spread of LSDV because it has been implicated as a potential vector (see Section 3.3.3). Figure 4 summarises the detection of *A. aegypti* in Australia as determined through trapping events. Figure 5 shows work from the Department aimed at visually representing weather systems that may assist with the movement of *A. aegypti* between neighbouring countries and Northern Australia.

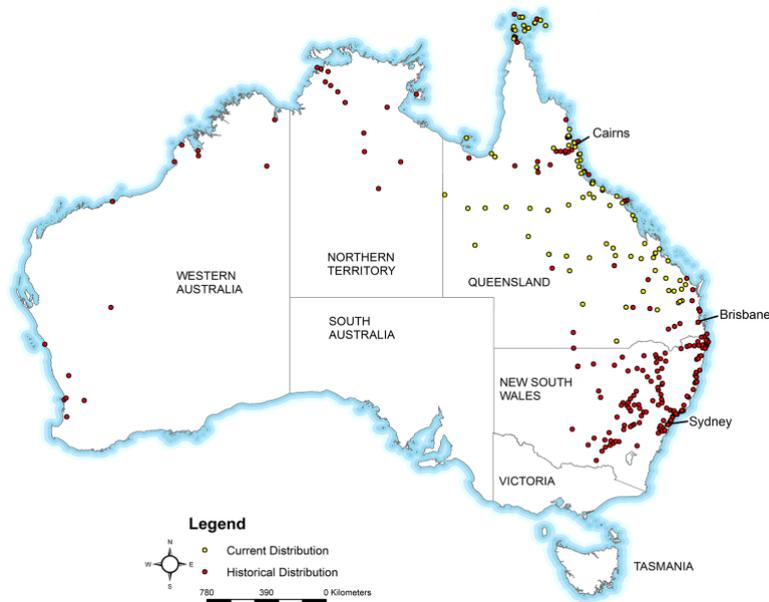


Figure 4 Historical (red dots) and contemporary (yellow dots) distribution records of *A. aegypti* in Australia 1887–2016 (Beebe et al., 2009; Trewin et al., 2017).

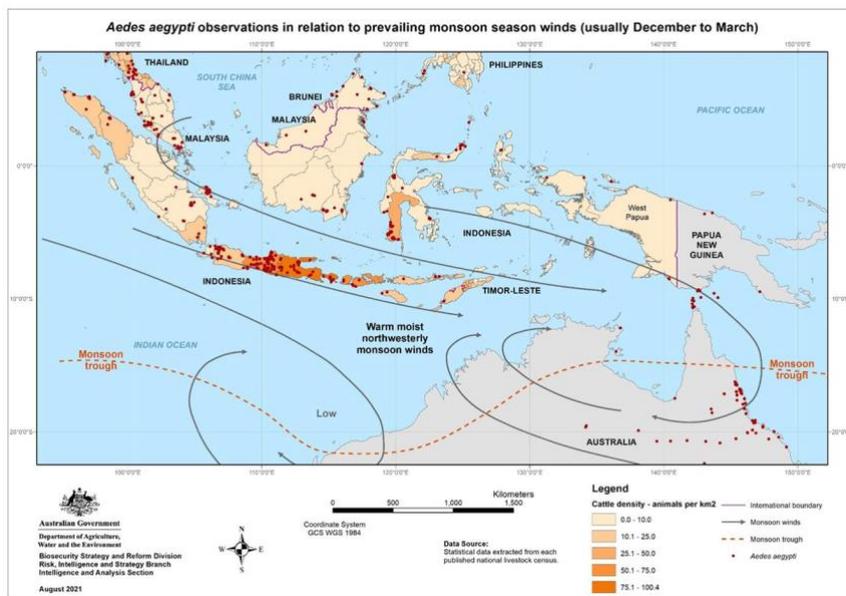


Figure 5 Monsoonal weather patterns relevant to the movement of *A. aegypti* in Northern Australia

### 5.2.3 Midges

Species from the family *Ceratopoginidae* are distributed worldwide on every continent except Antarctica (Boorman, 1993). The distribution of different species from this group within Australia is poorly

described and most studies focus primarily on the *Culicoides* spp. that are capable of transmitting BTV (Tay et al., 2016).

Figure 6 shows detections of *Culicoides* spp. from the trapping that takes place as part of the Australian National Arbovirus Monitoring Program (NAMP). More recent trapping results can be obtained with the relevant permissions through NAMP. This map gives an indication of where the *Culicoides* spp. relevant to BTV transmission have been detected in relation to cattle density. Figure 7 shows work from the Department aimed at visually representing weather systems that may assist with the movement of *Culicoides* spp. between Northern Australia and neighbouring countries.

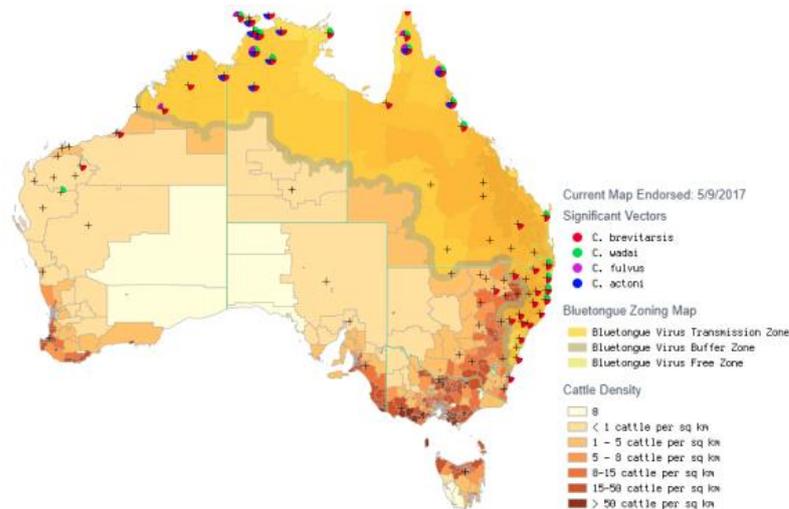


Figure 6 *Culicoides* trapping results from September 2016–August 2017 with cattle density (MLA, 2017)

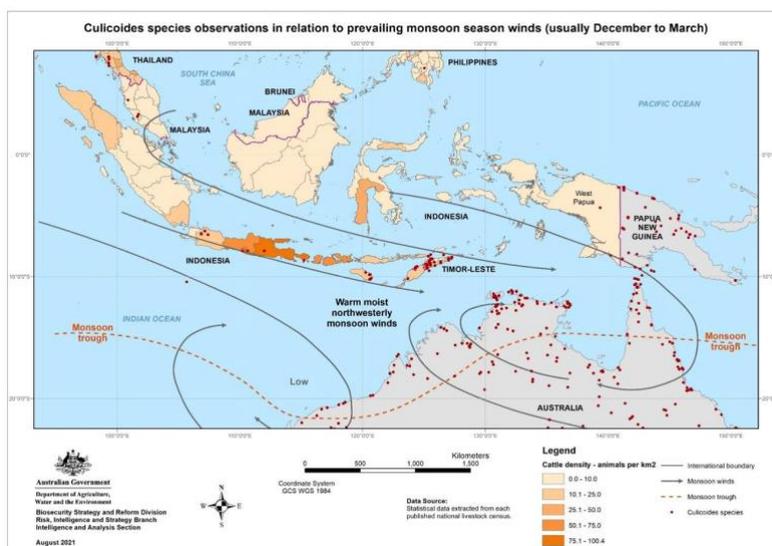


Figure 7 Monsoonal weather patterns relevant to the movement of *Culicoides* spp. in Northern Australia

### 5.2.4 Tabanidae

The family *Tabanidae* occur throughout Australia. Figure 8 shows a distribution map compiled of occurrence reports entered into the Atlas of Living Australia. Many of these reports come from renowned

organisations such as Museums Victoria but others are entered by citizen scientists. Nonetheless, the map gives an indication of the wide distribution of these species.

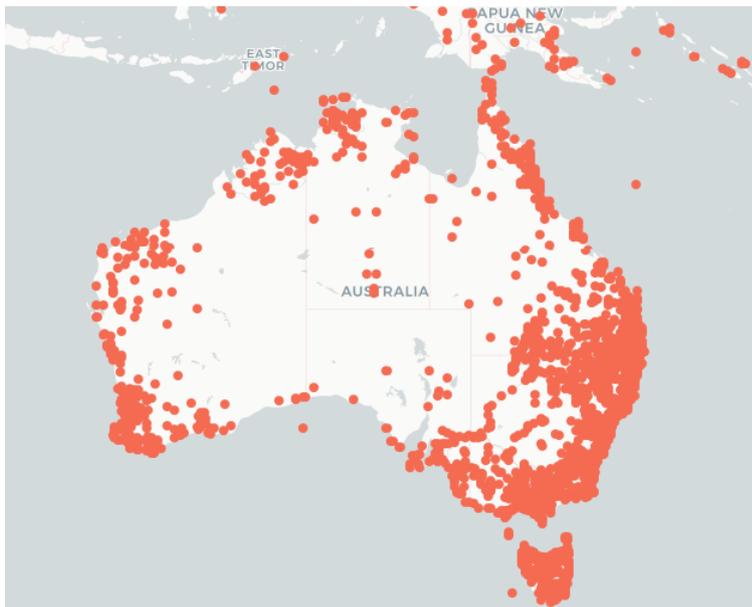


Figure 8 Occurrence reports of *Tabanidae* spp. (Atlas of living Australia, 2022)

### 5.2.5 Hard ticks

There are around 70 species of ticks in Australia, most of which are hard ticks (family *Ixodidae*) (Barker et al., 2014). The tick species studied in relation to LSDV transmission (see Section 3.3.3) are not present in Australia and ticks are unlikely to be involved in disease introduction (Barker et al., 2014). They could, however, become important vectors if LSDV ever established in Australia.

Perhaps of most relevance to LSDV transmission is the distribution of ticks that infect cattle. In Australia the ‘tick line’ divides areas where cattle ticks are expected, or endemic, and areas in which their presence is notifiable. Each jurisdiction has its own regulations around tick control and reporting such that tick zone updates are best sought from jurisdictional websites. Figure 9 shows an approximation of the ‘tick line’ across all relevant jurisdictions.

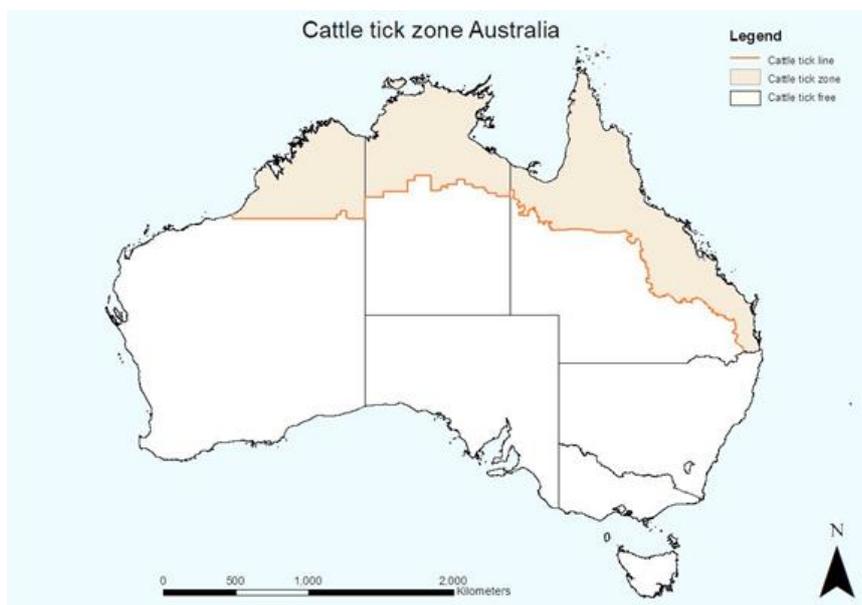


Figure 9 Approximate of Australian 'tick line' (MLA, 2022b)

## 5.3 Density and distribution of relevant livestock species in Australia

### 5.3.1 Domestic cattle

The presence of capable vectors can potentially be assumed, but another critical factor to the probability of LSDV entering and establishing in Australia is the density of domestic cattle in Australia, particularly around points where infected vectors could enter. Figure 10 shows the density of cattle in Australia, based on estimates from the 2016 Agricultural Census.

