IMPACTS OF CLIMATE CHANGE ON TICK-BORNE DISEASES IN LIVESTOCK: CASE STUDY OF *THEILERIA* IN CATTLE IN NEW ZEALAND.

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Abstract.

Aims: This paper aimed to investigate the potential influence of climate change variables on the distribution of *Theileria orientalis* in cattle species across New Zealand from 2012 to 2024. The research paper is divided into two main components: a systematic review and a temporal-spatial analysis of *Theileria* case counts. The systematic review aims to identify and synthesise published evidence on the relationship between climate-driven factors and *Theileria orientalis* Ikeda from 2017 to 2025. The analytical component aimed to explore temporal trends of *Theileria orientalis* cases at the district level to assess spatial variation in New Zealand from 2012 to 2024.

Methods: The systematic review was conducted using two electronic databases: Scopus and PubMed—a total of 40 abstracts qualified for inclusion after the implementation of predefined scoring criteria for qualitative synthesis. The review identified key climatic factors, including rainfall, temperature, humidity and seasonal variation, as associated with tick-borne diseases, such as *Theileria orientalis*. The research findings from the systematic review were used to identify the gaps in knowledge such as — limited temporal analyses, lack of exposure intensity data, and underrepresentation of extreme weather events—justify the subsequent longitudinal analyses in this thesis.

By using laboratory reports for *Theileria* case data sourced from the Ministry for Primary Industries (MPI) broader passive surveillance system. The climatic data was sourced from the National Institute of Water and Atmospheric Research (NIWA), from which the pre-processed monthly and zonal mean formatted data was used for analysis in this study. A total of 47 climatic, demographic and spatial variables were analysed by fitting univariable negative binomial models to assess individual association with *Theileria* case counts.

Results: From the analysis, five climatic predictors are observed to be strongly associated with *Theileria orientalis* cases in cattle. The lagged months going back three months were also included to capture delayed effects. Higher wind speeds (m/s) was positively associated with 78% (RR: 1.780, 95% CI: 1.609–1.969, $p < 0.001$) in the current month and remained elevated at 1-month 51% ((RR: 1.508, 95% CI: 1.366–1.665, $p < 0.001$) and 2-month lags 35% (RR: 1.345, 95% CI: 1.214–1.490, $p < 0.001$) risk increase in *Theileria* cases. Median vapour pressure from February to April was also positively associated with 45% (RR: 1.446, 95% CI: 1.351–1.548, $p < 0.001$) risk increase of *Theileria* cases. Potential evapotranspiration showed a temporal gradient: in the current month, 15% (RR: 1.149, 95% CI: 1.103–1.197, $p < 0.001$), increased disease risk, whereas lagged values suggested a protective effect. Temperature exhibited strong lag effects a showing significant negative association with *Theileria* cases. The mean annual temperature was statistically significant with a positive association contributing to 27% (RR: 1.272, 95%CI: 1.094, 1.479, $p<0.01$) risk increase in cases. While current month rainfall was not significantly associated, rainfall at a 2-month 4% (RR: 1.042, 95% CI: 1.019–1.066, $p < 0.001$) and at a 3-month lags with 5% (RR: 1.049, 95% CI: 1.026–1.073, $p < 0.001$) were positively associated with increased risk of *Theileria* cases. Similarly, relative humidity at a 2-month lag was 3% (RR: 1.030, 95%CI: 1.021, 1.040, $p< 0.001$) and at a 3-month lag was 6% (RR: 1.055, 95% CI: 1.045–1.064, $p < 0.001$), indicating a positive associated with an increase of *Theileria* cases. Apart from climatic variables, demographic and spatial predictor variables are also observed to be statistically associated with *Theileria* cases from the analysis.

Conclusion: In conclusion, cases of *Theileria orientalis* in cattle across New Zealand from 2012 to 2024 were strongly associated with specific climate variables. These included wind speed, median vapour pressure (February–April), potential evapotranspiration, temperature, rainfall, and relative humidity. These patterns suggest that climate may play an influential role in disease dynamics. However, univariable analysis cannot account for complex interactions between variables or establish causal relationships, particularly given the ecological nature of the data. The results from this research, based on these associations, serve as a foundation for future multivariable modelling. Further analysis can be done to better understand the interplay of climatic and ecological factors influencing *Theileria orientalis* transmission in New Zealand.

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Table of Contents.

List of Tables.

List of Figures.

Chapter 1 Introduction.

Animal health systems are increasingly challenged by climate change, which poses a significant environmental challenge and a threat to animal health. The IPCC (2022) and WHO (2022) have identified climate change as one of the most critical global issues of the 21st century, with evidence of impacts observed on agricultural production, ecosystems and health systems. There are also growing concerns about the influence of climate change on animal disease patterns and trends (Gayatri et al., 2013).

Climate change is widely recognised as a key driver in the spread of tick-borne diseases, posing a significant threat to both animal and human health. It is reported that changing weather patterns create more favourable conditions for tick survival, increased incidence, and transmission rates of tick-borne diseases (Alkishe et al., 2021; Nuttall, 2022; Tsoumani et al., 2023).

The relationship between climate change and tick-borne diseases has been studied in various regions worldwide over the years. Mainly highlighting the impacts of climate change on the transmission of different tick pathogens and their vectors. Focusing on New Zealand, research has indicated that the only type of tick species present is the *Haemaphysalis longicornis*, which is responsible for transmitting *Theileria orientalis* Ikeda in bovine species (Heath, 2016).

Before 2012, cases of *Theileria orientalis* in New Zealand were sporadic. Since 2006, clinical outbreaks have increased, especially those caused by the pathogenic Ikeda (Type 2) genotype (Lakew et al., 2023). Retrospective testing of samples identified the more virulent Ikeda strain in spring 2011, with the first official diagnosis in August 2012 during an outbreak of bovine theileriosis (Lawrence et al., 2021; McFadden et al., 2011). The emergence marked a significant shift in the disease landscape, as the Ikeda strain led to widespread cases of *Theileria*-associated bovine anaemia (TABA), initially in Northland and Waikato, and subsequently spread southwards. The outbreak prompted national surveillance and biosecurity responses due to considerable impacts on cattle health and productivity (Lawrence et al., 2021; Lawrence et al., 2013; Vallee et al., 2020). Such studies have provided local context on understanding the potential of climate change on tick-borne diseases in New Zealand livestock.

Studies in New Zealand during the early phase of the *Theileria* epidemic period (August 2012 to September 2013) reported a high incidence risk, with a total of 2,847 cattle affected, with mortality rates of 17% at the herd level observed over the study period (Vink et al., 2016). Despite the significant challenges posed by theileriosis, researchers suggest that other transmission routes, such as mechanical vectors, also play a role in the spread of tick-borne disease, complicating control efforts further (Lakew et al., 2023). New Zealand's seasonal cattle farming systems may also further complicate the epidemiology of *Theileria*, as climatic variations can affect vector populations and disease transmission dynamics (Lawrence et al., 2021). Studies by Lawrence et al. (2017) describe the spatial distribution of *Haemaphysalis longicornis* in New Zealand from 2012 to 2014 using a maxent rule-based envelope model, assessing climatic variables such as—mean annual rainfall, mean annual temperature, mean annual frost, mean July maximum temperature, mean July minimum temperature and elevation thresholds—to describe suitable habitats. Research to date, including studies such as Lawrence et al. (2021), has primarily focused on the outbreak and clinical manifestation of *Theileria orientalis* Ikeda in New Zealand.

Studies have shown that higher temperatures, altered rainfall patterns, and specific humidity levels correlate with increased incidence of *Theileria* infections in cattle (Brock, 2011; Wilson et al., 2011). Tick populations are also reported to be expanding into previously unaffected areas (Lawrence et al., 2017). These changes and adaptations suggest that theileriosis, which depends on the presence of *Haemaphysalis longicornis*, is most likely to become more prevalent as climate patterns change in New Zealand (Vallee et al., 2020).

The aim of this thesis is to examine how climate change variables may have affected the spatial and temporal distribution of *Theileria orientalis* in New Zealand cattle between 2012 and 2024. The thesis is divided into two parts. The first part, Chapters 2 and 3, is a review of the literature. The first part of the review is a narrative literature review of the global distribution of tick-borne diseases. The second part of the review is a systematic review exploring the review of studies (from 2017 to early 2025), assessing the climate sensitivity of *Theileria orientalis* Ikeda. The next three chapters, Chapters 4 to 7, describe the analysis of longitudinal data exploring the relationship between climate predictors and the number of *Theileria* cases (from 2012 to 2024). To achieve this aim, the objectives of the study were to (1) investigate the associations between climate predictor variables and the case counts of *Theileria orientalis* in New Zealand from 2012 to 2024. The study tested the hypothesis that there is a significant relationship between climate variable predictors and the number of *Theileria* cases in the New Zealand cattle population from 2012 to 2024. The scope of the thesis includes analysing climatic drives, long-term temporal patterns, and *Theileria orientalis* case data in New Zealand cattle populations using existing datasets. Aspects that would require new data collection are out of scope and beyond the aims of this research, therefore, are not captured or assessed.

Chapter 2 Literature Review.

2.1 Introduction.

The increasing distribution and frequency of tick-borne diseases (TDBs) pose significant global challenges, resulting in rising infection rates across multiple host species (Botero-Cañola et al., 2024). This chapter provides a narrative literature review of tick-borne disease distribution, both globally and in New Zealand as a case study. It highlights key themes such as outbreak dynamics, vector ecology, modelling approaches, climatic drivers, and diagnostic methods. The review aims to integrate fundamental knowledge to provide a conceptual foundation for understanding climate-driven epidemiological patterns observed worldwide, with relevance to studies on *Theileria orientalis* Ikeda in New Zealand.

2.2 Tick-borne disease ecology.

TBDs are complex, arising from the dynamic interactions among pathogens, vectors and susceptible hosts within specific environmental conditions. Understanding these interactions provides a framework for interpreting patterns of disease distribution, emergence and transmission. These insights are important for predicting disease risk and implementing effective management strategies.

2.2.1 Susceptible hosts.

Susceptible hosts are vertebrates that support pathogen replication and enable transmission by tick vectors. Host susceptibility varies according to species, breed, age, immune status, and previous exposure, with certain mammals and birds being important for maintenance and amplification. Livestock, especially cattle, can significantly influence local tick populations; for example, a study in Spain reported that higher cattle density increased the risk of infection by certain TDBs like *Anaplasma phagocytophilum,* while potentially reducing the risk of others like *Borrelia burgdorferi* (Ruiz-Fons et al., 2012). Overall, livestock density highlights the complex and pathogen-specific roles that host populations play in tick-borne disease dynamics.

Although humans are not reservoir hosts, they can become susceptible to infections through tick bites. In the United States, cases of Lyme disease caused by *Borrelia burgdorferi* and babesiosis caused by *Babesia microti* have been reported to be increasing (Mahon & Rohr, 2020; Wellins, 2017). The transmission dynamics in human hosts are further complicated by the presence of multiple pathogens, which increase public health risks (Rocha et al., 2022). High density of susceptible hosts in an area provides more feeding opportunities, leading to high survival and reproduction rates of ticks. Overall, host abundance, distribution and behaviour determine contact rates with vectors and the efficiency of pathogen spread. Hosts play a significant role in shaping the epidemiology of tick-borne diseases.

Apart from human and domesticated livestock hosts, the presence of various wildlife species can also create complex ecological interactions that influence tick populations. A study in Sweden reported that the presence of certain deer species was associated with increased tick density and higher incidence of TBDs, such as tick-borne encephalitis (Jaenson et al., 2018). Several species of rodents, deer and birds also serve as primary reservoirs for pathogens such as *Borrelia* and *Babesia*, facilitating the transmission to ticks and, subsequently, to humans (Brown et al., 2005; Mahon & Rohr, 2020; Rocha et al., 2022). These findings suggest that wildlife species may function as alternative or reservoir hosts, influencing pathogen persistence and spillover risk. Therefore, understanding the type of hosts present within a geographical region is crucial for determining susceptibility and infection risk of TBDs, because not all hosts play the same role in the disease cycle.

2.2.2 Tick vectors.

Ticks are among the most important vectors of infectious diseases globally, directly transmitting pathogens to humans, livestock, and wildlife (Botero-Cañola et al., 2024). TBDs occur mainly in areas where competent tick vectors, susceptible hosts and suitable environmental conditions coexist (Brown et al., 2005; Tonk-Rügen et al., 2025). Different tick species act as vectors, and their interaction with the host is shaped by ecological and biological factors. Vector ecology—including species distribution, host preference, and life cycle—is a key determinant of disease risk, as it directly influences host contact rates and pathogen transmission.

Ticks from the families Ixodidae (hard ticks) and Argasidae (soft ticks) are reported as the primary vectors for pathogens affecting humans and animals (Estrada-Peña, 2015). Globally, approximately 867 tick species have been identified, of which 35 Ixodid and 10 Argasid species commonly bite humans (Brown et al., 2005). Notable TBDs transmitted by these vectors include Lyme disease, Rocky Mountain spotted fever, and tick-borne encephalitis (Goddard, 2008). Understanding the distribution, ecology, and host interactions of tick vectors is therefore critical for assessing disease risk and guiding the development of effective surveillance and control strategies.

2.2.3 Transmission dynamics across tick life cycle stages.

TBDs are transmitted to hosts during blood feeding by larval, nymphal, or adult ticks. While ticks progress through multiple developmental stages, transmission of pathogens occurs exclusively during feeding on a host. Ticks progress through four stages—egg, larva, nymph, and adult. Only larva, nymph, and adult stages take blood meals from the host and can transmit pathogens, whereas eggs do not feed and therefore do not contribute to pathogen transmission (Wu & Zhang, 2020). Because ticks can retain pathogens across life stages and sometimes pass them to offspring, they are highly effective vectors linking wildlife reservoirs to incidental hosts, including humans. (Eisen et al., 2018; Sonenshine, 2005).

During the larval stages, ticks typically feed on small mammals, reptiles and birds, which serve as competent reservoirs for pathogens (LoGiudice et al., 2003). Larvae are generally uninfected at emergence and rarely transmit pathogens directly to humans, as transovarial transmission is uncommon or absent for most medically important tick-borne pathogens (Karbowiak et al., 2016). Therefore, larval feeding on reservoir hosts is a critical step for pathogen acquisition, with infections maintained through transstadial transmission, making nymphs and adults the primary stages responsible for transmitting pathogens to humans and other vertebrate hosts.

The nymphal stage is epidemiologically the most important for human infection. Nymphs often carry infections because they feed early on animals that carry the pathogens, and their small size makes them difficult to detect (Eisen et al., 2018). Their extended attachment allows pathogens such as *Borrelia burgdorferi*, which require prolonged feeding periods to be efficiently transmitted (Eisen et al., 2018). In the United States, nymphs are responsible for most human cases of Lyme disease, anaplasmosis, and babesiosis (Karbowiak & Biernat, 2016). They can also transmit pathogens such as *Anaplasma phagocytophilum* and tick-borne encephalitis virus (TBEV) during the peak spring and early summer activity, coinciding with periods of high human outdoor exposure (Karbowiak & Biernat, 2016). Collectively, due to their high infection prevalence, small size, and prolonged feeding behaviour, nymphs represent the primary stage responsible for transmitting tick-borne pathogens, highlighting their significant role in the epidemiology of TBDs.

Adult ticks are primarily responsible for transmitting infections to larger mammals, and can also pass pathogens to the next generation through transovarial transmission (Karbowiak & Beata., 2016). Pathogens are transmitted systematically during feeding, as infected ticks transfer pathogens directly to hosts (Karbowiak et al., 2018). Infected ticks can transmit pathogens to uninfected ticks through co-feeding, where pathogens replicate locally at the bite site without causing systemic infection (Rocha et al., 2022; Zhang & Wu, 2024). Understanding these stage-specific roles is essential for designing effective tick control strategies and reducing human and livestock exposure.

2.2.4 Pathogen types and expanding disease risks.

TBDs are caused by a diverse range of pathogens including, viruses, bacteria, and protozoa, with incidence increasing due to changing environmental conditions (Rochlin & Toledo, 2020). Among viral TBDs, several are of global importance due to increasing prevalence and geographic expansion, posing a significant risk to human health. For example, tick-borne encephalitis virus (TBEV) primarily affects human populations in Europe and Asia (Damian, 2024). Crimean-Congo haemorrhagic fever virus (CCHFV), which is associated with high mortality rates in humans, is endemic in the Balkans, Caucasus, and southern Europe and gradually spreading to new areas (Damian, 2024; Portillo et al., 2021). In North America, Powassan virus (POWV) incidence is increasing and can cause severe neurological complications in humans (Damian, 2024). Collectively, these patterns suggest that tick-borne viral diseases are an expanding global public health concern, underscoring the need for improved surveillance and proactive control measures.

Bacterial TBDs such as Lyme disease, anaplasmosis, and rickettsiosis continue to spread, particularly in temperate regions (Shah et al., 2023). The emergence of these bacterial TBDs depends on the geological expansion of tick vectors, notably *Ixodes scapularis* and *Amblyomma americanum* (Shah et al., 2023). Lyme disease, caused by *Borrelia* species, is prevalent in the Northern Hemisphere (Rochlin & Toledo, 2020). Anaplasmosis and ehrlichiosis are caused by *Anaplasma* and *Ehrlichia* species, respectively. They often show similar symptoms, which can make diagnosis difficult in humans and animals (Andonova et al., 2024). Despite increasing awareness, challenges remain in accurate diagnosis, treatment and management (Contreras-Ferro et al., 2024). Therefore, this highlights the need for robust, stage-specific surveillance and diagnostic techniques, particularly because many tick-borne diseases present with overlapping symptoms.

Protozoan TDBs primarily affect livestock, posing threats to livestock health, productivity and food security worldwide. One of the most important protozoan TBDs is babesiosis, which is caused by *Babesia* species, with increasing prevalence reported in both cattle and humans (Andonova et al., 2024; Bouchard et al., 2019; Nuttall, 2022). Another pathogen of economic importance is *Theileria* species, which are also transmitted through tick bites, similarly impacting livestock health and productivity across regions (Bishop et al., 2004). Because *Babesia* and *Theileria* infections have major health and economic impacts, it is important to study the global factors that influence tick populations and the spread of these pathogens, which determine where the diseases are most likely to occur and persist.

Most studies on tick-borne pathogens focus on prevalence and geographical distribution, but few examine how transmission efficiency changes under different environmental conditions. Transmission efficiency can vary between tick species, life stages, host populations, and pathogen strains. It is also strongly influenced by factors such as temperature, humidity, and habitat type. Measuring these interactions is difficult because it requires tracking how ticks acquire pathogens, how pathogens replicate in ticks, and how they are transmitted to hosts under real environmental conditions. As a result, there is a major gap in understanding how climate and ecology affect tick-borne diseases. This limits our ability to predict how these infections will respond to current and future environmental changes.

2.3 Global drivers of tick-borne diseases and distribution.

2.3.1 Environmental drivers of tick-borne diseases.

The increasing incidence and prevalence of both ticks and their associated pathogens are expanding geographically. Transmission risk depends on the geographic presence of competent tick vectors, pathogens, and susceptible hosts, influenced by environmentally driven changes in tick ecology (Brown et al., 2005). Among these factors, urbanisation can create new habitats for tick populations, thereby increasing human exposure to tick-borne pathogens (Rizzoli et al., 2014). In addition, non-climatic drives, such as land management, habitat fragmentation, and landscape connectivity, contribute in shaping tick movement, host-tick encounter rates, and local establishment patterns (Betancur et al., 2015; Medlock et al., 2013). These links reflect broader challenges in distinguishing climate-driven changes from concurrent shifts in ecology and land-use systems. Variability across studies highlights the need for integrated frameworks that assess environmental drivers across both the tick life cycle and the pathogen transmission, rather than treating them separately. While non-climatic environmental factors play a role in shaping tick ecology and disease risk, climatic changes add an additional layer of influence, driving shifts in tick distributions, seasonal activity, and pathogen transmission dynamics.

Climate change is contributing to the expansion of tick ranges, potentially increasing the size of endemic zones and altering disease distribution patterns (Medlock et al., 2013; Tonk-Rügen et al., 2025; Tsoumani et al., 2023). Change in temperature and humidity influences tick survival, development rates, and reproductive success, thereby facilitating the spread of TBDs into previously unaffected regions (Prakasan et al., 2020; Tonk-Rügen et al., 2025). For example, a study by Tsoumani et al. (2023) reported outbreaks of Lyme disease and tick-borne encephalitis in Europe, caused by warmer winters extending tick activity periods and increased transmission rates. However, research from non-endemic regions suggests that initial disease emergence often results from interactions among rising temperatures, humidity changes, and altered host distributions rather than climate alone (Ali et al., 2024). The interactions between climate factors, host availability, and ecology remain underexplored, particularly in newly affected regions. Therefore, more studies are needed to examine how these factors jointly influence tick-borne disease emergence and transmission dynamics.

Identifying the biological and ecological drivers of tick-borne diseases is essential for designing effective prevention and control strategies. Understanding interactions among ticks, pathogens and hosts enables science-based interventions to reduce infection and transmission risk (Botero-Cañola et al., 2024). However, technical measures alone are insufficient in controlling tick disease incidences. Sustainable tick control also depends on community awareness, government policies, biosecurity measures and multisectoral collaborations (Betancur et al., 2015). Integrating these human dimensions with ecological knowledge offers a more realistic pathway for reducing the long-term burden of tick-borne diseases. The literature shows substantial variation in how strongly different studies emphasise climatic, ecological, or anthropogenic drives, indicating ongoing debate regarding the dominant mechanisms shaping patterns of emergence.

2.3.2 Climatic drives of tick-borne diseases.

Climate change affects tick development, survival, and activity periods, often prolonging the season during which ticks are active. The length of tick active seasons is reported to be increasing, leading to extended periods in which humans and animals are susceptible to the risk of infection (Gray et al., 2009; Nuttall, 2021). The effects of climate change also include prompting the emergence of heat-tolerant and exotic tick species into previously unaffected regions, diversifying the range of tick-borne pathogens (Nuttall, 2021; Voyiatzaki et al., 2022).

The relationship between climate change and the expanding risk of tick-borne diseases has become more evident in recent years. Several studies have reported the increase in incidence of TBDs, driven by climatic, environmental and social factors (Deshpande et al., 2023; Lee & Chung, 2023; Voyiatzaki. et al., 2022). Abiotic factors, including temperature, relative humidity, and rainfall, play a crucial role in the development and spread of TBDs by shaping vector survival and activity patterns. In North America, higher temperature have been reported to elevate the risk of TBDs transmission, as warmer conditions promote higher tick survival, fast development rates and contribute to longer periods of host-seeking activity (Jensen, 2023; Ogden et al., 2020). Globally, these effects are expected to intensify under ongoing climate change, especially in tropical and subtropical regions, potentially increasing the size of endemic zones and altering disease distribution patterns.