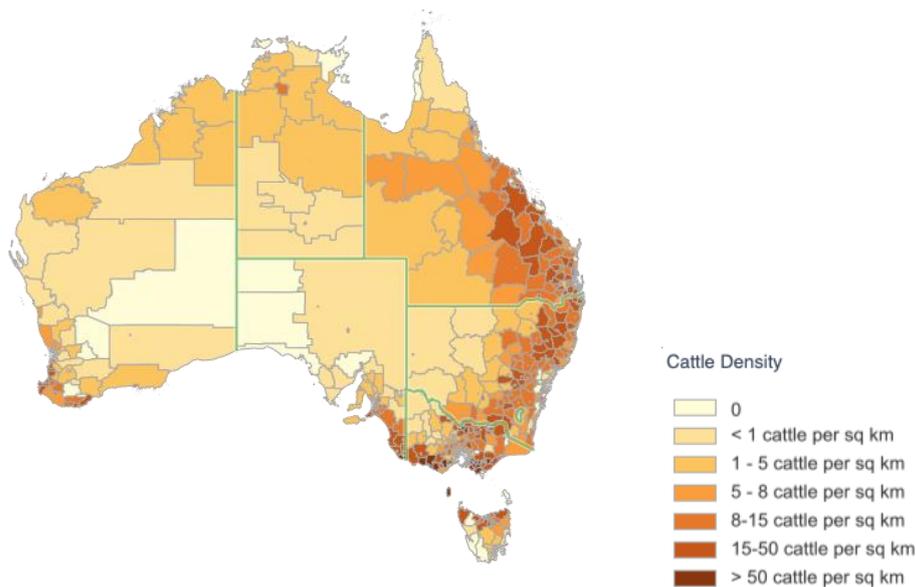


Figure 10 Cattle density in Australia

### 5.3.2 Feral species

Wild cattle (including *Bos javanicus*) and water buffalo (*Bubalus bubalis*) are both found in Australia, predominantly in the top end of the NT (Department of Sustainability, Environment, Water, Population and Communities, 2011; Murray and Snowdon, 1976). Water buffalo were imported into the Cobourg Peninsula in the NT as a meat source during the 19th century and subsequently dispersed into nearby swamps and floodplains (Department of Sustainability, Environment, Water, Population and Communities, 2011). Peak populations, prior to the Brucellosis and Tuberculosis Eradication Campaign of the 1980s, were estimated at 350,000 individuals but numbers have reduced considerably since then (Corner, 2006; Department of Sustainability, Environment, Water, Population and Communities, 2011). Population densities for buffalo can reportedly reach 34 head per km<sup>2</sup> during the wet season (Department of Sustainability, Environment, Water, Population and Communities, 2011).

The risk of pathogen transmission from buffalo to livestock was extensively considered during the brucellosis and tuberculosis eradication campaign. Although the grazing range overlapped during the dry season, there was limited direct contact between these species and buffalo; transmission was considered

unlikely (Corner, 2006). The risk of transmission is likely to be greater with LSDV due to the importance of mechanical vector-borne transmission.

Feral cattle of domestic species occur around most pastoral areas, but at lower densities than commercial cattle, and these will often be difficult to distinguish from domestic cattle anyway (Reid et al., 2020; Woolnough et al., 2005). In fact, the presence of a nearby pastoral station has been associated with the probability of feral cattle species occurring in that region (Reid et al., 2020).

## 5.4 Density and distribution of relevant livestock species in neighbouring countries

The density and distribution of cattle in neighbouring countries will be critical to assessing the risk of LSDV travelling from these countries to Australia via unregulated pathways.

Figure 11 shows the density of cattle in the Indonesian provinces closest to Australia.

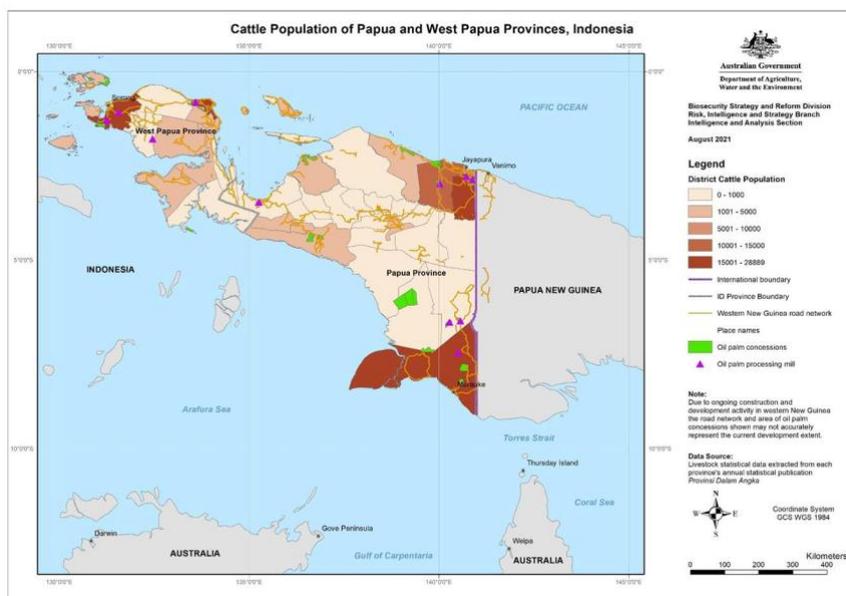


Figure 11 Cattle density of Papua and West Papua provinces of Indonesia

The 2019 Agricultural census in Timor Leste indicated that there are an estimated 286,558 cattle in the country and 127,475 buffalo (Republic of Timor-Leste, 2019). These figures have been broken down by municipality and will be mapped as part of the final report for this work. However, using the total landmass of Timor Leste this equates to cattle densities of approximately 19 head of cattle per km<sup>2</sup> and 8.5 head of buffalo per km<sup>2</sup>. This falls within the range associated with LSDV spread.

In PNG, there are an estimated 40,000 head of cattle, with the highest numbers in Morobe Province (approximately 17,000 head) (Papua New Guinea Government Official, 2021). These population densities will be mapped as part of the final report for this work. However, using the total landmass of PNG and Morobe Province, this equates to cattle densities of less than one per km<sup>2</sup> and approximately 2 per km<sup>2</sup>, respectively. These densities may not be sufficient for LSDV to spread easily within PNG.

## 6 The role of climate change in the spread of LSDV

---

The aim of this section is to answer the research question - What is the role of climate change in the future spread of LSDV and how will extreme climate change scenarios impact the potential entry and establishment of LSDV in Australia in 10 years' time?

From its earliest days, it was observed that unusually heavy rains often preceded LSD outbreaks (Woods, 1988). 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 both changes in vector survival, geographical range expansion and changes in vector activity, efficiency and susceptibility to infection (Ali et al., 2020). Extreme weather events may also play a role (such as cyclones assisting windborne movement), but these are associated with even more uncertainty than general global warming (Thornton et al., 2009). Prior to its rapid spread through Asia, Tuppurainen et al (year) observed that the impact of global climate change on vector distribution suggested a real risk of LSDV establishing itself in the Middle East and Asia, as well as spreading further (Tuppurainen et al., 2017). In addition, Wittmann et al (2001) suggested that an increase in environmental temperature of 2 °C could result in extensive expansion of the range of *Culicoides imicola*, a vector responsible for the transmission of BTV (Wittmann et al., 2001).

Despite this, it is difficult to predict how global climate change may affect vector abundance and distribution in the future because there are too many uncertainties (Rocklöv and Dubrow, 2020; Tuppurainen and Oura, 2012). Firstly, the level of climate change will depend greatly on the intensity of human action taken to reduce greenhouse gas emissions (Rocklöv and Dubrow, 2020). Secondly, predictions need to account for non-climatic drivers of infectious disease incidence, such as a political will to control disease transmission, many of which are also highly unpredictable (Rocklöv and Dubrow, 2020).

There have been several attempts to develop models to gain an understanding of future situations (Rocklöv and Dubrow, 2020). The Intergovernmental Panel on Climate Change (IPCC) have developed four Representative Concentration Pathway (RCP) scenarios for greenhouse gas emissions that range from high emissions ('business as usual' approach) to low emissions brought about by aggressive global mitigation (Rocklöv and Dubrow, 2020). For each scenario, temperatures, precipitation and humidity are predicted to 2100 and beyond (Rocklöv and Dubrow, 2020). The IPCC has also developed five Shared Socioeconomic Pathways (SSPs) that describe alternative scenarios for socioeconomic change up until 2100 (Rocklöv and Dubrow, 2020). Climate-based scenarios (e.g., RCPs) and non-climate based scenarios (e.g., SSPs) can be used in combination to make projections about the future of vector-borne diseases (Rocklöv and Dubrow, 2020).

In one such study on future dengue virus occurrence, global distribution was found to be highly dependent on the RCP-SSP scenario applied (Messina et al., 2019). In another study on the impact of climate change on global malaria distribution that utilised RCPs and SSPs, modelling found consistent increases in the length of the malaria transmission season in highland regions, along with consistent decreases in tropical regions (Caminade et al., 2014). The net effect of future climate change appeared to be small, although there were large regional differences (Caminade et al., 2014). Lastly, another study used mosquito distribution data, meteorological variables and demographic variables to build a model of historical spatial spread for *Aedes aegypti* and *A. albopictus* (Kraemer et al., 2019). These were used to

project future spread until 2080 under different RCPs (Kraemer et al., 2019). The study found that historical spread of these vectors and projected spread in the next 5–15 years is mostly explained by human movement patterns, whereas in later years expansion will be more climate driven (Kraemer et al., 2019). No studies could be found that utilised RCPs and SSPs to predict future spread of LSDV.

Climate modelling approaches for any vector-borne disease risk assessment must consider both the positive and negative impacts of altered climate across different spatial and temporal scales (Tjaden et al., 2018). Global warming might increase climatically suitable regions for vector establishment and disease transmission to higher latitudes and elevations; it may also limit transmission of vector-borne disease in the warmest places where temperature thresholds for vector or pathogen survival may actually be exceeded (Altizer et al., 2013; Mordecai et al., 2017; Tjaden et al., 2018).

## 7 Risk assessment related to Lumpy Skin Disease

---

The aim of this section is to answer the research question - Have there been risk assessments on LSD in other countries and what can they tell us about appropriate frameworks for this risk assessment?