In Michigan, Jensen (2023) reported that Lyme disease cases increased with higher average temperatures and more rainfall, especially during warmer months above 15–20°C, and were further influenced by extreme weather events. Similarly, in Europe, warmer winters extended the active season of ticks, increasing contact between tick and hosts and increasing opportunities for pathogen transmission (Tsoumani et al., 2023). In California, the abundance of juvenile ticks was influenced by the seasonal temperature changes, which may extend the periods of pathogen transmission (Sambado et al., 2024). Other studies have shown higher levels of temperature and vapour pressure as key factors of tick ecology and creating favourable conditions for disease spread across various regions (Dumic & Severnini, 2018; Tsoumani et al., 2023). Together, these findings show that temperature drives tick activity and tick-borne disease risk across different regions. While warmer temperatures and winters generally increase tick activity and disease incidence, the strength and direction of these relationships are not uniform. These relationships across regions highlight a critical gap and indicate a need for more context-specific studies.

Rainfall exerts a dual influence on tick distributions and pathogen transmission, with effects varying across vector species and ecological context. While higher rainfall is often associated with a higher incidence of TBDs, the relationship is not uniform. For example, Jensen (2023) reported a correlation between rainfall and disease incidence in regions with heterogeneous population densities, suggesting that human exposure patterns may mediate climate effects. In the United States, Dumic and Severnini (2018) found that the incidence of Lyme disease increased at temperatures between 7-15 ˚C and at annual rainfall levels below 70 cm and above

270 cm, indicating that both low and very high rainfall can influence tick ecology. However, the evidence remains somewhat inconsistent, while rainfall is clearly an important driver, its ecological and epidemiological effects require more nuanced, context-specific interpretation.

Environmental water availability can have contrasting effects on TBDs dynamics. Moderate moisture in the habitats, including soil and vegetation humidity, supports tick survival and reproduction, whereas excessive rainfall may disrupt microhabitats or reduce the viability of certain hemoparasites (Abdullah et al., 2019). Abdullah et al. (2019) illustrate this complexity in Iraq, where Spearman-rank analysis showed that temperature was strongly positively correlated with *Theileria* species. infection in cattle ($R^2 = 0.90$, p=0.001), while rainfall exhibited a strong negative correlation $R^2 = -83$, p=0.001). These findings suggest that higher rainfall was linked to lower disease incidence in this context. Overall, the relationship between rainfall, tick ecology, and pathogen transmission appears to be context-dependent rather than universally linear. They also highlight the importance of considering both climatic and ecological factors, as pathogen responses can vary between regions, hosts, and tick species. Simple assumptions that more rainfall always increases disease risk may be misleading.

Beyond immediate effects, rainfall can influence tick-borne disease dynamics through lagged impacts. For instance, Giesen et al. (2024) reported that an additional inch of rainfall increases the odds of Lyme disease seropositivity in the following season by approximately 2% (Giesen et al., 2024). Similarly, Espich et al. (2020) observed that increases in rainfall during one season often precede rises in tick-borne disease cases in the subsequent seasons, reflecting the time required for tick development (Espich et al., 2020). These findings highlight the importance of considering the magnitude and timing of precipitation when assessing its effects on tick biology and disease risk. Overall, these studies suggest that rainfall influences vector and pathogen ecology in multifaceted way.

Relative humidity, together with other climatic factors, also contributes to tick ecology. Studies have shown that tick species such as *Ixodes scapularis* and *Ixodes ricinus,* which are the primary vectors for Lyme disease and tick-borne encephalitis, respectively, are influenced by higher relative humidity in the air and greater moisture availability in the microhabitats, such as lead and soil (Espich et al., 2020; Petersen et al., 2022; Wu et al., 2025). Prolonged periods of low humidity or drought can increase tick mortality, whereas favourable moist conditions support larger tick populations and increase the risk of disease transmission (Petersen et al., 2022; Tytar et al., 2024). While these studies provide valuable insights into the role of humidity to support tick abundance and transmission, the magnitude of these effects likely depends on local environment conditions, host availability and species-specific ecological factors.

Long-term warming trends and extreme weather events are increasingly linked to changes in tick behaviour, prevalence and disease incidence (Bouchard et al., 2019; Lee & Chung, 2023). For instance, warmer winters are reported to prolong the active season of ticks, increasing the risk of exposure for both humans and animals (Tsoumani et al., 2023). In contrast, extreme events such as flooding or heatwaves can disrupt the existing tick habitats, often reducing tick survival and transmission potential (Ogden et al., 2021). The impacts of such events vary depending on local environmental conditions and the availability of refuges that protect ticks from extreme stress (Ogden et al., 2021). Projections indicate that these climatic shifts have facilitated ticks' expansion towards higher latitudes and elevation, thereby increasing the probability of TBDs in many regions that were previously unaffected (Ogden et al., 2021; Pavia et al., 2025). However, the magnitude of this risk is linked to non-climatic factors such as human behaviour, land use and socioeconomic conditions, which either contribute or mitigate disease emergence (Randolph, 2010). Sudden spikes in tick-borne disease incidence often result from the interaction of extreme weather with ecological or social factors (Estrada-Peña et al., 2012). These outcomes highlight the gaps in current knowledge as most studies could be observational or mode-based, and the experimental evidence on the effects of extreme weather on ticks' survival and behaviour remain limited.

2.3.3 Regional variation and phenological patterns.

Spatial and seasonal variation are also associated with tick activity and tick-borne disease risk. Geographic differences in tick species behaviour and disease prevalence further complicate the dynamics and occurrences of tick-borne diseases. A study by Beckley et al. (2016) in West Africa reported that the prevalence of *Theileria* species was significantly higher in regions with specific vegetation, such as coastal savannahs, and influenced by rainfall patterns in the region. Comparable studies in Algeria and Iraq also indicate that the prevalence of *Theileria* species varies between bioclimatic areas, with humid and semi-arid areas showing differences in summer incidence (Abdullah & Ali, 2021; Ziam et al., 2020). Environmental changes such as habitat fragmentation that increase forest edges, combined with warmer temperatures, have been associated with elevated exposure risk, although the magnitude of this effect vary depending on local ecology (Iijima et al., 2025). While these studies consistently link environmental conditions to tick prevalence, the observational nature of much of this work and variations in sampling methods suggest caution in directly comparing absolute prevalence values across regions.

Seasonal variation further contributes to tick populations and disease transmission. The period of tick activity is linked to the seasonal patterns, directly influencing the risk for disease occurrence (Goren et al., 2023). Studies by Eisen (2025) in the United States reported that patterns of *Ixodes scapularis* and *Ixodes pacificus* species show distinct seasonal patterns of tick activity, with nymphs and adults peaking at different times of the year depending on regional climate (Eisen, 2025). Notably, adult tick activity in colder climates can be bimodal, peaking in both autumn and spring, whereas in warmer regions, activity may be more continuous or shifted earlier in the year (Eisen, 2025). Similarly, Monoldorova et al. (2024) in South Korea reported that the adult stage of *Haemaphysalis longicornis* was higher in late spring and summer, while larvae peaked in late summer or early autumn. Across multiple regions, seasonal peaks in Lyme disease in Northern Europe and the United States are occurring earlier than in previous decades, likely due to climate change (Goren et al., 2023; McClung et al., 2023).

Several tick-borne pathogens of importance that are also influenced by seasonality are *Borrelia, Anaplasma, Bebesia* and *Theileria*, which are exhibiting seasonal variation, typically peaking in late spring or summer, coinciding with periods of high tick activity (Hancock et al., 2011). Fluctuations in seasonal temperature are associated with the emergence and early onset of tick activity, leading to an increased risk of disease transmission (Bournez et al., 2020). The interaction between climate, tick phenology, host dynamics and human behaviour complicates the efforts to forecast and predict disease risk and requires further studies (Nah & Wu, 2021; Sambado et al., 2024). These limitations hinder the ability to make robust predictions about future trends for monitoring and preparedness efforts in the region.

Collectively, these studies demonstrate that both spatial and seasonal variation are critical determinants of tick-borne disease risk. However, the diversity of geographic contexts, species-specific life cycles, and methodological differences across studies underscores the need for high-quality, region-specific data to reliably interpret trends and forecast disease risk. Observed shifts, such as earlier seasonal peaks, indicate climate mediated effects, but distinguishing these from other environmental factors could remain a challenge.

2.3.4 Global distribution of *Theileria* species.

The distribution and spread of *Theileria* species, which cause theileriosis, are influenced by host and vector availability, as well as ecological and management factors. These important hemoprotozoan parasites affect a wide range of livestock species, leading to significant economic loss and animal health issues (Bishop et al., 2004). In China and Iran, *Hyalomma* and *Rhipicephalus* species are identified as primary vectors for *Theileria* transmission (Sun et al., 2019; Zarei et al., 2019). In Pakistan, phylogenetic analyses of *Theileria ovis* and *Theileria lestoquardi* showed clustering with sequences from other countries (Raza et al., 2024).

Beyond vector and host distributions, climatic conditions that also influence and shape the epidemiology of specific *Theileria* species have been studied globally. Studies in India show that increases in minimum temperature (r=0.460, p=0.005) and mean daily temperatures (r=0.400, p=0.016) are significantly associated with higher incidence of *Theileria orientalis* (Deepa et al., 2024). These findings suggest that *Theileria orientalis* incidence is more strongly influenced by sustained baseline warming than by extreme daytime heat, highlighting the importance of persistent thermal suitability for tick survival and pathogen transmission. Similarly, the prevalence of *Theileria orientalis* in South Korea was significantly higher during the warm period (43.0%) compared with the cold period (13.5%) (Espiritu et al., 2024). Additional studies from South Korea indicate that increasing temperatures are associated with more tick-borne infections and the appearance of new disease hotspots (Lee & Chung, 2023). These findings suggest that tick development and survival rates are higher in warmer environments compared to colder environments.

High temperature has shown to enhance pathogen transmission dynamics. For instance, virus replication within ticks increases substantially at higher temperature, raising the probability of infection per tick bite during hot periods (Daniel et al., 2018; Ogden et al., 2020). Host-related factors also play a crucial role. In Pakistan, *Theileria Ovis* and *Theileria lestoquardi* were detected in 14% of sampled sheep and goats, with higher prevalence in sheet (19%) than goats (8%), and younger sheep exhibited a higher susceptibility (Riaz et al., 2024). *Theileria parva*, which causes East Coast fever (ECF), is a significant protozoan pathogen of cattle. It is primarily transmitted by *Rhipicephalus appendiculatus* and occurs across Europe, central, and southern Africa (Ndungu et al., 2021). The genetic diversity of *Theileria parva* is notably higher in African buffalo species compared to cattle, complicating control measures and emphasising the role of wildlife reservoirs in maintaining infection cycles (Allan et al., 2021).

East Coast fever can lead to mortality exceeding 80% in susceptible cattle populations, affecting 11 countries across eastern, southern, and central Africa (Toye & Ballantyne, 2015). These findings highlight the importance of host susceptibility, wildlife reservoirs and movement management in influencing disease spread.

Epidemiological studies demonstrate diagnostic challenges and variable infection rates across hosts for *Theileria*. In Pakistan, *Theileria equi* was detected in 10% of working horses by microscopy and 21% by competitive ELISA, while *Theileria annulata* occurred in roughly 13% of cattle by microscopy and 24% by PCR (Raza et al., 2024; Shah et al., 2022). These findings underscore the impact of diagnostic methods on prevalence estimates for *Theileria* infections, with PCR and ELISA approaches detecting higher infection rates than microscopy. The variation highlights that many infections may be subclinical or missed by traditional microscopy techniques, suggesting the need for sensitive diagnostic tools to accurately analyse disease burden and inform control strategies in animal species.