Several countries have conducted risk assessments related to LSD.

In 2015, Berg et al (2015) assessed the risk of LSDV entering the European Union (EU) prior to its actual introduction (Berg et al., 2015). Based on a literature review and knowledge of import practices, they considered the illegal movement of infected animals to be the most likely pathway of introduction for LSDV (Berg et al., 2015). Using probability theory and estimates of seroprevalence from different countries that already have LSDV, they made quantitative estimates of how many animals would need to be moved illegally to create a 0.05–0.95 probability of introduction of LSDV into the EU (Berg et al., 2015). Using a seroprevalence of 30% (based on the estimated seroprevalence in Ethiopia), they estimated 1301 animals would need to be moved illegally from to create a 0.95 probability of introducing the disease (Berg et al., 2015). Conversely, the movement of 25 animals would result in a probability of introduction of less than 0.05 (Berg et al., 2015). If the country of origin had a seroprevalence of 5%, the number of animals that would need to be moved would be 140 or 7809 to create probabilities of 0.05 and 0.95, respectively (Berg et al., 2015). They concluded (accurately in the end) that whilst infection was likely to spread in Bulgaria and Greece (with less spread seen when culling is initiated quickly), it is unlikely that the disease would become endemic in the EU (Berg et al., 2015).

Gale et al (2016) conducted a qualitative risk assessment of the entry of capripoxviruses into Great Britain from the EU through the importation of hides, skin or wool (Gale et al., 2016). They developed a simple risk pathway and made an informed qualitative assessment of the probability of each step occurring, along with detailing the level of uncertainty and key assumptions (Gale et al., 2016). They concluded that the risk of importation of LSDV virus via cattle hide/skin is low.

Horigan et al (2018) performed a qualitative risk assessment on the introduction and onward transmission of LSDV into the UK (Horigan et al., 2018). They mapped potential basic risk pathways and assigned an informed qualitative probability of each for introduction and onward transmission, as well as outlining uncertainties and data sources that were used to arrive at estimates (Horigan et al., 2018). They determined that the probability of introduction via vectors or livestock trade (both legal and illegal live animals and animal products) was very low (Horigan et al., 2018). All other routes were considered negligible (Horigan et al., 2018).

Taylor et al (2019) described a generic framework for spatial quantitative risk assessments of infectious diseases using LSD as a case study (Taylor et al., 2019). They outlined a generic risk pathway for any infectious pathogen to move from an infected country into a non-infected country (and infect susceptible species) (Taylor et al., 2019). For each step in the generic risk pathway they proposed a mathematical formula for calculating the probability, which relies on basic parameters such as prevalence of the disease in the infected country (Taylor et al., 2019). They then used this generic framework to assess the risk of LSDV infecting other countries in Europe following its introduction into the Balkans in 2016 (Taylor et al., 2019). They found that Croatia had the highest mean probability of infection, followed by Italy, Hungary and Spain (Taylor et al., 2019). Interestingly, LSD was never reported in any of these countries during the European outbreaks of 2015, 2016 and 2017 (OIE, 2022).

Saegerman et al (2018) developed a quantitative import risk analysis to assess the risk of LSD being introduced into France by imports of cattle (Saegerman et al., 2019). Using a stochastic model and based on the information available, they estimated that the probability of the first outbreak of LSD occurring following import of infected live cattle for breeding or fattening was  $5.4 \times 10^{-4}$  (95% probability interval

(PI):  $0.4 \times 10^{-4}$ ;  $28.7 \times 10^{-4}$ ) in the summer months and  $1.8 \times 10^{-4}$  (95% PI  $0.14 \times 10^{-4}$ ;  $15 \times 10^{-4}$ ) in the winter months (Saegerman et al., 2019).

The Food and Agricultural Organisation (FAO) conducted a qualitative risk assessment on the likelihood of introduction and spread of LSD in 23 countries in South, East and Southeast Asia in 2020 (Roche et al., 2021). They distributed a questionnaire to the countries being evaluated that aimed to determine the presence or absence of several risk factors (e.g informal and formal trade volumes, veterinary service capacity etc) (Roche et al., 2021). Where countries did not respond, alternative data sources were sourced (Roche et al., 2021). They assessed Cambodia, Laos, Myanmar, Thailand and Vietnam as having the highest risk of introduction and spread (of the countries that weren't already infected) (Roche et al., 2021). As it happens, these countries were the next to be infected, with some of the countries they assessed as being low to moderate risk becoming infected at later dates (such as Malaysia and Indonesia).

## 8 Relevant research gaps

There are several research areas of interest to the upcoming LSD risk assessment for which the literature review failed to find publications or grey literature of sufficient detail to inform the assessment. This will inevitably result in uncertainty when assigning qualitative values in our assessment. Relevant potential research gaps and methods to reduce the uncertainty around these have been summarised in Table 1.

**Table 1 Research gaps relevant to upcoming risk assessment for LSD**

Research gap	Approach to addressing associated uncertainty
Potential risk pathways applicable to the Australian context	Expert consultation with the Department and the Northern Australian Quarantine Service Scientific Discipline Meeting participants
Effect of climate change on wind-assisted transport of vectors	Expert consultation with Dr Andrew Watkins, head of Operational Climate Services at the BOM, in combination with consultation from Medical Entomologist, Dr Mike Mueller
Survival of potential vector species on cargo ships, people and their belongings	Expert consultation with Medical Entomologist, Dr Mike Mueller
Detailed data on livestock populations in PNG	Current estimates provided from the Department will be mapped and compared to the FAO gridded livestock data. Further information may be sought from within PNG
Probability of vectors with high relevance to Australia such as the buffalo fly being able to transmit LSDV	Expert consultation with Medical Entomologist, Dr Mike Mueller

In addition, there are research areas discussed in the literature but not reviewed here that are of interest to the Australian agricultural sector and to the Department; namely LSD control and eradication and the role of vaccination. Australia's most recently published disease-specific AUSVETPLAN on LSD was completed in 2009. Since then, the disease has spread considerably and been effectively controlled in Europe. There is much to learn from recent experiences in how best to prepare for an LSD incursion and options for control or eradication. Ausvet recommends further work in reviewing these areas.

## 9 References

---

- Abera, Z., Degefu, H., Gari, G., Kidane, M., 2015. Sero-prevalence of lumpy skin disease in selected districts of West Wollega zone, Ethiopia. *BMC Vet. Res.* 11, 1–9.
- Abutarbush, S.M., Hananeh, W.M., Ramadan, W., Sheyab, O.M., Alnajjar, A.R., Zoubi, I.G., 2016. Adverse reactions to field vaccination against lumpy skin disease in Jordan. *Transbound Emerg Dis* 63. <https://doi.org/10.1111/tbed.12257>
- Acharya, K., Subedi, D., 2020. First outbreak of lumpy skin disease in Nepal. *Transbound. Emerg. Dis.* 67, 2280–2281. <https://doi.org/10.1111/tbed.13815>
- Agianniotaki, E.I., Tasioudi, K.E., Chaintoutis, S.C., Iliadou, P., Mangana-Vougiouka, O., Kirtzalidou, A., 2017. Lumpy skin disease outbreaks in Greece during 2015–16, implementation of emergency immunization and genetic differentiation between field isolates and vaccine virus strains. *Vet Microbiol* 201. <https://doi.org/10.1016/j.vetmic.2016.12.037>
- Aleksandr, K., Olga, B., David, W., Pavel, P., Yana, P., Svetlana, K., Alexander, N., Vladimir, R., Dmitriy, L., Alexander, S., 2020. Non-vector-borne transmission of lumpy skin disease virus. *Sci. Rep.* 10. <https://doi.org/10.1038/s41598-020-64029-w>
- Ali, A.A., Esmat, M., Attia, H., Selim, A., Abdel-Hamid, Y.M., 1990. Clinical and pathological studies of lumpy skin disease in Egypt. *Vet. Rec.* 127, 549–550.
- Ali, M., Carlile, G., Giasuddin, M., 2020. Impact of global climate change on livestock health: Bangladesh perspective. *OPEN Vet. J.* 10, 178–188. <https://doi.org/10.4314/ovj.v10i2.7>
- Alkhamis, M.A., VanderWaal, K., 2016. Spatial and temporal epidemiology of lumpy skin disease in the Middle East, 2012–2015. *Front. Vet. Sci.* 3, 19.
- Allepuz, A., Casal, J., Beltran-Alcrudo, D., 2019. Spatial analysis of lumpy skin disease in Eurasia—Predicting areas at risk for further spread within the region. *Transbound. Emerg. Dis.* 66, 813–822. <https://doi.org/10.1111/tbed.13090>
- Altizer, S., Ostfeld, R.S., Johnson, P.T., Kutz, S., Harvell, C.D., 2013. Climate change and infectious diseases: from evidence to a predictive framework. *science* 341, 514–519.
- Anderson, J.F., Magnarelli, L.A., 2008. Biology of ticks. *Infect. Dis. Clin. North Am.* 22, 195–215.
- Answorth, R., 2021. Indonesians to start negotiations with Mexican live exporters as Aussie feeder cattle rise to record prices. *Beef Cent.*
- Ardestani, E., Mokhtari, A., 2020. Modeling the lumpy skin disease risk probability in central Zagros Mountains of Iran. *Prev. Vet. Med.* 176. <https://doi.org/10.1016/j.prevetmed.2020.104887>
- Arijkumpa, O., Suwannaboon, M., Boonrawd, M., Punyawan, I., Laobannu, P., Yantaphan, S., Bungwai, A., Ponyium, V., Suwankitwat, N., Boonpornprasert, P., Nuansrichay, B., Kaewkalong, S., Ounpomma, D., Charoenlarp, W., Pamaranon, N., Prakotcheo, R., Buameetooop, N., Punyapornwithaya, V., Songkasupa, T., 2021. First emergence of lumpy skin disease in cattle in Thailand, 2021. *Transbound. Emerg. Dis.* 68, 3002–3004. <https://doi.org/10.1111/tbed.14246>
- Atlas of living Australia, 2022. Atlas of living Australia [WWW Document]. URL [ala.org.au](http://ala.org.au)
- Australian Bureau of Meteorology, 2022. Bureau of Meteorology Climate Data [WWW Document]. URL <http://www.bom.gov.au/cgi-bin/climate/change/averagemaps.cgi?map=dtr&season=0112>
- Azeem, S., Sharma, B., Shabir, S., Akbar, H., Venter, E., 2022. Lumpy skin disease is expanding its geographic range: A challenge for Asian livestock management and food security. *Vet. J.* 279, 105785.
- Babiuk, S., Bowden, T.R., Boyle, D.B., Wallace, D.B., Kitching, R.P., 2008. Capripoxviruses: an emerging worldwide threat to sheep, goats and cattle. *Transbound. Emerg. Dis.* 55, 263–272.
- Badhy, S.C., Chowdhury, M.G.A., Settypalli, T.B.K., Cattoli, G., Lamien, C.E., Fakir, M.A.U., Akter, S., Osmani, M.G., Talukdar, F., Begum, N., 2021. Molecular characterization of lumpy skin disease virus (LSDV) emerged in Bangladesh reveals unique genetic features compared to contemporary field strains. *BMC Vet. Res.* 17, 1–11.
- Balinsky, C.A., Delhon, G., Smoliga, G., Prarat, M., French, R.A., Geary, S.J., 2008. Rapid preclinical detection of sheeppox virus by a real-time PCR assay. *J Clin Microbiol* 46. <https://doi.org/10.1128/JCM.01953-07>
- Barker, S.C., Walker, A.R., Campelo, D., 2014. A list of the 70 species of Australian ticks; diagnostic guides to and species accounts of *Ixodes holocyclus* (paralysis tick), *Ixodes cornuatus* (southern

- paralysis tick) and *Rhipicephalus australis* (Australian cattle tick); and consideration of the place of Australia in the evolution of ticks with comments on four controversial ideas. *Int. J. Parasitol.* 44, 941–953.
- Barnard, B.J.H., 1997. Antibodies against some viruses of domestic animals in southern African wild animals. *Onderstepoort J Vet Res* 64, 95–110.
- Beebe, N.W., Cooper, R.D., Mottram, P., Sweeney, A.W., 2009. Australia's dengue risk driven by human adaptation to climate change. *PLoS Negl. Trop. Dis.* 3, e429.
- Berg, C., Botner, A., Browman, H., De Koeijer, A., Depner, K., Domingo, M., Ducrot, C., Edwards, S., Fourichon, C., Koenen, F., More, S., Raj, M., Sihvonen, L., Spoolder, H., Stegeman, J., Thulke, H., Vagsholm, L., Velarde, A., Willeberg, P., Zientara, S., EFSA Panel Anim Hlth & Welf AHAW, 2015. Scientific Opinion on lumpy skin disease. *EFSA J.* 13. <https://doi.org/10.2903/j.efsa.2015.3986>
- Boorman, J., 1993. Biting midges (Ceratopogonidae), in: *Medical Insects and Arachnids*. Springer, pp. 288–309.
- Bowden, T.R., Babiuk, S.L., Parkyn, G.R., Coppins, J.S., Boyle, D.B., 2008. Capripoxvirus tissue tropism and shedding: a quantitative study in experimentally infected sheep and goats. *Virology* 371. <https://doi.org/10.1016/j.virol.2007.10.002>
- Bunmee, T., Chaiwang, N., Kaewkot, C., Jaturasitha, S., 2018. Current situation and future prospects for beef production in Thailand—A review. *Asian-Australas. J. Anim. Sci.* 31, 968.
- Calistri, P., DeClercq, K., De Vleeschauwer, A., Gubbins, S., Klement, E., Stegeman, A., Cortiñas Abrahantes, J., Antoniou, S.-E., Broglia, A., 2018. Lumpy skin disease: scientific and technical assistance on control and surveillance activities. *EFSA J.* 16, e05452.
- Caminade, C., Kovats, S., Rocklov, J., Tompkins, A.M., Morse, A.P., Colón-González, F.J., Stenlund, H., Martens, P., Lloyd, S.J., 2014. Impact of climate change on global malaria distribution. *Proc. Natl. Acad. Sci.* 111, 3286–3291.
- Carn, V.M., Kitching, R.P., 1995. An investigation of possible routes of transmission of lumpy skin disease virus (Neethling). *Epidemiol. Infect.* 114, 219–226.
- Centre for Disease Control and Prevention, 2022. Centre for Disease Control and Prevention - Mosquitoes [WWW Document]. URL <https://www.cdc.gov/mosquitoes/about/where-mosquitoes-live.html#:~:text=Habitats,with%20little%20or%20no%20flow>
- Chihota, C., Rennie, L., Kitching, R., Mellor, P., 2003. Attempted mechanical transmission of lumpy skin disease virus by biting insects. *Med. Vet. Entomol.* 17, 294–300. <https://doi.org/10.1046/j.1365-2915.2003.00445.x>
- Chihota, C., Rennie, L., Kitching, R., Mellor, P., 2001. Mechanical transmission of lumpy skin disease virus by *Aedes aegypti* (Diptera : Culicidae). *Epidemiol. Infect.* 126, 317–321. <https://doi.org/10.1017/S0950268801005179>
- Corner, L.A., 2006. The role of wild animal populations in the epidemiology of tuberculosis in domestic animals: how to assess the risk. *Vet. Microbiol.* 112, 303–312.
- Davies, F.G., 1991. Lumpy skin disease, an African capripox virus disease of cattle. *Br. Vet. J.* 147, 489–503.
- Dehghani, M., Kazemi Shariat Panahi, H., Holmes, E.C., Hudson, B.J., Schloeffel, R., Guillemin, G.J., 2019. Human tick-borne diseases in Australia. *Front. Cell. Infect. Microbiol.* 3.
- Department of Sustainability, Environment, Water, Population and Communities, 2011. The feral water buffalo (*Bubalus bubalis*).
- Eagles, D., Melville, L., Weir, R., Davis, S., Bellis, G., Zalucki, M.P., Walker, P.J., Durr, P.A., 2014. Long-distance aerial dispersal modelling of Culicoides biting midges: case studies of incursions into Australia. *BMC Vet. Res.* 10, 1–10.
- EFSA, 2018. Lumpy skin disease II. Data collection and analysis. *EFSA J.* 16. <https://doi.org/10.2903/j.efsa.2018.5176>
- EFSA AHAW Panel, 2016. Statement: Urgent advice on lumpy skin disease. *EFSA J.* 14, 4573.
- EFSA, Calistri, P., DeClercq, K., Gubbins, S., Klement, E., Stegeman, A., Cortiñas Abrahantes, J., Antoniou, S.-E., Broglia, A., Gogin, A., 2019. Lumpy skin disease: III. Data collection and analysis. *EFSA J.* 17, e05638.
- Fagbo, S., Coetzer, J.A., Venter, E.H., 2014. Seroprevalence of Rift Valley fever and lumpy skin disease in African buffalo (*Syncerus caffer*) in the Kruger National Park and Hluhluwe-iMfolozi Park, South Africa. *J. S. Afr. Vet. Assoc.* 85, 1–7.

- FAO, 2016. Report of the FAO Ad Hoc Group Meeting on Lumpy Skin Disease.
- Fernández-Carrión, E., Ivorra, B., Ramos, Á.M., Martínez-Lopez, B., Aguilar-Vega, C., Sánchez-Vizcaíno, J.M., 2018. An advection-deposition-survival model to assess the risk of introduction of vector-borne diseases through the wind: Application to bluetongue outbreaks in Spain. *PloS One* 13, e0194573.
- Flannery, J., Shih, B., Haga, I., Ashby, M., Corla, A., King, S., Freimanis, G., Polo, N., Tse, A., Brackman, C., Chan, J., Pun, P., Ferguson, A., Law, A., Lycett, S., Batten, C., Beard, P., 2021. A novel strain of lumpy skin disease virus causes clinical disease in cattle in Hong Kong. *Transbound. Emerg. Dis.* <https://doi.org/10.1111/tbed.14304>
- Gale, P., Kelly, L., Snary, E., 2016. Qualitative assessment of the entry of capripoxviruses into Great Britain from the European Union through importation of ruminant hides, skins and wool. *Microb. RISK Anal.* 1, 13–18. <https://doi.org/10.1016/j.mran.2015.07.001>
- Gari, G., Bonnet, P., Roger, F., Waret-Szkuta, A., 2011. Epidemiological aspects and financial impact of lumpy skin disease in Ethiopia. *Prev. Vet. Med.* 102, 274–283.
- Gelaye, E., Belay, A., Ayelet, G., Jenberie, S., Yami, M., Loitsch, A., 2015. Capripox disease in Ethiopia : Genetic differences between field isolates and vaccine strain , and implications for vaccination failure. *Antivir Res* 119. <https://doi.org/10.1016/j.antiviral.2015.04.008>
- Gelaye, E., Lamien, C.E., Silber, R., Tuppurainen, E.S.M., Grabherr, R., Diallo, A., 2013. Development of a cost-effective method for Capripoxvirus genotyping using snapback primer and dsDNA intercalating dye. *PLoS One* 8. <https://doi.org/10.1371/journal.pone.0075971>
- Gelaye, E., Mach, L., Kolodziejek, J., Grabherr, R., Loitsch, A., Achenbach, J.E., 2017. A novel HRM assay for the simultaneous detection and differentiation of eight poxviruses of medical and veterinary importance. *Sci Rep* 7. <https://doi.org/10.1038/srep42892>
- Godwin, R.M., Mayer, D.G., Brown, G.W., Leemon, D.M., James, P.J., 2017. Predicting nuisance fly outbreaks on cattle feedlots in subtropical Australia. *Anim. Prod. Sci.* 58, 343–349.
- Goff, C., Lamien, C.E., Fakhfakh, E., Chadeyras, A., Aba-Adulugba, E., Libeau, G., 2009. Capripoxvirus G-protein-coupled chemokine receptor: a host-range gene suitable for virus animal origin discrimination. *J Gen Virol* 90. <https://doi.org/10.1099/vir.0.010686-0>
- Gortazar, C., Barroso, P., Nova, R., Caceres, G., 2021. The role of wildlife in the epidemiology and control of Foot-and-mouth-disease And Similar Transboundary (FAST) animal diseases: A review. *Transbound. Emerg. Dis.* <https://doi.org/10.1111/tbed.14235>
- Greta, A., Gourreau, J.M., Vassart, M., Wyers, M., Lefevre, P.C., 1992. Capripoxvirus disease in an Arabian oryx (*Oryx leucoryx*) from Saudi Arabia. *J. Wildl. Dis.* 28, 295–300.
- Gubbins, S., 2019. Using the basic reproduction number to assess the risk of transmission of lumpy skin disease virus by biting insects. *Transbound. Emerg. Dis.* 66, 1873–1883. <https://doi.org/10.1111/tbed.13216>
- Gupta, T., Patial, V., Bali, D., Angaria, S., Sharma, M., Chahota, R., 2020. A review: Lumpy skin disease and its emergence in India. *Vet. Res. Commun.* 44, 111–118. <https://doi.org/10.1007/s11259-020-09780-1>
- Haegeman, A., Zro, K., Vandenbussche, F., Demeestere, L., Campe, W., Ennaji, M.M., 2013. Development and validation of three Capripoxvirus real-time PCRs for parallel testing. *J Virol Methods* 193. <https://doi.org/10.1016/j.jviromet.2013.07.010>
- Heine, H.G., Stevens, M.P., Foord, A.J., Boyle, D.B., 1999. A capripoxvirus detection PCR and antibody ELISA based on the major antigen P32, the homolog of the vaccinia virus H3L gene. *J. Immunol. Methods* 227, 187–196.
- Hendrickx, G., Gilbert, M., Staubach, C., Elbers, A., Mintiens, K., Gerbier, G., Ducheyne, E., 2008. A wind density model to quantify the airborne spread of *Culicoides* species during north-western Europe bluetongue epidemic, 2006. *Prev. Vet. Med.* 87, 162–181.
- Hogsette, J.A., Urech, R., Green, P.E., Skerman, A., Elson-Harris, M., Bright, R.L., Brown, G.W., 2012. Nuisance flies on Australian cattle feedlots: immature populations. *Med. Vet. Entomol.* 26, 46–55.
- Horigan, V., Beard, P., Roberts, H., Adkin, A., Gale, P., Batten, C., Kelly, L., 2018. Assessing the probability of introduction and transmission of Lumpy skin disease virus within the United Kingdom. *Microb. RISK Anal.* 9, 1–10. <https://doi.org/10.1016/j.mran.2018.05.001>