Cross-species transmission and geographic spread are further influenced by climate, host movement, and vector distribution. In Egypt, *Theileria equi* was detected in 26% of the canine population using PCR analysis, with seasonal and breed variations (Hegab et al., 2023). In New Zealand, *Theileria orientalis* Ikeda was detected in 10% of red deer, suggesting potential wildlife reservoirs, while no infections were observed in horses or working farm dogs (Lawrence et al., 2024). These findings point out the widespread geographic distribution of *Theileria* spp and suggest a strong potential for cross-species transmission of tick-borne pathogens, particularly in regions with high livestock movement and trade. While theileriosis is a major concern for livestock health, some species may cause subclinical infections, which complicates the understanding of their overall impact on animal health and productivity (Zarei et al., 2019).

Despite growing evidence that *Theileria* transmission is shaped by interactions among climate, vector, ecology, host susceptibility, and pathogen diversity, existing studies are geographically concentrated and system specific. Research in Asia, the Middle East, Africa, and Europe demonstrates that climatic drives such as high temperatures, vector availability, host composition, and wildlife reservoirs influence *Theileria* dynamics (Bishop et al., 2004; Deepa et al., 2024; Espiritu et al., 2024; Zarei et al., 2019). However, the strength and direction of these relations vary across regions, tick species, and *Theileria* taxa, limiting the transferability of findings to other ecological contexts.

In particular, quantitative assessments linking sustained warming to *Theileria orientalis* transmission remain scarce outside a small number of regional studies, and host-related factors are often examined independently of climatic drives (Riaz et al., 2024). Furthermore, while phylogenetic analyses reveal regional connectivity and genetic diversity among *Theileria* species, the implications of this diversity for climate-driven transmission dynamics remain poorly resolved (Allan et al., 2021; Riaz et al., 2024). These gaps identified highlight the need for more recent region specific investigations, such as those in New Zealand. These regional differences emphasise that the distribution and spread of theileriosis result from the combined influence of ecological, climatic, host-related, and management factors. However, it remains unclear why certain tick species are restricted to specific regions and what environmental or climatic conditions could allow their establishment in new areas. Given ongoing climate change, shifts in temperature and humidity may create suitable conditions for non-native tick species to survive and transmit *Theileria*, raising the possibility that species currently restricted to certain regions could establish in New Zealand in the future due to climate change. Investigating these dynamics is therefore crucial to understanding the emergence of theileriosis and predicting future risks of tick-borne infections under changing environmental conditions.

2.4 *Theileria orientalis* and *Haemaphysalis longicornis* in New Zealand.

Studies conducted in New Zealand highlight the considerable consequences of *Theileria orientalis* for cattle health. *Haemaphysalis longicornis* is the only tick vector, predominantly affecting cattle and is associated with the development of cattle anaemia with occasional mortality (Lakew et al., 2023; Lawrence et al., 2021; Lawrence et al., 2013). Since the identification of *Theileria orientalis* Ikeda in 2012, it has become an endemic concern in New Zealand (Lawrence et al., 2021). In contrast to many other regions, New Zealand lacks most pathogenic tick-borne hemoparasites of cattle, which reduces the likelihood of co-infections (Lawrence et al., 2021). The absence of other haemoparasites highlights the susceptibility of cattle to *Theileria orientalis* and demonstrates the successful establishment and adaptability of *Haemaphysalis longicornis* under New Zealand's environmental conditions. In New Zealand, seasonal patterns also influence the epidemiological trends of *Theileria* in the beef and dairy sectors, resulting in unique outbreak patterns when compared to those observed in other countries (Lawrence et al., 2021). Climate change may facilitate the geographic spread of *Haemaphysalis longicornis*, thereby expanding the areas at risk for *Theileria orientalis* infections (Okely et al., 2025)

However, the adaptability of *Haemaphysalis longicornis*, particularly at the larval, nymphal, and adult stages, allows the tick to persist across diverse environments despite climatic variability, complicating disease prediction and control efforts; egg stages remain more sensitive to temperature and humidity extremes (Marendy et al., 2020). These findings underscore the importance of considering abiotic factors, vector ecology, and environmental adaptability when assessing the spread and future risk of tick-borne disease.

The incidence of *Theileria orientalis* is significantly higher in regions such as Northland and Waikato, where the environmental conditions favor the survival and reproduction of its vector, the tick *Haemaphysalis longicornis* (McFadden et al., 2016). Early case counts from Northland to the Waikato region were initially low from December 2012 to March 2013 (Lawrence, 2020). Seasonal variation further shapes the epidemiological trends of *Theileria* in the beef and dairy sectors, contributing to outbreak patterns distinct from those observed internationally

(Lawrence et al., 2021). These regional and seasonal patterns underscore the importance of environmental conditions in determining tick distribution and disease risk.

Environmental conditions strongly influence tick distribution. Climate change may facilitate the geographic spread of *Haemaphysalis longicornis*, thereby expanding the areas at risk for *Theileria orientalis* infections (Okely et al., 2025). *Haemaphysalis longicornis* can survive in temperatures between approximately 12°C and nearly 40°C and favours warm, humid environments that are projected to expand with climate change (Heath, 2016). Warmer and wetter conditions are expected to increase tick numbers and transmission potential, particularly for the pathogenic *Theileria orientalis* Ikeda genotype (Lakew et al., 2023; McFadden et al., 2016). However, some studies predict a decline in tick populations under drier, warmer scenarios, suggesting uncertainty regarding the net effect of climate change on future disease risk (Heath, 2021; Marendy et al., 2020). Studies in New Zealand by Heath (2021) mention that increased humidity enhances tick survival and reproduction, leading to higher tick populations and high transmission rates of *Theileria orientalis.* These differing projections highlight variability in model assumptions and underscore the need for more robust datasets to improve predictive accuracy.

Modern predictive modelling techniques have become valuable tools for monitoring and forecasting the impacts of climate change on tick-borne diseases. Such approaches integrate climatic, ecological and social factors to identify spatial distribution and future risk hotspots (Deshpande et al., 2023). Lawrence et al. (2017) applied a Maxent modelling to assess the environmental stability of *Haemaphysalis longicornis* using long-term averages climate data (reflecting current climatic conditions at the time of the study), predicting that 89% of New Zealand cattle farms provide suitable environments for tick survival and *Theileria* transmission. The study further suggests that areas currently suitable may experience ongoing cases, whereas regions with low transmission potential may experience sporadic and severe outbreaks. These observations and predictions are consistent with reported regional patterns.

Despite extensive research on *Theileria orientalis* and its vector, *Haemaphysalis longicorns* in New Zealand, several knowledge gaps remain. The net impact of climate change on tick population and disease risk is uncertain, with studies predicting both increases and declines under different environmental scenarios (Heath, 2021; Marendy et al., 2020). While regional and seasonal incidence patterns are documented, the specific environmental and ecological drivers of outbreak, particularly in low-transmission areas, are not fully understood (Lawrence et al., 2021; Lawrence et al., 2017; McFadden et al., 2016). Additionally, predictive models such as Maxent have assessed environmental suitability under current conditions but do not directly link variables to case counts over time. The current thesis addresses these gaps by investigating the associations between climate variables and *Theileria orientalis* case counts in New Zealand cattle from 2012 to 2024. By analysing longitudinal data, the study examines how specific climatic drivers shape regional and seasonal disease patterns, providing empirical evidence to clarify the climate–disease relationship.

2.5 Conclusion.

The literature review demonstrates the complex and multifaceted interactions between climate, environment and tick-host-pathogen dynamics. The review highlights that climate variability, habitat changes, and seasonal patterns influence tick distribution, abundance, and disease transmission potential globally. Although previous studies have examined the distribution, vectors, and general climate associations of *Theileria orientalis* and its vectors, the evidence remains limited. Quantitative relationships between specific climatic variables—such as temperature thresholds, rainfall intensity, and seasonal patterns—and disease incidence are not well characterised. Furthermore, while most studies examine global trends or restricted regional observations, there is limited understanding of how additional climatic variables influence disease transmission in New Zealand during time periods.

These gaps highlight the need for a systematic assessment of climatic susceptibility, particularly to evaluate the intensity, duration, and temporal patterns of climate exposure in relation to disease outcomes. To address these gaps and systematically evaluate the role of climate variables in shaping the distribution and epidemiology of *Theileria orientalis* in New Zealand cattle. The next chapter presents a structured systematic review of the existing evidence on the climatic susceptibility of *Theileria orientalis* Ikeda genotype and its vector, *Haemaphysalis longicornis*. This review aims to map the current evidence, identify consistent patterns, and highlight areas requiring further research, thereby providing a robust foundation for the subsequent longitudinal analysis of climate predictors and *Theileria orientalis* case counts in New Zealand cattle.

Chapter 3

Systematic Review of climatic susceptibility of *Theileria orientalis* Ikeda in cattle.

3.1 Objectives.

A systematic review was conducted to explore how climate change may influence the distribution of *Theileria orientalis* in cattle, aligning with the overarching research question of this thesis. This systematic review had two objectives: (1) to systematically identify and synthesise published evidence on the relationship between climate change factors and *Theileria orientalis* Ikeda; (2) to identify gaps in the current literature related to climate-driven changes in *T. orientalis* distribution and epidemiology.

3.2 Reviewing methodology.

The systematic review adopted a structured approach from Vallee et al. (2020), incorporating a consistent methodology to assess climate-driven impacts on *Theileria* in New Zealand. Building upon the previous study by Vallee et al. (2020), which reviewed literature from 1914 to 2017, this review extended the synthesis to cover recent publications from 2017 to 2025. This review incorporates several modifications from the previous study conducted by Vallee et.al (2020), particularly the inclusion criteria to enhance the relevance and applicability of outcomes to the current research scope.

The review was conducted using two electronic databases: Scopus and PubMed (as detailed in Tables 1 and 2). Literature published from 2017 to early 2025 was included in the search. Although it was included in the previous study, the Web of Science database was excluded due to a lack of authorised access through Massey University. Similarly, SciQuest was excluded from the database selection due to its limited geographical coverage and constrained search capabilities, which restricted its feasibility for capturing the broader international relevance required for this systematic review.

Search terms used in the systematic review are outlined in Tables 1 and 2. Table 1 lists the terms used to capture studies related to *Theileria orientalis*, its tick vector (*Haemaphysalis longicornis*), and relevant bovine host species. These biological terms were used consistently across all searches. Table 2 lists climate and environment-related search terms (e.g. temperature, rainfall, extreme weather events), which were added **individually** to the biological terms from Table 1 using the Boolean operator **AND**. This approach allowed the review to explore the literature on each climatic variable separately. Search syntax was adapted slightly between Scopus and PubMed to reflect the indexing conventions of each database.

The search results, including abstracts and complete reference details, were exported to the EndNote library. Within EndNote, customised groups were created for each climatic variable—temperature, rainfall, and extreme weather events—to organise, score, and filter each article’s abstract accordingly. The number of articles retrieved from each database was recorded before merging, and duplicates were removed within each climatic variable group. Additionally, articles previously assessed in the 2017 review by Vallee et al. (2020) were excluded, with only new articles beyond the original review period included in this analysis. The systematic search and data organisation were conducted over the period from 24th March to the 4th of April 2025.

Table 1: Search terms used in this systematic review from two databases for *Theileria* caused by the tick vector *Haemaphysalis longicorn* in the bovine species.