- Hosamani, M., Mondal, B., Tembhurne, P.A., Bandyopadhyay, S.K., Singh, R.K., Rasool, T.J., 2004. Differentiation of sheep pox and goat poxviruses by sequence analysis and PCR-RFLP of P32 gene. *Virus Genes* 29. <https://doi.org/10.1023/B:VIRU.0000032790.16751.13>
- House, J.A., Wilson, T.M., Nakashly, S.E., Karim, I.A., Ismail, I., Danaf, N.E., Moussa, A.M., Ayoub, N.N., 1990. The isolation of lumpy skin disease virus and bovine herpesvirus-from cattle in Egypt. *J. Vet. Diagn. Invest.* 2, 111–115.
- Inspector General of Biosecurity, 2017. Review of Department of Agriculture and Water Resources management of biosecurity risks posed by invasive vector mosquitoes.
- Ireland, D.C., Binopal, Y.S., 1998. Improved detection of capripoxvirus in biopsy samples by PCR. *J. Virol. Methods* 74, 1–7.
- Issimov, A., Kutumbetov, L., Orynbayev, M., Khairullin, B., Myrzakhmetova, B., Sultankulova, K., White, P., 2020. Mechanical Transmission of Lumpy Skin Disease Virus by *Stomoxys* spp. (*Stomoxys calcitrans*, *Stomoxys sitiens*, *Stomoxys indica*), Diptera: Muscidae. *ANIMALS* 10. <https://doi.org/10.3390/ani10030477>
- Issimov, A., Taylor, D., Shalmenov, M., Nurgaliyev, B., Zhubantayev, I., Abekeshev, N., Kushaliyev, K., Kereyev, A., Kutumbetov, L., Zhanabayev, A., Zhakiyanova, Y., White, P., 2021. Retention of lumpy skin disease virus in *Stomoxys* spp (*Stomoxys calcitrans*, *Stomoxys sitiens*, *Stomoxys indica*) following intrathoracic inoculation, Diptera: Muscidae. *PLOS ONE* 16. <https://doi.org/10.1371/journal.pone.0238210>
- Kahana-Sutin, E., Klement, E., Lensky, I., Gottlieb, Y., 2017. High relative abundance of the stable fly *Stomoxys calcitrans* is associated with lumpy skin disease outbreaks in Israeli dairy farms. *Med. Vet. Entomol.* 31, 150–160.
- Kara, P.D., Afonso, C.L., Wallace, D.B., Kutish, G.F., Abolnik, C., Lu, Z., 2003. Comparative sequence analysis of the south African vaccine strain and two virulent field isolates of lumpy skin disease virus. *Arch Virol* 148. <https://doi.org/10.1007/s00705-003-0102-0>
- Khan, Y., Ali, A., Hussain, K., Ijaz, M., Rabbani, A., Khan, R., Abbas, S., Aziz, M., Ghaffar, A., Sajid, H., 2021. A review: Surveillance of lumpy skin disease (LSD) a growing problem in Asia. *Microb. Pathog.* 158. <https://doi.org/10.1016/j.micpath.2021.105050>
- Klausner, Z., Fattal, E., Klement, E., 2017. Using synoptic systems' typical wind trajectories for the analysis of potential atmospheric long-distance dispersal of lumpy skin disease virus. *Transbound. Emerg. Dis.* 64, 398–410.
- Kononov, A., Byadovskaya, O., Kononova, S., Yashin, R., Zinyakov, N., Mischenko, V., 2019. Detection of vaccine-like strains of lumpy skin disease virus in outbreaks in Russia in 2017. *Arch Virol* 164. <https://doi.org/10.1007/s00705-019-04229-6>
- Kononov, Prutnikov, P., Shumilova, I., Kononova, S., Nesterov, A., Byadovskaya, O., Pestova, Y., Diev, V., Sprygin, A., 2019. Determination of lumpy skin disease virus in bovine meat and offal products following experimental infection. *Transbound. Emerg. Dis.* 66, 1332–1340. <https://doi.org/10.1111/tbed.13158>
- Kraemer, M.U., Reiner, R.C., Brady, O.J., Messina, J.P., Gilbert, M., Pigott, D.M., Yi, D., Johnson, K., Earl, L., Marczak, L.B., 2019. Past and future spread of the arbovirus vectors *Aedes aegypti* and *Aedes albopictus*. *Nat. Microbiol.* 4, 854–863.
- Kumar, P., Kumari, R., Devi, S., Tripathi, M., Singh, J., Kumar, R., Kumar, M., 2021. Emergence and transboundary spread of lumpy skin disease in South Asia. *Indian J. Anim. Sci.* 91, 507–517.
- Lamien, C.E., Le Goff, C., Silber, R., Wallace, D.B., Gulyaz, V., Tuppurainen, E., Madani, H., Caufour, P., Adam, T., El Harrak, M., 2011. Use of the Capripoxvirus homologue of Vaccinia virus 30 kDa RNA polymerase subunit (RPO30) gene as a novel diagnostic and genotyping target: Development of a classical PCR method to differentiate Goat poxvirus from Sheep poxvirus. *Vet. Microbiol.* 149, 30–39.
- Lessard, B., 2013. The taxonomy, systematics and biogeography of the austral horse fly tribe scionini (Diptera: Tabanidae).
- Lu, G., Xie, J., Luo, J., Shao, R., Jia, K., Li, S., 2021. Lumpy skin disease outbreaks in China, since 3 August 2019. *Transbound. Emerg. Dis.* 68, 216–219. <https://doi.org/10.1111/tbed.13898>
- Lubinga, J., Clift, S., Tuppurainen, E., Stoltz, W., Babiuk, S., Coetzer, J., Venter, E., 2014a. Demonstration of lumpy skin disease virus infection in *Amblyomma hebraeum* and *Rhipicephalus appendiculatus* ticks using immunohistochemistry. *TICKS TICK-BORNE Dis.* 5, 113–120. <https://doi.org/10.1016/j.ttbdis.2013.09.010>

- Lubinga, J., Tuppurainen, E., Coetzer, J., Stoltz, W., Venter, E., 2014b. Transovarial passage and transmission of LSDV by *Amblyomma hebraeum*, *Rhipicephalus appendiculatus* and *Rhipicephalus decoloratus*. *Exp. Appl. Acarol.* 62, 67–75. <https://doi.org/10.1007/s10493-013-9722-6>
- Lubinga, J., Tuppurainen, E., Mahlare, R., Coetzer, J., Stoltz, W., Venter, E., 2015. Evidence of Transstadial and Mechanical Transmission of Lumpy Skin Disease Virus by *Amblyomma hebraeum* Ticks. *Transbound. Emerg. Dis.* 62, 174–182. <https://doi.org/10.1111/tbed.12102>
- Machado, G., Korennoy, F., Alvarez, J., Picasso-Risso, C., Perez, A., VanderWaal, K., 2019. Mapping changes in the spatiotemporal distribution of lumpy skin disease virus. *Transbound. Emerg. Dis.* 66, 2045–2057. <https://doi.org/10.1111/tbed.13253>
- Magori-Cohen, R., Louzoun, Y., Herziger, Y., Oron, E., Arazi, A., Tuppurainen, E., Shpigel, N., Klement, E., 2012. Mathematical modelling and evaluation of the different routes of transmission of lumpy skin disease virus. *Vet. Res.* 43. <https://doi.org/10.1186/1297-9716-43-1>
- Menasherow, S., Erster, O., Rubinstein-Giuni, M., Kovtunenکو, A., Eyngor, E., Gelman, B., 2016. A high-resolution melting (HRM) assay for the differentiation between Israeli field and Neethling vaccine lumpy skin disease viruses. *J Virol Methods* 232. <https://doi.org/10.1016/j.jviromet.2016.02.008>
- Menasherow, S., Rubinstein-Giuni, M., Kovtunenکو, A., Eyngor, Y., Fridgut, O., Rotenberg, D., 2014. Development of an assay to differentiate between virulent and vaccine strains of lumpy skin disease virus (LSDV). *J Virol Methods* 199. <https://doi.org/10.1016/j.jviromet.2013.12.013>
- Messina, J.P., Brady, O.J., Golding, N., Kraemer, M.U., Wint, G.R., Ray, S.E., Pigott, D.M., Shearer, F.M., Johnson, K., Earl, L., 2019. The current and future global distribution and population at risk of dengue. *Nat. Microbiol.* 4, 1508–1515.
- MLA, 2022a. Meat and Livestock Australia - Flies [WWW Document]. URL <https://www.mla.com.au/research-and-development/animal-health-welfare-and-biosecurity/parasites/identification/flies/#:~:text=The%20buffalo%20fly%20is%20primarily,Wales%20to%20northern%20Western%20Australia.>
- MLA, 2022b. Meat and Livestock Australia - Tick regulations [WWW Document]. URL <https://www.mla.com.au/news-and-events/industry-news/what-are-the-cattle-tick-regulations-in-your-state/>
- MLA, 2017. National Arbovirus Monitoring Program 2014-2017 Report.
- Molla, W., Frankena, K., De Jong, M.C.M., 2017. Transmission dynamics of lumpy skin disease in Ethiopia. *Epidemiol. Infect.* 145, 2856–2863.
- Mordecai, E.A., Cohen, J.M., Evans, M.V., Gudapati, P., Johnson, L.R., Lippi, C.A., Miazgowiec, K., Murdock, C.C., Rohr, J.R., Ryan, S.J., 2017. Detecting the impact of temperature on transmission of Zika, dengue, and chikungunya using mechanistic models. *PLoS Negl. Trop. Dis.* 11, e0005568.
- Morris, J.P.A., 1930. Pseudo-urticaria. *North. Rhod. Dept Anim Health Ann Rpt* 12.
- Murray, M.D., Snowdon, W.A., 1976. The role of wild animals in the spread of exotic diseases in Australia. *Aust. Vet. J.* 52, 547–554.
- Namazi, F., Tafti, A., 2021. Lumpy skin disease, an emerging transboundary viral disease: A review. *Vet. Med. Sci.* 7, 888–896. <https://doi.org/10.1002/vms3.434>
- OIE, 2022. World Animal Health Information System.
- OIE, 2010. Chapter 2.7. 14 Sheep pox and goat pox in manual of Diagnostic Tests and Vaccines for Terrestrial Animals. 1-12. and Chapter 2.4. 1 4. Lumpy Skin Dis.
- Papua New Guinea Government Official, 2021. Personal communications.
- Paslaru, A.I., Verhulst, N.O., Maurer, L.M., Brendle, A., Pauli, N., Vöglin, A., Renzullo, S., Ruedin, Y., Hoffmann, B., Torgerson, P.R., 2021. Potential mechanical transmission of Lumpy skin disease virus (LSDV) by the stable fly (*Stomoxys calcitrans*) through regurgitation and defecation. *Curr. Res. Insect Sci.* 1, 100007.
- Patching, M., 2022. Personal Communications. Boralis group.
- Reid, A.M., Murphy, B.P., Vigilante, T., Corporation, W.G.A., Bowman, D.M., 2020. Distribution and abundance of large herbivores in a northern Australian tropical savanna: A multi-scale approach. *Austral Ecol.* 45, 529–547.
- Republic of Timor-Leste, 2019. Timor-Leste Agricultural Census Final Report.

- Ritchie, S.A., Rochester, W., 2001. Wind-blown mosquitoes and introduction of Japanese encephalitis into Australia. *Emerg. Infect. Dis.* 7, 900–903.
- Roche, X., Rozstalnyy, A., TagoPacheco, D., Pittiglio, C., Kamata, A., Beltran Alcrudo, D., Bisht, K., Karki, S., Kayamori, J., Larfaoui, F., 2021. Introduction and spread of lumpy skin disease in South, East and Southeast Asia: Qualitative risk assessment and management. *Food & Agriculture Org.*
- Rocklöv, J., Dubrow, R., 2020. Climate change: an enduring challenge for vector-borne disease prevention and control. *Nat. Immunol.* 21, 479–483.
- Rouby, S., Aboulsoud, E., 2016. Evidence of intrauterine transmission of lumpy skin disease virus. *Vet. J.* 209, 193–195.
- Saegerman, C., Bertagnoli, S., Meyer, G., Ganieri, J., Caufour, P., De Clercq, K., Jacquiet, P., Hautefeuille, C., Etoire, F., Casal, J., 2019. Risk of introduction of Lumpy Skin Disease into France through imports of cattle. *Transbound. Emerg. Dis.* 66, 957–967. <https://doi.org/10.1111/tbed.13111>
- Sanz-Bernardo, B., Haga, I., Wijesiriwardana, N., Basu, S., Larner, W., Diaz, A., Langlands, Z., Denison, E., Stoner, J., White, M., Sanders, C., Hawes, P., Wilson, A., Atkinson, J., Batten, C., Alphey, L., Darpel, K., Gubbins, S., Beard, P., 2021. Quantifying and Modeling the Acquisition and Retention of Lumpy Skin Disease Virus by Hematophagus Insects Reveals Clinically but Not Subclinically Affected Cattle Are Promoters of Viral Transmission and Key Targets for Control of Disease Outbreaks. *J. Virol.* 95. <https://doi.org/10.1128/JVI.02239-20>
- Schaffner, F., Medlock, J.M., Van Bortel, W., 2013. Public health significance of invasive mosquitoes in Europe. *Clin. Microbiol. Infect.* 19, 685–692.
- Şevik, M., Doğan, M., 2017. Epidemiological and molecular studies on lumpy skin disease outbreaks in Turkey during 2014–2015. *Transbound. Emerg. Dis.* 64, 1268–1279.
- Shirakawa, H., Ishibashi, K., Ogawa, T., 1994. A comparison of the epidemiology of bovine ephemeral fever in South Korea and south-western Japan. *Aust. Vet. J.* 71, 50–52.
- Smith, P., Bourgeois Luethi, N., Huachun, L., Naing Oo, K., Phonvisay, A., Premashthira, S., Abila, R., Widders, P., Kukreja, K., Miller, C., 2015. Movement pathways and market chains of large ruminants in the Greater Mekong Sub-region.
- Sohier, C., Haegeman, A., Mostin, L., De Leeuw, I., Van Campe, W., De Vleeschauwer, A., Tuppurainen, E., van den Berg, T., De Regge, N., De Clercq, K., 2019. Experimental evidence of mechanical lumpy skin disease virus transmission by *Stomoxys calcitrans* biting flies and *Haematopota* spp. horseflies. *Sci. Rep.* 9. <https://doi.org/10.1038/s41598-019-56605-6>
- Sprygin, A., Babin, Y., Pestova, Y., Kononova, S., Wallace, D.B., Van Schalkwyk, A., Byadovskaya, O., Diev, V., Lozovoy, D., Kononov, A., 2018. Analysis and insights into recombination signals in lumpy skin disease virus recovered in the field. *PLoS One* 13, e0207480.
- Sprygin, Babin, Y., Pestova, Y., Kononova, S., Wallace, D.B., Schalkwyk, A., 2018a. Analysis and insights into recombination signals in lumpy skin disease virus recovered in the field. *PLoS One* 13. <https://doi.org/10.1371/journal.pone.0207480>
- Sprygin, Pestova, Y., Bjadovskaya, O., Prutnikov, P., Zinyakov, N., Kononova, S., 2020. Evidence of recombination of vaccine strains of lumpy skin disease virus with field strains, causing disease. *PLoS One* 15. <https://doi.org/10.1371/journal.pone.0232584>
- Sprygin, Pestova, Y., Prutnikov, P., Kononov, A., 2018b. Detection of vaccine-like lumpy skin disease virus in cattle and *Musca domestica* L. flies in an outbreak of lumpy skin disease in Russia in 2017. *Transbound. Emerg. Dis.* 65, 1137–1144. <https://doi.org/10.1111/tbed.12897>
- Sprygin, Pestova, Y., Wallace, D., Tuppurainen, E., Kononov, A., 2019. Transmission of lumpy skin disease virus: A short review. *Virus Res.* 269. <https://doi.org/10.1016/j.virusres.2019.05.015>
- Stram, Y., Kuznetzova, L., Friedgut, O., Gelman, B., Yadin, H., Rubinstein-Guini, M., 2008. The use of lumpy skin disease virus genome termini for detection and phylogenetic analysis. *J Virol Methods* 151. <https://doi.org/10.1016/j.jviromet.2008.05.003>
- Stubbs, S., Oura, C.A.L., Henstock, M., Bowden, T.R., King, D.P., Tuppurainen, E.S.M., 2012. Validation of a high-throughput real-time polymerase chain reaction assay for the detection of capripoxviral DNA. *J Virol Methods* 179. <https://doi.org/10.1016/j.jviromet.2011.11.015>
- Tay, W.T., Kerr, P.J., Jermin, L.S., 2016. Population genetic structure and potential incursion pathways of the bluetongue virus vector *Culicoides brevitarsis* (Diptera: Ceratopogonidae) in Australia. *PLoS One* 11, e0146699.

- Taylor, R., Berriman, A., Gale, P., Kelly, L., Snary, E., 2019. A generic framework for spatial quantitative risk assessments of infectious diseases: Lumpy skin disease case study. *Transbound. Emerg. Dis.* 66, 131–143. <https://doi.org/10.1111/tbed.12993>
- Telfer, D., 2018. *Advanced Stable Fly Management for Vegetable Producers*.
- Thornton, P.K., van de Steeg, J., Notenbaert, A., Herrero, M., 2009. The impacts of climate change on livestock and livestock systems in developing countries: A review of what we know and what we need to know. *Agric. Syst.* 101, 113–127.
- Tjaden, N.B., Caminade, C., Beierkuhnlein, C., Thomas, S.M., 2018. Mosquito-borne diseases: advances in modelling climate-change impacts. *Trends Parasitol.* 34, 227–245.
- Trewin, B.J., Darbro, J.M., Jansen, C.C., Schellhorn, N.A., Zalucki, M.P., Hurst, T.P., Devine, G.J., 2017. The elimination of the dengue vector, *Aedes aegypti*, from Brisbane, Australia: The role of surveillance, larval habitat removal and policy. *PLoS Negl. Trop. Dis.* 11, e0005848.
- Tulman, E.R., Afonso, C.L., Lu, Z., Zsak, L., Kutish, G.F., Rock, D.L., 2001. Genome of lumpy skin disease virus. *J Virol* 75. <https://doi.org/10.1128/JVI.75.15.7122-7130.2001>
- Tuppurainen, E., Lubinga, J., Stoltz, W., Troskie, M., Carpenter, S., Coetzer, J., Venter, E., Oura, C., 2013a. Mechanical transmission of lumpy skin disease virus by *Rhipicephalus appendiculatus* male ticks. *Epidemiol. Infect.* 141, 425–430. <https://doi.org/10.1017/S0950268812000805>
- Tuppurainen, E., Lubinga, J., Stoltz, W., Troskie, M., Carpenter, S., Coetzer, J., Venter, E., Oura, C., 2013b. Evidence of vertical transmission of lumpy skin disease virus in *Rhipicephalus decoloratus* ticks. *Ticks Tick-Borne Dis.* 4, 329–333. <https://doi.org/10.1016/j.ttbdis.2013.01.006>
- Tuppurainen, E., Oura, C., 2012. Review: Lumpy Skin Disease: An Emerging Threat to Europe, the Middle East and Asia. *Transbound. Emerg. Dis.* 59, 40–48. <https://doi.org/10.1111/j.1865-1682.2011.01242.x>
- Tuppurainen, E., Stoltz, W., Troskie, M., Wallace, D., Oura, C., Mellor, P., Coetzer, J., Venter, E., 2011. A Potential Role for Ixodid (Hard) Tick Vectors in the Transmission of Lumpy Skin Disease Virus in Cattle. *Transbound. Emerg. Dis.* 58, 93–104. <https://doi.org/10.1111/j.1865-1682.2010.01184.x>
- Tuppurainen, E., Venter, E., Shisler, J., Gari, G., Mekonnen, G., Juleff, N., Lyons, N., De Clercq, K., Upton, C., Bowden, T., Babiuk, S., Babiuk, L., 2017. Review: Capripoxvirus Diseases: Current Status and Opportunities for Control. *Transbound. Emerg. Dis.* 64, 729–745. <https://doi.org/10.1111/tbed.12444>
- University of Sydney, 2022. University of Sydney Entomology Department [WWW Document]. URL <https://medent.usyd.edu.au/fact/biting%20flies.htm>
- Waldron, S., Pham, L., Smith, D., Hieu, P.S., Xiaoxia, D., Brown, C., 2018. Macro developments in the China and Southeast Asia beef sector. *Anim. Prod. Sci.* 59, 1001–1015.
- Wang, Y., Zhao, L., Yang, J., Shi, M., Nie, F., Liu, S., Wang, Z., Huang, D., Wu, H., Li, D., Lin, H., Li, Y., 2021. Analysis of vaccine-like lumpy skin disease virus from flies near the western border of China. *Transbound. Emerg. Dis.* <https://doi.org/10.1111/tbed.14159>
- Weiss, K.E., 1968. Lumpy skin disease virus, in: *Cytomegaloviruses. Rinderpest Virus. Lumpy Skin Disease Virus*. Springer, pp. 111–131.
- Wittmann, E.J., Mellor, P.S., Baylis, M., 2001. Using climate data to map the potential distribution of *Culicoides imicola* (Diptera: Ceratopogonidae) in Europe. *Rev. Sci. Tech.-Off. Int. Epizoot.* 20, 731–740.
- Woods, J., 1988. Lumpy skin disease - a review. *Trop. Anim. Health Prod.* 20, 11–17. <https://doi.org/10.1007/BF02239636>
- Woolnough, A., Gray, G., Lowe, T., Kirkpatrick, W., Rose, K., Martin, G., 2005. Distribution and Abundance of Pest Animals in Western Australia.
- Yerulam, I., Nir, O., Braverman, Y., Davidson, M., Grinstein, H., Haymovitch, M., Zamir, O., 1995. Spread of lumpy skin disease in Israeli dairy herds. *Vet. Rec.* 137, 91–91.
- Young, E., Basson, P.A., Weiss, K.E., 1970. Experimental infection of game animals with lumpy skin disease virus (prototype strain Neethling).