Search Concept	Search terms Scopus	Search terms PubMed
Theileria/Vector terms	TITLE-ABS-KEY ((theileria* OR “haemaphysalis longicorn” OR “Theileria orientalis Ikeda” OR” Theileria-associated bovine anaemia” OR "cattle tick”)	(theileria* OR “haemaphysalis longicorn” OR “Theileria orientalis Ikeda “OR” Theileria-associated bovine anaemia “OR “cattle tick ")
Host terms (bovine-related)	TITLE-ABS-KEY (cattle OR cow OR cows OR calf OR calves OR bull OR bulls OR heifer* OR bovin)	(Cattle OR cow OR cows OR calf OR calves OR bull OR bulls OR heifer* OR bovin)

Table 2: The search terms used for each climatic variable in the two databases.

Climatic variable	Search terms Scopus	Search terms PubMed
Temperature	TITLE-ABS-KEY ("air temperature*" OR "ambient temperature*" OR "elevated temperature*" OR freezing OR "high temperature*" OR "higher temperature*" OR "increased temperature*" OR "low temperature*" OR "lower temperature*" OR "maximum temperature*" OR "mean annual temperature*" OR "mean temperature*" OR "minimum temperature*" OR "summer temperature*" OR "warm temperature*" OR "warm year*" OR "warmer temperature*" OR "winter temperature*" OR frost OR "extreme temperature*" OR "autumn temperature*" OR "spring temperature*")	("air temperature*" OR "ambient temperature*" OR "elevated temperature*" OR freezing OR "high temperature*" OR "higher temperature*" OR "increased temperature*" OR "low temperature*" OR "lower temperature*" OR "maximum temperature*" OR "mean annual temperature*" OR "mean temperature*" OR "minimum temperature*" OR "summer temperature*" OR "warm temperature*" OR "warm year*" OR "warmer temperature*" OR "winter temperature*" OR frost OR "extreme temperature*" OR "autumn temperature*" OR "spring temperature*")
Rainfall	TITLE-ABS-KEY (drought OR monsoon OR precipitation OR rain OR rainfall OR "rainy season" OR runoff OR "wet condition" OR "wet season")	(drought OR monsoon OR precipitation OR rain OR rainfall OR "rainy season" OR runoff OR "wet condition" OR "wet season")
Extreme Weather Event	TITLE-ABS-KEY (cyclone OR "extreme weather" OR flood OR flooding OR "heat wave" OR hurricane OR storm OR wildfire OR inundation)	(cyclone OR "extreme weather" OR flood OR flooding OR "heat wave" OR hurricane OR storm OR wildfire OR inundation)

3.2.1 Abstract Screening and scoring criteria.

Each abstract was evaluated and screened for relevance based on its relationship to *Theileria orientalis* and the designated climate variable. Article abstracts that did not meet the predefined criteria were excluded. Scoring was conducted using a structured framework, assessing relevance according to the presence of specific keywords and alignment with each climatic variable used to measure *Theileria*.

Each article's abstract was scored accordingly, even if it appeared multiple times within different climatic variable groups in the EndNote library. If the abstract provided insufficient information for scoring, the full article was reviewed for relevance. Scoring was based on the criteria outlined in the framework presented in Table 3. The scoring framework was implemented to priorities abstracts according to the direct quantitative evidence, according to the scoring criteria. Based on the scoring framework criteria, the abstracts were classified accordingly.

Table 3:The scoring criteria used to measure relevance for each climatic variable.

Scoring Criteria for *Theileria* in Bovine	
Climatic Variable	Measuring Criteria
Temperature	Does the article abstract contain evidence linking temperature to *Theileria* and the vector *(Haemaphysalis longicornis)* distribution in bovine species? 0. No mention of temperature effects on *Theileria* and vector distribution. 1. General mention of temperature trends but not quantitative evidence: similar diseases (different gene, different species), distribution of vectors of similar species. 2. Provides quantitative data on temperature's effects on incidence and prevalence of similar diseases (e.g., same genus but different species), distribution of vectors (e.g., ticks), or risk factors associated with diseases of interest. 3. Direct quantification of temperature's impact on *Theileria* prevalence and distribution of *Haemaphysalis longicornis* in bovine species.
Rainfall	Does the article abstract contain evidence linking rainfall to *Theileria* and the vector *(Haemaphysalis longicornis*) distribution in bovine species? 0. No mention of rainfall effects on *Theileria* and vector distribution. 1. General mention of rainfall trends but not quantitative evidence: similar diseases (different gene, different species), distribution of vectors of similar species. 2. Provides quantitative data on rainfall effects on incidence and prevalence of similar diseases (e.g., same genus but different species), distribution of vectors (e.g., ticks), or risk factors associated with diseases of interest. 3. Direct quantification of rainfall impact on *Theileria* prevalence and distribution of *Haemaphysalis longicornis* in bovine species.
Extreme weather events	Does the article abstract contain evidence linking extreme weather events to *Theileria* and the vector *(Haemaphysalis longicornis)* distribution in bovine species? 0. No mention of extreme weather events effects on *Theileria* and vector distribution. 1. General mention of extreme weather events trends but not quantitative evidence: similar diseases (different gene, different species), distribution of vectors of similar species. 2. Provides quantitative data on extreme weather events effects on incidence and prevalence of similar diseases (e.g., same genus but different species), distribution of vectors (e.g., ticks), or risk factors associated with diseases of interest. 3. Direct quantification of extreme weather events impact on *Theileria* prevalence and distribution of *Haemaphysalis longicornis* in bovine species.

3.3 Results.

A total of 119 abstracts were retrieved from Scopus (n=77) and PubMed (n=42), and categorised under the three climate variables—temperature, rainfall and extreme weather events — in Endnote library. Following the removal of 45 duplicates, 74 abstracts were screened using the predefined eligibility and scoring framework. Abstracts scoring zero across all criteria (n=34) were excluded, leaving 40 abstracts retained for qualitative synthesis. These were distributed across scoring level: score 1 (n=9), score 2 (n=21) and score 3 (n=10) as illustrated in Figure 1 and 2, and detailed in Table 4.

The 40 included studies represented a broad global distribution across multiple climatic zones, livestock systems and ecological settings as illustrated in Table 5. The data illustrates findings across multiple continents and climate zones, illustrating a widespread interest in understanding how climatic variables shape disease dynamics in livestock systems. The studies were done mainly in multiple regions including India (Bhanot, 2020; Debbarma et al., 2020; Ghosh et al., 2020; Jayalakshmi et al., 2022; Krishnamoorthy et al., 2021; Niranjan et al., 2023; Shit et al., 2023), China (Chen et al., 2022), Pakistan (Ali et al., 2024; Shoaib et al., 2022), Uzbekistan (Abdurasulov et al., 2024), Ethiopia (Hadgu et al., 2019; Tarekegn et al., 2025; Yenew et al., 2025), Uganda (Etiang et al., 2024; Obara et al., 2020), Zimbabwe (Manyenyeka et al., 2022; Nemaungwe et al., 2023), Ghana (Tawiah-Mensah et al., 2024), Kenya (Chepkwony et al., 2020), Botswana (Babayani & Makati, 2021), Brazil (Cruz et al., 2020; Nicaretta et al., 2021; Oshiro et al., 2021; Puentes & Riet-Correa, 2023; Sales et al., 2024), Colombia (Zapata et al., 2024), Ecuador (Pérez-Otáñez et al., 2024), Argentina (Nava et al., 2022), Iraq (Abdullah et al., 2019; Zangana & Tawfeq, 2021), Iran (Patial et al., 2021), Algeria (Ziam et al., 2020), Thailand (Sri-In et al., 2024), Spain (Calleja-Bueno et al., 2022), USA (Leal et al., 2018; Zamora et al., 2020) and New Zealand (Heath, 2021).

Collectively, the studies done demonstrate an increasing global recognition of the complex relationship between climate and the epidemiology of tick-borne disease in livestock. The analysis of the 40 abstracts revealed that the main climatic variables included, rainfall, temperature (n=30), relative humidity (n=26) and broader seasonal variation (n=18). Additional environmental parameters such as, altitude, latitude and land cover also appeared in several studies.

Flow process for identification of studies from databases.

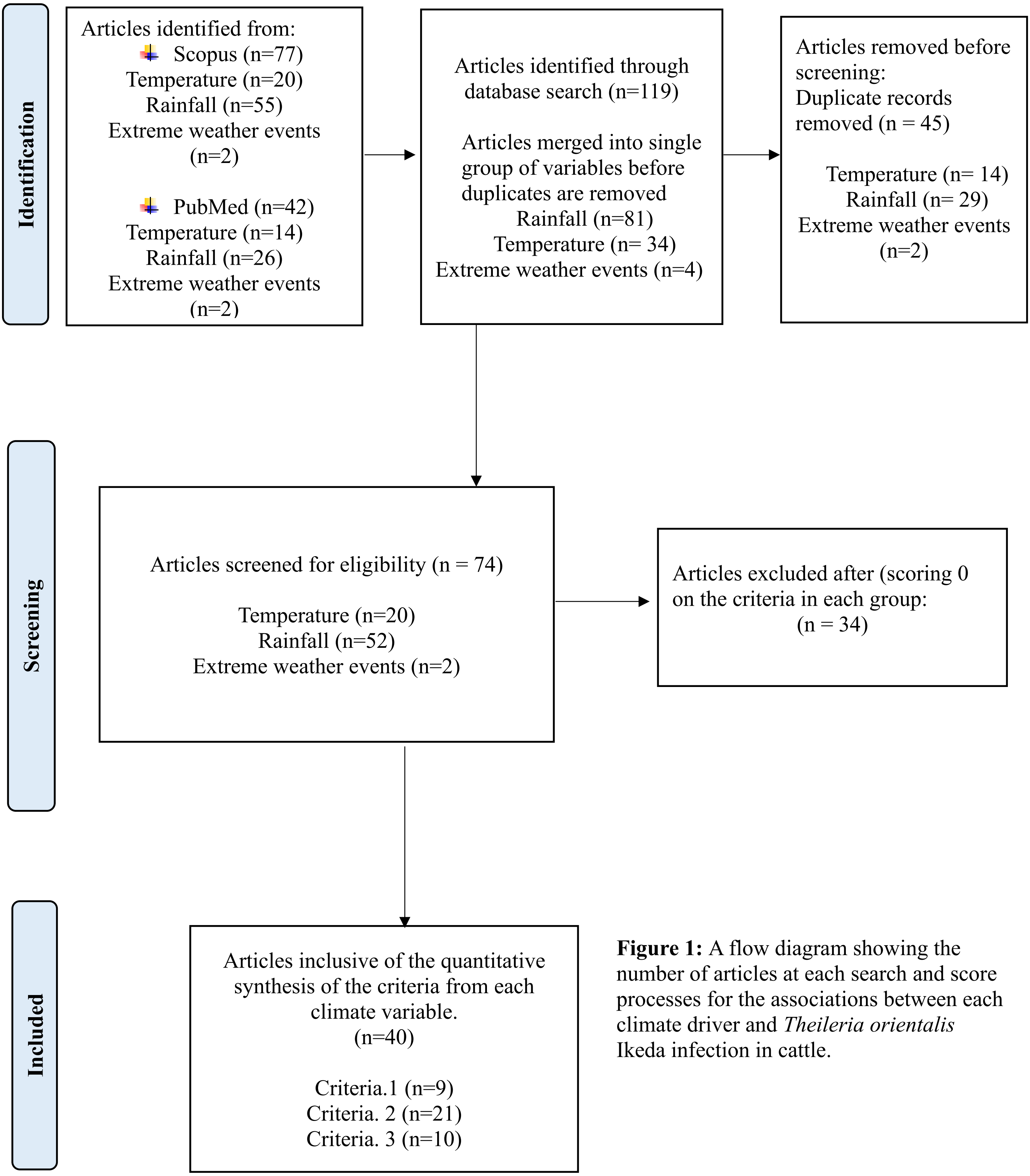

Figure 1: A flow diagram showing the number of articles at each search and score processes for the associations between each climate driver and *Theileria orientalis* Ikeda infection in cattle.