# Appendix One

---

## Search terms

- a) 'Lumpy skin disease' and 'Asia' or 'Pacific'
- b) 'Lumpy skin disease' and 'transmission'
- c) 'Lumpy skin disease' and 'epidemiology'
- d) 'Lumpy skin disease' and 'vector'
- e) An identified vector (identified through review) and 'distribution in Australia' and 'distribution in Asia' and 'distribution in the Pacific'
- f) An identified vector (identified through review) and 'climate'
- g) 'Lumpy skin disease' and 'risk'

# Appendix Two

---

## Livestock movement report

This report was written by Dr Michael Patching of Boralis Group.

Lumpy skin disease (LSD) is an economically significant viral infection of cattle. It presents clinically as itchy nodules on the skin that impact production and can result in secondary infection and death in some weaker livestock or those that have not previously been exposed to the virus. Control options include limiting movement of livestock, vaccination programs and culling of infected animals. Due to the aetiology of the virus the successful control in Europe and Africa has been limited. It is important that Australia is prepared for the potential movement of the virus from South East Asia into Northern Australia.

This section of the report will consider the 2019-2021 movement of LSD in South East Asia and some factors to consider as early warning indicators for Australia as well as areas for further consideration or investigation.

### **Trading Routes in Southern Asia - Trends**

Similar to the difficulties in controlling the spread in Europe, South East Asia also comprises a group of nations sharing either land or sea borders and a complex history of war, isolation, and the legacy of Colonialism. While these nations have come together through the Association of Southeast Asian Nations (ASEAN) this body is designed to support common interests and foster relationships and trade, not to provide prescriptive and common standards like the European Union (EU). Goods are able to move freely between nations either officially or unofficially and disease responses vary in the region. Cattle, pigs, and poultry are amongst the produce that are traded within and between nations in the region largely due to livestock economic value, weak border controls, and known trading relationships.

Understanding the dynamics of these movements has been proposed as a way to provide some insights into the development of modelling tools to reduce risk factors for disease entry into Australia.

### Trends in Cattle Movement in Southern Asia

For the cattle sector movement in mainland SouthEast Asia generally flows in an eastern and northern direction. When the cattle originate in Myanmar they move direct into China or east into Thailand. Cattle in Thailand move either South into Malaysia, East through Laos or Cambodia into Vietnam and north through Laos into China.

The majority of the ongoing research into movement of livestock in the region has been focused on foot and mouth disease (FMD) transmission. Reports conducted by the OIE in 2015 (Smith, 2015) and then economic modelling by ACIAR up to 2017 (Waldron, 2018) provide an accurate estimation of general cattle movements in the region and some economic impacts on the trade.



Figure 1: General movement trends in Southern Asian mainland(Smith, 2015)

### Movement within high Risk Countries

From an Australian perspective, the movement of LSD and other transboundary diseases is mainly a concern from Indonesia, Timor Leste, and PNG. These nations will become the early warning system for vector movement into northern Australia.

There are no official movements of cattle into the islands from mainland South East Asia, although there are movements from Indonesia and East Malaysia into Malaysia. Unlike the mainland, unofficial movement of livestock from the mainland to the islands is unlikely, although not impossible.

With the price of Australian cattle likely to remain high until 2023, Indonesia continues to look to South America and Mexico to decrease reliance on Australia as a sole trading partner. Importers are actively exploring the possibility of importing cattle from Brazil however previous attempts to import cattle from Mexico have failed (Answorth, 2021). The risk of transmission from imported cattle needs to be considered.

Cattle are also transported between Indonesian islands. The Indonesian Government has supported the construction of a livestock carrier to operate between the island of Nusa Tenggara (NTT) into Jakarta ([www.pelni.co.id](http://www.pelni.co.id)). The KM Camara Nusantara is managed by PELNI and delivered a total of 7,899 head in 2019. It takes a route of Kupang - Waingapu - Tg. Priok - Cirebon - Kupang.

There are also known informal movements of cattle between Indonesia into Timor Leste (Waldron, 2015) including an estimated 5,000 annually in 2015 from TL into Indonesia.

### **LSD - Predicted Movements**

Even with known models for the movement livestock through Asia there remain challenges in accurately modelling the direction of movement of any disease through the region.

The Promed database on reports of LSD in the region (appendix A) provides a good source of information on how the disease movement was officially reported.

It is likely that the virus moved South from China into Vietnam from an outbreak in Eastern China in July 2020. This goes against the normal flow of livestock movements from Vietnam and South East Asia north into China. By the end of the year there was clinical disease in Myanmar. It is unclear if this originated from northern or eastern China, or from some other origin to the West.

Clinical disease continued down the coast of Vietnam throughout 2020 and by the middle 2021 it was being reported in Ha Tinh Province. Anecdotally there was widespread outbreak of the disease in feedlots

in northern and central Vietnam for the first half of 2021. One feedlot owner with large numbers of Australian cattle reported to be suffering significant production losses in some lines of cattle and there was communication between Vietnamese cattle farmers about purchase and use of the vaccine.

The feedlots were also known to be trying to sell infected cattle into abattoirs without reporting but in some cases the clinical signs meant that the hides had lost value.

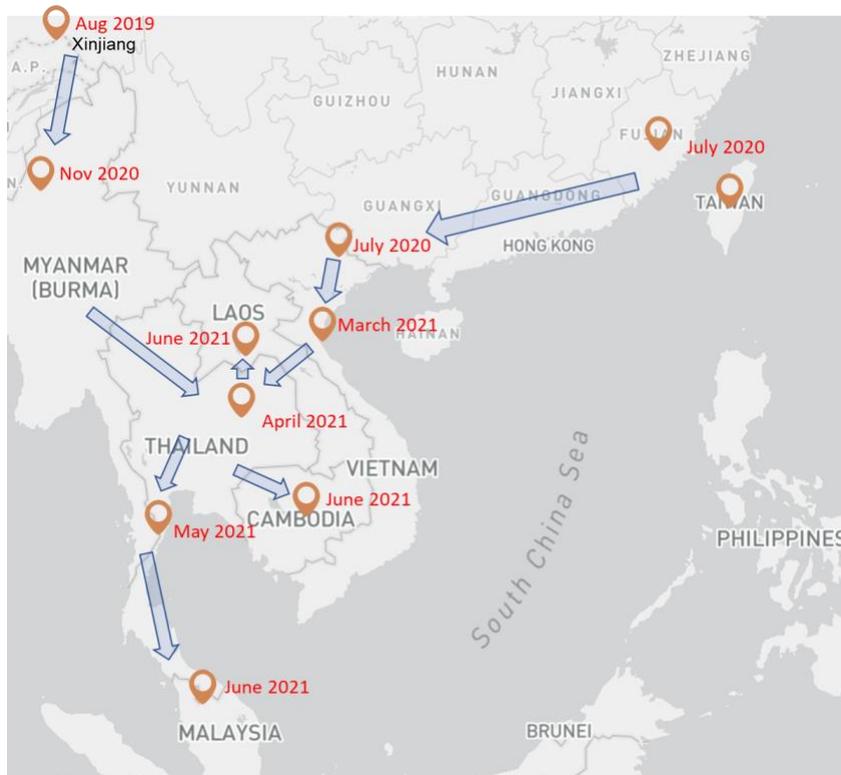
The first clinical signs of the virus were observed in eastern Thailand by April and it is likely that the virus movement was related to the trucking of cattle back across the border from Vietnam. It has been claimed by some traders that infected cattle from Vietnam were being moved into Vietnamese provinces and into Laos, Cambodia, and Laos as they were cheap due to the inability to be sold in Vietnamese abattoirs.

It is also possible that the virus infection in cattle in Thailand originated from the movement of cattle from China or Myanmar. Thailand commonly feeds cattle from Myanmar and it is a known source of FMD infection into Thailand and the region. The main cattle production region in Thailand is in the north east where the outbreak was first observed and is an important transition hub for movement throughout the region.

The movement of the virus likely followed traditional trading routes. South into Malaysia and would have circulated east back through Cambodia and Laos into Vietnam. It is also possible that there were cattle traded from Vietnam into Laos and Cambodia against historical trading routes due to a discounted price as noted above and this could have contributed to the spread.

Interestingly there have been no significant official or unofficial reports of LSD in southern Vietnam, at least with Australian cattle feedlots. The feedlots in Southern Vietnam have greater biosecurity and less movement of local cattle into them. They also had more time to vaccinate their cattle against the disease or slaughter early.

While the movement of the virus generally followed the traditional routes, there were exceptions to this which will be explored in more detail below. Irregular trading patterns makes disease monitoring a challenge.



## Factors Impacting Identification of LSD Movement

### Impact of Different Country Reporting Ability and Willingness

During the recent African Swine Fever (ASF) outbreak, there was a notable difference in reporting by neighbouring countries and sometimes provinces. ASF infected pigs were seen transported in both China and throughout Asia to ensure that farmers received some income or to avoid their farm being quarantined. Similarly during the outbreak of LSD in Vietnam there were reports that cattle were being traded into abattoirs to avoid quarantine restrictions on farm and production loss. Reportedly, some severely affected cattle were not able to enter any abattoir due to the damage to the hides and therefore were not financially worthwhile to slaughter. It is likely these cattle were traded to other properties, over further distances, or remained as high viral shedders and would have been the main contributors to the viral transmission in the region.

With LSD the anecdotal reports of infection occurred before any official reports. The below photo was sent from a Malaysian farm in May 2021 and outbreaks were not reported in Malaysia until 3rd June 2021.



Similar issues were observed in Laos where personal communications through photos were being shared from in-market traders as early as April 2021. This was done without awareness of what the disease was, how to treat it, or capability or desire to report it to officials. These behaviours result in movement of livestock out of regions before national programs can be implemented. The fact that the first incident of LSD was reported in June 2021 *after* it was observed in Thailand and Malaysia is an indication that the disease was being underreported.

Delays or absence in reporting of cases to the OIE makes disease-control modelling from an Australian perspective challenging. Establishing a network of early responding experts in the region or alternative positive reporting mechanisms to encourage farmers to increase reporting is an important goal but remains elusive in the entire region.

### Trading Systems

There are broadly two cattle trading systems that operate in the region 1) local traders that are involved in spot trading often between a farms into a regional abattoir 2) International traders (including those from Australia) that have the ability and networks to maintain relationships across borders and are often trading larger volumes.

These two trading mechanisms work independently from each other but also overlap, and so different disruptions to trade will impact these two groups differently. Generally you can consider the local traders as having greater influence within their smaller network but do not individually have the ability to have a large impact on trade flows. They can trade cattle domestically or internationally but are characterised by being more sporadic and opportunistic which makes them difficult to regulate. Local traders remain important to ensure disconnected and low volume farmers can access markets, but this also means they contribute to fragmentation in the market. They need to be a key consideration for real disease movement in the region as it is these traders that are responsible for facilitating the movement of infected animals off farms quickly and into abattoirs beyond the view or record of regulators.

International traders have a greater ability to fundamentally impact and disrupt historical cattle trading patterns due to trading higher volumes or by establishing new trading channels. They can leverage local traders to sell their cattle in times of high competition or if they are entering a new market channel, but they will eventually displace the local traders and sell direct to higher volume abattoirs or routes. This includes the establishment of official and unofficial livestock markets domestically or in border regions.

Therefore as a general rule, when there are consistent and favourable conditions for trade the international traders dominate and livestock movements are more predictable.