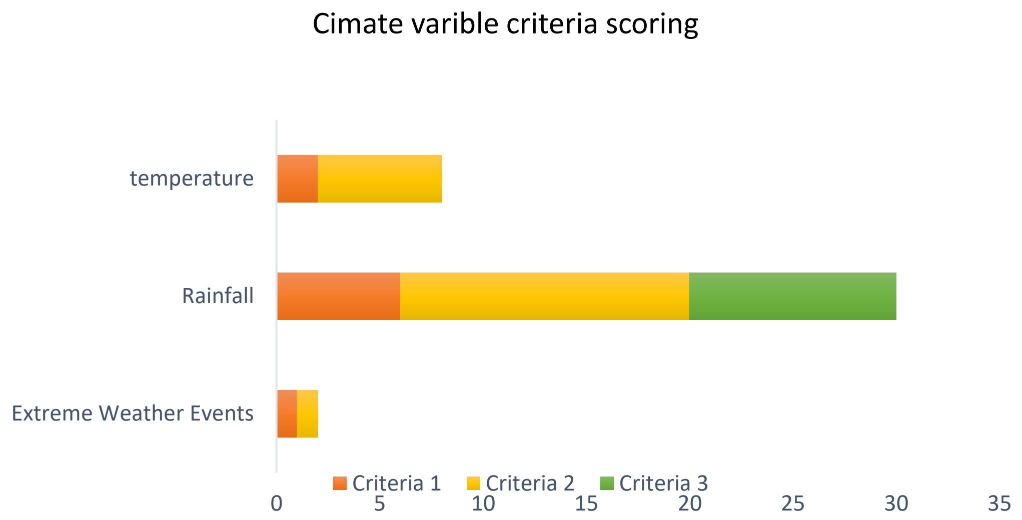

Figure 2: Graph showing the scoring outcomes for each abstract under each climate variable and the relevance to the study. Articles scoring (0) were excluded from this analysis.

Table 4: The number of abstracts scored under each climatic variable, with criterion 3 showing the highest relevance.

Variable	Criteria 1	Criteria 2	Criteria 3
Extreme Weather Events	1	1	0
Rainfall	6	1 4	10
temperature	2	6	0
Total	9	21	10

Table 5: Summary of 40 abstracts capturing the key findings for each country and the climatic variables that are measured in each country.

Country	Climate Variables	Disease measures	Key findings	Source.
Algeria	Rainfall (seasonality)	Prevalence and clinical signs of bovine piroplasmosis, anaplasmosis, and tropical theileriosis	*Theileria annulata* incidence peaked in July, aligning with elevated temperature and humidity, indicating seasonally driven transmission	Ziam et al. (2020)
Argentina	Temperature and seasonality variety.	Incidence of *Rhipicephalus* (Boophilus) *microplus* in Cattle.	A temperature increase during the autumn and winter months will increase infection.	Nava et al. (2022)
Botswana	Seasonality yearly, stocking density, normalized difference vegetation index values.	Prevalence of tick species in livestock-wildlife interface.	Season and microclimatic factors, such as seasonal flooding and the driest of the seasons have a major impact on tick abundance.	Babayani and Makati (2021).
Brazil	Temperature, humidity, rainfall, and seasonal/extreme weather variation	Prevalence and dynamics of *Rhipicephalus microplus* and associated haemoparasites in cattle	Tick prevalence and distribution were influenced by seasonal rainfall patterns, with higher infections during rainy or humid periods. Dry seasons and floods reduced prevalence, while temperature and ground-level humidity significantly affected tick biology and survival.	Sales et al. (2024), Puentes and Riet-Correa (2023), Cruz et al. (2020)et al., Oshiro et al. (2021), Nicaretta et al. (2021)
Central Spain	Altitude and relative humidity and temperature.	Prevalence of *Anaplasma marginale* and *Babesia bigemina* in cattle.	Both agents were detected in regions with lower temperatures, greater altitude and relative humidity.	Calleja-Bueno et al. (2022)
China	longitude, latitude, precipitation, temperature, humidity, and altitude	Prevalence of *Theileria spp*. in cattle	Longitude, latitude, precipitation, humidity, and temperature were associated with *Theileria* prevalence.	Chen et al. (2022)
Colombia	Rainfall and temperature	Prevalence of *Rhipicephalus microplus* in cattle.	Temperature and moderate rainfall had impacts on the prevalence *of Rhipicephalus microplus* in cattle.	Zapata et al. (2024) et al.

Ecuador	isothermality, precipitation and seasonality.	Spatial distribution of *Rhipicephalus microplus* and *Amblyomma cajennense s.l.* ticks	Precipitation levels and isothermality impacted the distribution. Seasonality was clearly visible in the distribution across the coast areas.	Pérez-Otáñez et al. (2024)
Ethiopia	Seasonal variation (dry/wet seasons, temperature, and precipitation)	Prevalence and distribution of tick-borne pathogens (e.g., Ixodid, *Rhipicephalus spp.*) in cattle	Tick-borne disease prevalence in cattle is seasonally influenced, with higher rates during rainy periods. Prevalence is further affected by agroecology, vegetation, livestock management, and long-term temperature rise	Yenew et al. (2025) et al, Tarekegn et al. (2025), Hadgu et al. (2019) et al.
Ghana	Seasonal Variety (dry and wet seasons).	Incidence of *Rhipicephalus microplus*, *Hyalomma rufipes* and *Amblyomma variegatum* in cattle.	There tick species and seasons were significantly correlated ($p < 0.001$).	Tawiah-Mensah et al. (2024).
India	Seasonal variation (monsoon, summer, winter, rainy season)	Prevalence of tick-borne haemoparasites including *Theileria*, *Anaplasma*, *Babesia*, *Hyalomma*, *Rhipicephalus (Boophilus)* species, and *Trypanosoma* spp. in cattle	*Theileria* is the most prevalent tick-borne pathogen in cattle, with infections peaking during wet, summer, and monsoon seasons. The monsoon strongly influences tick distribution and disease prevalence, while winter months show the lowest infection rates. *Anaplasma marginale* is also common, with its spread affected by both epidemiological and climate factors. Overall, seasonal variations significantly impact tick-borne disease dynamics in cattle.	Shit et al. (2023), Krishnamoorthy et al. (2021), Debbarma et al. (2020), Ghosh et al. (2020), Jayalakshmi et al. (2019), Bhanot (2020), Kaur et al. (2021), Niranjan et al. (2023).
Iraq	Temperature, humidity, and rainfall, along with seasonal changes (winter and summer)	Prevalence of theileriosis, babesiosis, (*Anaplasma spp.*, *Babesia spp.*, and *Theileria spp.* in cattle and goats is closely influenced by climate	*Theileria* was the most prevalent infection, with higher cases in summer and lowest in winter. Temperature promoted infection development, while rainfall and relative humidity tended to reduce it. Cattle showed the highest prevalence of *Theileria spp.*	Zangana and Tawfeq (2021), Abdullah et al. (2019).

Kenya	Seasonal variety (rainfall)	Incidence of anaplasmosis and babesiosis in cattle.	The monthly rainfall had no correlation with infection rates.	Chepkwony et al. (2020).
New Zealand	Temperature and humidity	Prevalence of arthropod parasites in domestic animals	Tick prevalence rises in warm, humid weather. Ectoparasites may be less common in warmer, drier climates.	Heath (2021)
Pakistan	Seasonal variation, including summer, winter, and rainy seasons, along with temperature and humidity, significantly influence tick-borne disease prevalence.	prevalence of *Rhipicephalus microplus* and other tick species influenced by local environmental and climatic conditions	Elevated temperature and humidity during summer and wet seasons drive increased tick dispersion and infection prevalence, while winter months show the lowest rates.	Ali et al. (2019), Shoaib et al. (2022)
Thailand	Rainfall, (season)	Tick diversity and molecular detection of *Anaplasma*, *Babesia*, and *Theileria.*	Rainfall had negative impact on tick population of ticks, whereas temperature and relative humidity did not exhibit similar effects.	Sri-In et al. (2024)et al.
Uganda	Rainfall (rainy and dry season).	Prevalence of ixodid ticks-*Rhipicephalus appendiculatus.*	Tick infections peaked during the rainy and dry seasons, though unknown factors may limit accurate distribution forecasts in areas with higher rainfall.	Etiang et al. (2024), Obara et al. (2020).
USA (Taxes)	Relative humidity ambient temperatures, and precipitation,	Prevalence of *Rhipicephalus* (Boophillus) *annulatus* (Acari: Ixodidae) and measure of climatic variables	Relative humidity, along with its interaction with canopy habitat occupancy, plays a highly significant role in infection rates, as tick survival is strongly influenced by the combined effects of habitat and seasonal conditions.	Zamora et al. (2020), Leal et al. (2018)
Uzbekistan	Temperature and relative humidity.	Immunobiological properties of theileriosis in cattle breeding	The virulence of *Theileria annulata* can decrease under unfavourable environmental conditions, with low humidity and elevated temperatures weakening the virus.	Abdurasulov et al. (2024)

Zimbabwe	Temperature and precipitation.; Seasonality variety (hot and wet season).	climate-disease dynamics of *Rhipicephalus appendiculatus* in livestock.; Spatio-temporal clustering and risk factor analysis of *Theileria parva* in bovine species.	Maxent modelling predicts that by 2050, climate change will reduce viable habitats for ticks, pushing them toward cooler, higher elevations. Currently, the highest incidence of *Theileria parva* occurs during the hot, rainy season.	Nemaungwe et al. (2023), Manyenyeka et al. (2022)

3.4 Discussion.

The systematic review synthesised evidence from 40 studies investigating how climatic variables influence the distribution of *Theileria orientalis* and other tick-borne diseases in cattle across diverse global regions. While most of the included studies examined general tick-climate associations rather than *Theileria orientalis* specifically, the review extracted cross-cutting themes that provide insight into how climate variables shape vector ecology and pathogen transmission. Importantly, the review not only identifies *Haemaphysalis longicornis*—the established vector in New Zealand—but also a range of other tick species known to transmit different *Theileria* genotypes globally.

The number of studies identified in the review includes Asia (15), Africa (12), South America (9), Europe (1), North America (2) and New Zealand (1). The main climatic variables associated with consistently shaping tick abundance and pathogen prevalence in livestock were temperature, rainfall, humidity and seasonal variation. Rainfall was the most frequently examined climatic variable (20 studies), followed by temperature (15) and humidity (8). Although seasonality variation was also captured, it was rarely analysed as an isolated climatic factor and was often measured in relation to rainfall patterns or temperature cycles. The geographical spread of studies illustrates a strong global interest in climate impacts on tick ecology, also highlighting considerable regional variation. Global, warmer and more humid conditions favor higher vector activity and infection prevention. In New Zealand, *Haemaphysalis longicornis* exhibits greater activity and distribution in moist, warm-temperate environments, suggesting warmer and wetter conditions support the life cycle and protentional of *Theileria orientalis* Ikeda transmission (Heath, 2016).

From the review, it was evident that *Theileria* species were reported predominantly in Algeria and China. In Algeria, *Theileria annulata* caused by the *Hyalomma* ticks (*Hyalomma scupense* and *Hyalomma anatolicum*), peaks during the humid, warm months of July (Ziam et al., 2020). In China, multiple *Theileria* species, including *Theileria annulata*, *Theileria orientalis* and *Theileria sinensis*, occur across diverse agroecological zones, mainly transmitted by ticks such as *Haemaphysalis longicornis*, *Dermacentor silvarum*, and *Ixodes persulcatus* (Chen et al., 2022). The co-occurrence of *Theileria orientalis* and *Theileria sinensis* in northeastern China study highlights regional diversity. The systematic search identified only one New Zealand study by Heath (2021). However, as captured in the narrative literature review in Chapter 2, a broader body of research on *Theileria orientalis* in New Zealand exits, which was not captured by the database search in the systematic review due to limitations in the database index and variation in terminology but were identified through prior literature syntheses. Consequently, they were included in the overall analysis to ensure a comprehensive assessment of *Theileria orientalis* epidemiology and transmission in New Zealand. This highlights a gap in the systematic review process and emphasizes the importance of supplementary search strategies to capture regionally published work not indexed in major databases.

While the systematic review captured the association between climatic variables and tick-borne pathogens, it did not explicitly account for temporal lags, exposure intensity, or cumulative climate effects. Nonetheless, several studies provide indirect evidence of these dynamics. For example, in Algeria (Ziam et al., 2020) and Brazil (Puentes & Riet-Correa, 2023; Sales et al., 2024), seasonal peaks in prevalence correspond with periods of high temperature, humidity, or rainfall, indicating that climate impacts on tick abundance and *Theileria annulata and Rhipicephalus microplus* transmission follow environmental changes over time. Similarly, in Ethiopia, higher pathogen prevalence during rainy periods indicates a delayed response of disease dynamics to climatic conditions (Tarekegn et al., 2025; Yenew et al., 2025). Other regional examples further illustrate these patterns: in Argentina, moderate autumn and winter temperatures coincide with increased *Rhipicephalus microplus* prevalence in cattle (Nava et al., 2022). These seasonal patterns serve as proxies for temporal lag and cumulative exposure, highlighting how recurring wet or warm periods drive higher disease incidence over weeks or months. Future analyses could explicitly quantify these temporal and cumulative effects to improve predictions of disease risks under changing environmental conditions.

In India, the prevalence of *Theileria, Anaplasma*, *Babesia* and *Trypanosoma* peaked during the monsoon and summer seasons, with winter months showing the lowest infection rates (Bhanot, 2020; Debbarma et al., 2020; Jayalakshmi et al., 2022; Krishnamoorthy et al., 2021; Niranjan et al., 2023; Shit et al., 2023). Similarly, in Ethiopian studies reported higher prevalence of *Rhipicephalus* species during rain periods, and further moderated by agroecology, vegetation cover, livestock management, and long term temperature trends (Hadgu et al., 2019; Tarekegn et al., 2025; Yenew et al., 2025). These findings align with observations from Colombia, Ecuador, and Pakistan, where temperature and rainfall together influenced *Rhipicephalus species* distribution and disease prevalence (Ali et al., 2024; Pérez-Otáñez et al., 2024; Shoaib et al., 2022; Zapata et al., 2024). These patterns collectively support the conclusion that climatic drives operate across multiple ecological systems, through their intensity and expression vary by region, vector species and production systems.

Altitude, latitude, and land cover also appear to modulate vector and pathogen dynamics. In Spain, higher altitudes and cooler temperatures were associated with reduced prevalence of *Anaplasma marginale* and *Babesia bigemina* (Calleja-Bueno et al., 2022), whereas in Uzbekistan, low humidity and high temperatures were shown to weaken the virulence of *Theileria annulata* (Abdurasulov et al., 2024). In Zimbabwe, Maxent modelling predicts that climate change may push ticks to cooler, higher elevations by 2050, although current *Theileria parva* incidence remains highest during hot, rainy seasons (Manyenyeka et al., 2022; Nemaungwe et al., 2023). Despite these insights, the existing systematic review reveals several knowledge gaps. Very few studies quantitatively evaluate the intensity, duration, and cumulative exposure to climatic variables relative to disease outcomes.

Extreme weather events, such as flooding and drought, were also captured in several studies. In Botswana, seasonal flooding and dry periods strongly influenced tick prevalence at the livestock-wildlife interface, indicating the importance of microclimate and land in modulating disease risk (Babayani & Makati, 2021). Studies in Brazil, Cruz et al. (2020); Puentes and Riet-Correa (2023); Sales et al. (2024) found that *Rhipicephalus microplus* prevalence increased during rainy and humid periods, whereas extreme events like floods or droughts reduced tick survival. These results illustrate that both seasonal variation and extreme climatic events can shape disease dynamics in livestock systems. In contrast, in Thailand, rainfall had less pronounced effects, reflecting the complex interactions between multiple environmental factors (Sri-In et al., 2024). Despite these insights, several knowledge gaps remain such as assessing extreme weather events, such as droughts and floods, which are rarely incorporated into analyses, despite their potential to significantly influence tick populations and pathogen transmission.

Several limitations were identified in the review process. Only a single reviewer assessed abstracts, increasing the risk of bias. Search terms for extreme weather events were incomplete (e.g., excluding drought), potentially underrepresenting certain climatic impacts. Limiting searches to Scopus and PubMed may have omitted relevant studies in other databases or grey literature. Additionally, the keyword strategy may have excluded relevant studies, especially those addressing less documented climatic variables such as extreme weather events, potentially skewing results toward more commonly studied factors such as temperature and rainfall. Furthermore, to enhance robustness of the scoring process, the inclusion of a secondary reviewer, assessment of inter-rater reliability (e.g., using Cohen’s Kappa), and a pilot scoring phase to refine criteria would have improved consistency and validity of the review process.

Overall, the systematic review indicates that temperature, rainfall, humidity, and seasonal variation are consistently associated with tick abundance and pathogen prevalence across multiple ecological and climatic contexts. For New Zealand, these findings suggest that climatic factors, particularly warm and humid conditions, likely drive the distribution and epidemiology of *Theileria orientalis* Ikeda. However, the gaps identified—such as limited temporal analyses, lack of exposure intensity data, and underrepresentation of extreme weather events—justify the subsequent longitudinal analyses in this thesis. Chapters 4 to 7 will address these limitations by examining climate predictors and *Theileria orientalis* case counts in New Zealand cattle from 2012 to 2024, providing a robust, context-specific understanding of climate-driven disease dynamics.

Chapter 4 Materials and Methods.

This chapter describes the methods used to analyse the impacts of climate change variables on theileriosis in the New Zealand cattle population. The main objectives were (1) to describe temporal trends in *Theileria* incidence from 2012 to 2024 at a district level to understand spatial variations, and (2) to identify key climatic predictors associated with the *Theileria* case counts using the laboratory reports collected from passive surveillance.

4.1 Study area.

New Zealand is a unique island nation located in the Southwestern Pacific Ocean, with a population of approximately 5.3 million, and known for its ethnic diversity including significant Māori population (Streat, 2012). The country comprises two main islands, the North and South islands, along with over 700 smaller islands, covering a total area of 268,021 square kilometres (Streat, 2012). The country climate is varied, influenced by oceanic conditions with climate change posing risks to agricultural, economic stability and environmental sustainability (Hopkins et al., 2015). New Zealand's climate, particularly in the South Island, is influenced by the Southern Hemisphere westerlies interacting with the Southern Alps, with sea surface temperature variations affecting local climate and glacier mass balance changes (Kropac et al., 2023). The agriculture sector plays a crucial role in the New Zealand economy, particularly pastoral farming, which significantly contributes to greenhouse gas emissions (Hopkins et al., 2015). The economic burden of *T.orientalis* is significant, as it affects cattle health and productivity, requiring ongoing awareness and management practices to mitigate impacts in New Zealand over the years (Watts et al., 2016).

4.2 Datasets.

4.2.1 *Theileria* case data.

Theileria case data was sourced from the Ministry for Primary Industries (MPI) through its broader passive surveillance system. There is no active surveillance system dedicated to monitoring anaemia outbreaks; therefore, the *Theileria* case reports are based on farmers' observations and reports of illness, needing veterinary interventions. In this study, a case was defined as a cattle (including beef and dairy) farm where farmers detect clinical signs and a veterinarian visits, determines that laboratory testing is required, and collects samples for diagnosis, and the samples test positive for *Theileria orientalis* Ikeda.

The case dataset captures the laboratory submissions for diagnosed *Theileria* cases in New Zealand from the 1st of August 2012 to the 31st of August 2024. The laboratory submission data recorded details of the sampling record date, species, region, presenting signs, territorial authority, aetiological diagnosis, pathological diagnosis and test requested. A time series case count dataset was created, counting the diagnosed cases of *Theileria* by month and by territorial authority (TLA).

4.2.2 Climate data.

The original climatic data was sourced from the National Institute of Water and Atmospheric Research (NIWA) through the EpiCentre under a data-sharing agreement. This study used the data, which was already pre-processed into a monthly and zonal mean format from 2012 to 2024 by a data handler for analysis. The study also incorporated the climatic variables hypothesised as essential for tick survival and distribution in New Zealand, based on Neilson (1980) and Heath (1979, 1981, 2016); Heath (1975). These variables included annual mean rainfall, annual temperature, mean July maximum temperature (winter months), mean July minimum temperature (winter months), median vapour pressure, and median soil moisture for January months. Although they were found not important by Lawrence (2020), these variables were selected for investigation in this study because of their biological significance and their role in enhancing the survival and reproduction success of *H.longicornis* in New Zealand (Lawrence, 2020).

4.2.3 Spatial data

The spatial data in the shapefile format, containing polygons for the territorial authority, was sourced from the New Zealand stats website: (https://www.stats.govt.nz/). These data were used to visualise the *Theileria* case distribution, and to extract the centroids of the district for analysis. The coordinates of the district centroids were extracted from the NZ territorial authority polygons. The map in Figure 5 was created using the NZ spatial dataset with the package simple features library (sf) in R for spatial vector data analysis.

4.2.4 Census data.

Cattle farm population data was sourced from the agricultural census on the StatsNZ website (https://www.stats.govt.nz/), which contains farm count data for different farm types and territorial authorities (TLA) in New Zealand from records from 2012, 2017 and 2022. As the agricultural census in New Zealand are conducted every five years, data for intervening years were interpolated. This was done by assuming a linear relationship to create a complete annual dataset from 2012 to 2024 for integration with the main dataset. To perform a complete time series analysis, gap years in the annual cattle population counts were imputed using the function impute_linear () in R to perform linear model-based imputation. The function inputs a subset of the data corresponding to each unique combination of farm and territorial authority (TLA). For each group, a simple linear regression model was fitted using two data points, and predictions were generated for all years up to 2024. The imputation process was applied to all combinations of farm type and territorial authority (TLA) using the dplyr: group split () and purr: map2_df (), ensuring a robust and group-wise complete time series dataset.

4.2.5 Data integration.

All datasets were merged to create a single dataset that included all the primary predictor variables listed in Table 6. The climate dataset, which was already cleaned and formatted, was merged with the *Theileria* case dataset using year, month and territorial authority as the common fields. In addition, the data were merged to include time lags (-1 month, -2 month, and -3 month) to account for the potential delay between climate conditions and disease case reporting, including the circulation of *Theileria*, exposure to cattle, incubation periods, delays in reporting diagnosis and ecological interactions influencing disease transmission by *H. longicornis*. The four climate variables linked to tick survival (Mean July Tmax, Mean July Tmin, MedianVP Feb/Apr and MedianJansoil Moisture) were merged with the case count data, so that the climate variables preceded the case counts and corresponded to the immediate previous season. For example, the January 2023 data were merged with the July 2022 data, instead of the July 2023 data. The latitude and longitude coordinates of the centroids of territorial authorities were integrated into the dataset using the territorial authority as the joint field.

Table 6: Description of climatic, demographic and spatial variables sourced from the National Institute of Water and Atmospheric research (NIWA) used in the modelling to determine the impacts of *Theileria* cases in cattle in New Zealand.