However when unfavourable conditions are created due to high regional or international cattle prices, exchange rate volatility, or border closures due to pandemics, the local traders will exploit this opportunity and there will be erratic movement of livestock while the system finds a new equilibrium. The length of time the disruption lasts determines if new trading routes are established.

From a disease modelling perspective consideration needs to be given to the difficulty in predicting individual trades vs modelling general trading patterns. General patterns provide models of general risk, but individual movement of livestock is the cause for disease transmission.

Further to this the OIE has done countless investigations into trade in the region and mechanisms to make the trade more official (Widders, 2020) however this remains a challenge. And value chain analysis into regional movement of animals down to individual township level in some cases. Dr Tosapol Dejyong (2020) has done work through the FAO RAP ECTAD to use value chain analysis as a means to produce better tools for epidemiologists.

### Livestock Trends are Dynamic

The most important consideration for livestock movement in the region is that it is constantly changing. Several examples below demonstrate how changes in the market will continue to contribute to livestock movements.

The 2015 OIE report (Smith, 2015) identified several locations for movement of livestock across borders and physical livestock markets. A year later in 2016, an unofficial Meat & Livestock Australia (MLA) market visit in 2016 (Patching, 2022) visited the key markets and land crossings in the report and many of them had been relocated or were no longer operational.

Since 2019, China has been increasing their controls at the Vietnam border and these controls have been tightened since the COVID-19 outbreak. China and Vietnam share joint concerns over the illegal trading of people and goods across the border illegally in both directions (Qi, 2022). It has been increasingly

difficult, but not impossible, to move cattle across the northern Vietnam border into China and this has impacted some regional cattle movements.

Investment from China in the BRI throughout Laos and Myanmar has also contributed to tightening of border controls. And the more recent Chinese signing of separate health protocols with Laos and Myanmar will have potential impacts on the movement of livestock in the entire region in the near future.

Since 2014, Australia has exported significant numbers of feeder and direct-to-slaughter weight cattle into Vietnam as well as into Thailand, Malaysia, and Cambodia at different times. The regulated and restricted trading model that is required through the Exporter Supply Chain Assurance System (ESCAS) creates unnatural trading environments in Asia. The increased regulation and oversight has positively created greater investment in feedlots and abattoirs resulting in consolidation of the industry. In Vietnam feedlot capacity has gone from non-existent in 2013 to over 90,000 head in 2022 due to the import of Australian cattle (Nason, 2021). And the abattoir sector has gone from an average of 5 head per night to approximately 20 head per night per facility in the same time.

The increasing price of cattle in Australia and the restrictive nature of ESCAS created the catalyst for the first shipment of cattle to arrive from Brazil into Vietnam (Patching, Dyer, 2021). There have been no further shipments to date, but there is ongoing discussion of shipments into Indonesia from Brazil or Mexico which can create alternative disease transmission risks for Australia.

The above examples are important when considering disease movement in the region as they demonstrate the dynamic and constantly changing nature of cattle trade in the region.

### **Considerations in Modelling - Quantifying the Trade**

There are several known mechanisms to try to quantify livestock movements as a base for modelling.

#### Official Trade

Each country maintains a record of official trade. It is widely accepted with all livestock that these numbers are a poor indicator of true volume and movement as it is not in the interests of traders to go through official channels. Customs data is unofficially available from most nations in the region at a price and with the right contacts. This could be used as a means to track monthly recorded trades and look for trends in the data.

Trade modelling has also been conducted by the University of Queensland (Dong, 2018) who highlighted the challenges of monitoring disease movements due to the high volumes of unofficial trade and other barriers that are created due to the complex trading systems discussed above.

#### Unofficial Trade

As mentioned above unofficial (unrecorded) trade remains an important consideration for modelling the movement of any livestock species.

There are several known attempts to quantify movement of all livestock in the region in relative real time. Meat & Livestock Australia (MLA) partnered with the Vietnamese data collection company Agromonitor between 2015-17 to write monthly reports on the current movement of cattle officially and unofficially across the Cambodia and Laos border into Vietnam as an indicator of regional competition (not publicly available). This project was stopped as collecting this type of data in any meaningful format was difficult and at times dangerous.

Similar border monitoring has been done as components of various ACIAR projects with similar results. Unless there is a significant investment into border controls these are not sustainable as a means of quantifying livestock movements without encountering issues with suspicious local traders.

The OIE is currently underway in a project investigating the economic trends in the region and if this can be used as an indicator of movement of livestock for FMD outbreak control (Bolortuya, 2020). From personal correspondence with the OIE this is an internal project and not for wider distribution of results and use, but joint efforts in this type of approach may have some merit.

#### Variations with livestock class and time of year

It has already been established that livestock movements will not always follow the same general trends. It is also accurate that within the same species different classes of cattle follow different general trends.

A personal experience involving a shipment of Australian cattle into Cambodia illustrates this point. Cambodians generally prefer beef from older cows that have yellow fat and so they rejected the younger white fat cattle from Australia. This follows from conversations I have had with traders that sell cull female cows west into Cambodia and the feeder bulls east into Vietnam (Patching, 2022).

### **Predictions for next 5 years**

#### Impact of China Trade in the next 5 years

A more recent MLA commissioned report has looked at the movement of cattle in the region and how the official trade of cattle through Laos and/or Myanmar created through quarantine stations with China through the Belt and Road Initiative (BRI) could feasibly work. Theoretically if the trade were successful and prices remained high in China with increasing border controls this would have a significant impact on cattle in the region (Dyer, 2021). The health protocol requirements including freedom from skin lesions such as LSD could drive an increase in the desire for farmers to improve biosecurity in the region to eradicate diseases like FMD and LSD or at least create large areas of disease free zones.

Unfortunately at this stage there does not appear to be enough of an economic pull through this channel and COVID has distracted from efforts to make this channel more effective. There remain several commercial companies that are still heavily investing in the success of this so it is important to monitor (Patching, 2022).

#### Changes in Movement of Livestock on the Islands

Timor Leste and PNG both have ambitions for increasing national herd numbers but low consumer demand or ability to pay will mean that importing livestock will not be a reality unless it is government supported.

It is unlikely that cattle movements between the islands will progress beyond the Government funded livestock carriers due to financial constraints. Even if unofficial trade occurred, the low volume of this trade channel would limit the speed of transmission between the nations. This is compared to the high volume trade that exists in mainland Asia via land.

#### Reduction in Recent Virus Detection

Globally the control of LSD has been challenging. Vaccination programs, movement controls, vector control, and early detection are all needed in a coordinated manner to have impact. Without this done in a coordinated manner it will remain difficult to eliminate the virus from the region and it is likely that there will continue to be outbreaks. Larger commercial operations are now aware of the impact of the virus and they have reported that they are now vigilant when purchasing cattle or a more routine use of vaccine in regions that still have some virus such as northern Vietnam. This will reduce but not eliminate options for trading cattle across borders and should continue to minimise its ongoing spread.

Clinically the virus has been overreported in weak, sick, or poorly fed cattle. Local cattle that are not immunocompromised and have adequate nutrition on the same or neighboring properties seem to have some level of natural immunity and have generally not shown clinical signs. It has not yet been assessed if this corresponds to a decreased viral load in the cattle population but it is logical and likely. Given the overwhelming majority of cattle in the region are *bos indicus* cattle it is also possible that this natural immunity relates to breed and therefore it is possible that the impact will not be as significant as has been

observed in Europe. P, Smith & NB, Luthi & L, Huachun & KN, Oo & S, Phonvisay & Premashtira, Sith & R, Abila & Widders, Phil & Kukreja, Karan & C, Miller. (2015). Movement pathways and market chains of large ruminants in the Greater Mekong Sub-region.

## References

1. Waldron Scott, Pham Luong, Smith Dominic, Hieu Phan Sy, Xiaoxia Dong, Brown Colin (2018) Macro developments in the China and Southeast Asia beef sector. *Animal Production Science* 59, 1001-1015
2. Dong, X., S. Waldron, and C. B. J. Zhang. "Price Transmission in Regional Beef Markets: Australia, China and Southeast Asia". *Emirates Journal of Food and Agriculture*, Vol. 30, no. 2, Jan. 2018, pp. 99-06, doi:<https://doi.org/10.9755/ejfa.2018.v30.i2.1601>. Accessed 8 Feb. 2022.
3. Answorth, R. Beef Central. Indonesians to start negotiations with Mexican live exporters as Aussie feeder cattle rise to record prices. Jan. 25 2021. <https://www.beefcentral.com/live-export/indonesians-to-start-negotiations-with-mexican-live-exporters-in-response-to-record-high-aus-feeder-cattle-prices/> Accessed 5 Feb. 2022.
4. Widders, P. Traders' Incentives Study to Facilitate Safe Livestock Trade in the Upper Mekong Sub-Region. OIE Virtual Meeting Series of 23rd SEACFMD National Coordinators. June 5, 2020. [https://rr-asia.oie.int/wp-content/uploads/2020/07/3-6-traders-incentive-study\\_phil-widders.pdf](https://rr-asia.oie.int/wp-content/uploads/2020/07/3-6-traders-incentive-study_phil-widders.pdf)
5. Dejong, T. Updates on VC and cattle. PPT presentation SEACFMD National Coordinators Virtual Meeting June 5 2020 trade [https://rr-asia.oie.int/wp-content/uploads/2020/07/3-7-20200708-fao-vc-and-cattle-trade-update\\_tosapol.pdf](https://rr-asia.oie.int/wp-content/uploads/2020/07/3-7-20200708-fao-vc-and-cattle-trade-update_tosapol.pdf)
6. Scott Waldron (UQ), Vicente de Paulo Correia (UNTL), Adelino de Rego (UNTL) and Calisto da Costa Varela (MAFF) (2015), The Timor Leste Beef Industry in "Regional Workshop on Beef markets and trade in Southeast Asian and China", Ben Tre, Vietnam, 30th November – 3rd December, 2015
7. Patching, M 2022. Personal experience
8. Patching, M. Dyer, R. The Mekong Minute: Brazilian cattle to Vietnam highlight shifting ASEAN cattle trade dynamics 23/08/2021 <https://www.beefcentral.com/live-export/the-mekong-minute-brazilian-cattle-to-vietnam-highlight-shifting-asean-cattle-trade-dynamics/>
9. Liyan Qi, Keith Zhai and Lam Le Wall Street Journal Feb 2 2022 <https://www.wsj.com/articles/china-fortifies-its-borders-with-a-southern-great-wall-citing-covid-19-11643814716>
10. Nason, J. 8/4/2021 The rise, fall and rise again of Australia's cattle trade to Vietnam. Beef Central <https://www.beefcentral.com/live-export/the-rise-fall-and-rise-again-of-australias-cattle-trade-to-vietnam/>
11. Bolortuya, P Survey tool Price monitoring in the Region OIE Virtual Meeting Series of 23rd SEACFMD National Coordinators. June 5 2020. [https://rr-asia.oie.int/wp-content/uploads/2020/07/3-12-survey-tool\\_research\\_nc-meeting\\_bp\\_finalv1.pdf](https://rr-asia.oie.int/wp-content/uploads/2020/07/3-12-survey-tool_research_nc-meeting_bp_finalv1.pdf)
12. Dyer, R 2021. Meat & Livestock Australia report. Trade options for the movement of cattle into China through Laos and Myanmar. Not published.