Variable	Units	Description	Source
Tmax5k_i	°C	Monthly mean maximum temperature from 9 am local day, with i (0, 1, 2, 3) month lags.	NIWA
Tmin5k_i	°C	Monthly mean minimum temperature to 9 am local day, with i (0, 1, 2, 3) month lags.	NIWA
Rain5k_i	mm	Monthly mean rainfall to 9 am local day, with i (0, 1, 2, 3) month lags.	NIWA
RHum5k_i	%	Monthly mean relative humidity local day, with i (0, 1, 2, 3) month lags.	NIWA
SRad5k_i	MJ/m2	Monthly mean amount of accumulated global solar radiation from midnight local day, with i (0, 1, 2, 3) month lags.	NIWA
VP5k_i	hPa	Monthly mean vapour pressure at 9 am local day, with i (0, 1, 2, 3) month lags.	NIWA
mslp5k_i	hPa	Monthly mean Atmospheric pressure reduced to mean sea level at 9 am local day.	NIWA
PETo_clidb5k_i	mm	Monthly mean of Penman Potential Evapotranspiration total from 9 am local day., with i (0, 1, 2, 3) month lags.	NIWA
SMD5k_i	mm	Monthly mean Soil moisture from 9 am local day calculated from rainfall and evapotranspiration. The base value is -150 mm ("permanent wilting point") based on "soil store capacity". A value of "0" indicates the soil is at "field capacity" (amount of water held in the soil after the excess has drained away). A value greater than 0 indicates runoff. With i (0, 1, 2, 3) month lags.	NIWA
Wind_i	m/s	Monthly mean wind speed at 10 m above ground level over 24 hours from midnight local day, with i (0, 1, 2, 3) month lags.	NIWA
Meanrain	mm/year	The mean annual rainfall for years 2012- 2024	NIWA
Meantemp	°C	The mean annual temperature for years 2012-2024	NIWA
Mean July Tmax	°C	The mean July daily maximum temperature to illustrate winter months for years 2012- 2024.	NIWA
Mean July Tmin	°C	The mean July daily minimum temperature to illustrate winter months from 2012- 2024	NIWA
MedianVP Feb/Apr	hPa	The median Vapour pressure at 9 am local day of months February, March, and April for years 2012- 2024	NIWA
MedianJansoil Moisture	mm	Soil moisture from 9 am local day for month of January for years 2012- 2024.	NIWA
Dairy cattle farm population	Farms per district	Dairy cattle farm count.	StatsNZ agricultural census 2012, 2017, 2022.
Beef farm populations	Farms per district	Beef cattle farm count.	StatsNZ agricultural census 2012, 2017, 2022.
Latitude and Longitude	Centroids	NZ territorial authority polygon	statsNZ

4.2.6 Statistical analysis.

All the data processing and analyses in this study were conducted using the statistical software R [version 4.5.0 (2025-04-11 ucrt)] (R Core Team, 2024). The R packages used were dplyr (Wickham.H et al., 2025), glmmTMB (McGillycuddy M et al., 2025), sf (Pebesma, 2018), plyr (Wickham, 2011), ggplot2 (Wilkinson, 2011), mass (Venables & Ripley, 2013), car (Fox & Weisberg, 2018), purrr (Henry & Wickham, 2017), reshape2 (Wickham, 2007), tidyverse (Wickham, 2020), lubridate (Grolemund & Wickham, 2011), DHARMa (Hartig, 2016, 2022), caret (Kuhn, 2008), performance (Lüdecke et al., 2019)

4.2.7 Modelling approach.

Poisson regression and negative binomial modelling approaches were considered for the analysis. The outcome count data was observed to be over-dispersed, and according to the Akaike information criterion (AIC) between the Poisson and negative binomial models, the negative binomial was considered a better fit. All models were fitted using the glmmTMB package, which allows inclusion of fixed and random effects. The models included a random effect for territorial authority (TLA) to capture unmeasured spatial heterogeneity. The negative binomial distribution assumes the following variance structure:

$$Var(Y) = \mu + \frac{\mu^2}{\varphi}$$

where, Y= is the response variable (count),

μ = is the expected value (mean) of Y,

φ = is the dispersion parameter (estimated by the model),

A total of 47 predictor variables were analysed by fitting univariable negative binomial models to assess individual association with the response variable, which is the *Theileria* case counts. Each baseline univariable model included individual climatic variable predictors as the fixed effect and territorial authority as a random effect to establish the standalone effect of each climate variable on counts, which was initially assessed. To improve interpretability, coefficients were exponentiated to derive relative risks (RRs), which reflect the multiplicative changes in expected case count for a one-unit increase in each predictor.

A custom function was defined in R to compute the risk ratio and 95% confidence intervals (CI) for each fixed effect using the standard normal approximation to assume asymptotic normality of the parameter estimates. The 1.96 multiplier in the formula corresponds to the 97.5th percentile of the standard normal distribution, appropriate for contrasting a two-sided 95% CI.

The transformation applied was.

Risk Ratio: $Risk\ Ratio\ (RR) = e\beta$

Where; β = estimated coefficient on log scale, eβ = yields the relative risk.

Predictors with Risk Ratio > 1: The predictor is positively associated with an increase in the risk of the outcome.

Predictors with Risk Ratio <1: The predictor is negatively associated with the risk of the outcome.

95% Confidence Intervals:

The lower and upper confidence limits were calculated using the standard deviation of the estimates:

$$Lower\ CI = e^{\beta - 1.96 \times SE}$$

$$Upper\ CI = e^{\beta + 1.96 \times SE}$$

Where; β is the regression coefficient, and the *SE* is Standard error of the coefficient. 1.96 is the critical value for a 95% confidence level in a standard normal distribution.

If the 95% confidence interval included 1, the association is not statistically significant, indicating that the predictor may have no meaningful effect on the outcome. Conversely, if the confidence interval does not include 1, the risk ratio is statistically significant, suggesting that the predictor has significant negative or positive associations with the outcome. This approach allowed for an interpretation of the effect size and significance of each covariate included in the negative binomial mixed models.

Chapter 5 Results.

There were 11,417 confirmed cases from the 1st of September 2012 to the 30th of August 2024. As shown in Table 7 and Figure 3, *Theileria* cases were heavily concentrated in the North Island, particularly in Waikato, which experienced a major outbreak between 2013 and 2016. These regions accounted for over 80% of national cases, while the South Island remained minimally affected throughout the study period. Figure 4 suggests a possible seasonal pattern, with higher case counts observed in spring months across multiple years. However, no statistical testing was conducted to confirm whether these seasonal differences are significant.

Several climatic variables showed significant associations with *Theileria* case counts, with wind speed, vapour pressure for February to April, potential evapotranspiration at the current month, rainfall and relative humidity among the strongest positive predictors. Temperature-related variables tended to show negative associations. Figure 5 illustrates the spatial location and livestock density also contributed significantly to disease risk. Figure 6 shows the regional variation of incidence rates per 1,000 farms in New Zealand from 2012 to 2024. Figure 7 presents the epidemic curve of incidence rates among at-risk cattle populations from 2012 to 2024.

Table 8 presents the results of 47 univariable negative binomial models that were fit to analyse the associations between climatic, demographic and spatial predictors against the outcome variable. The results in Table 8 outline the risk ratio (RR), 95% confidence intervals and p-values from the analysis done to identify which predictors are significantly associated with higher or lower *Theileria* case counts in New Zealand from 2012 to 2024.

Table 7: The number and percentage of *Theileria* case counts in each region stratified in 2012, 2013 to 2016, 2017-2020 and 2021 to 2024.

Region	Number and (percentage **%**).				
	2012	2013-2016	2017-2020	2021-2024	All years
Waikato	8 (30)	3, 413 (55.4)	983 (32.9)	954 (42.5)	5358 (46.9)
Bay of Plenty	0	854 (13.9)	338 (11.3)	148 (6.6)	1340 (11.7)
Taranaki	0	254 (4.1)	524 (17.6)	422 (18.8)	1200 (10.5)
Manawatu-Whanganui	0	383 (6.2)	494 (16.6)	317 (14.1)	1194 (10.5)
Northland	18 (67)	454 (7.4)	188 (6.3)	104 (4.6)	769 (6.7)
Auckland	1(4)	507 (8.2)	88 (3)	39 (2)	635 (5.6)
Hawke's Bay	0	93 (2)	117 (3.9)	101 (4.5)	311 (2.7)
Wellington	0	24 (0.4)	86 (3)	35 (2)	145 (1.3)
Gisborne	0	80 (1)	26 (1)	18 (1)	124 (1.1)
Tasman	0	26 (0.4)	31 (1)	38 (2)	95 (1)
Canterbury	0	42 (0.7)	21 (1)	19 (1)	83 (1)
Melborough	0	12 (0.2)	41 (1)	26 (1)	79 (1)
West Coast	0	8 (0.1)	34 (1)	9 (0.4)	51 (1)
Nelson	0	7 (0.1)	11 (0.4)	11 (1)	29 (0.3)
Southland	0	0	1 (0.03)	1 (0.05)	2 (0.02)
Otago	0	0	0	2 (0.1)	2 (0.02)
All regions	27 (100%)	6,157 (100%)	2,984 (100%)	2,244 (100%)	11,417 (100%)

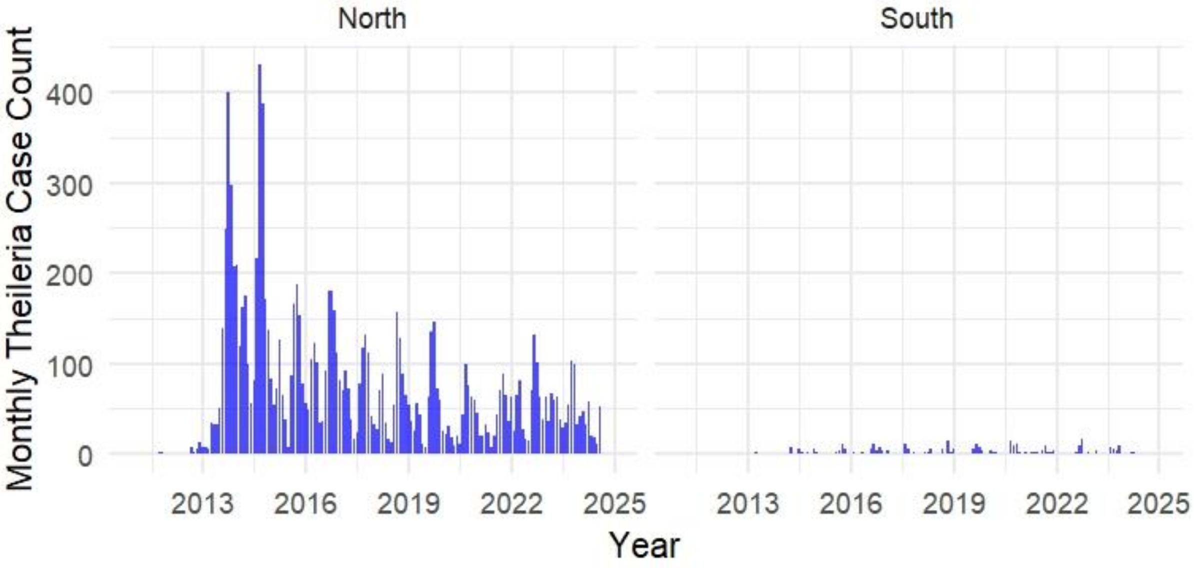

Figure 3: Stratified time-series plot highlighting the disparity in *Theileria* case counts between the North Island and South Island over time.

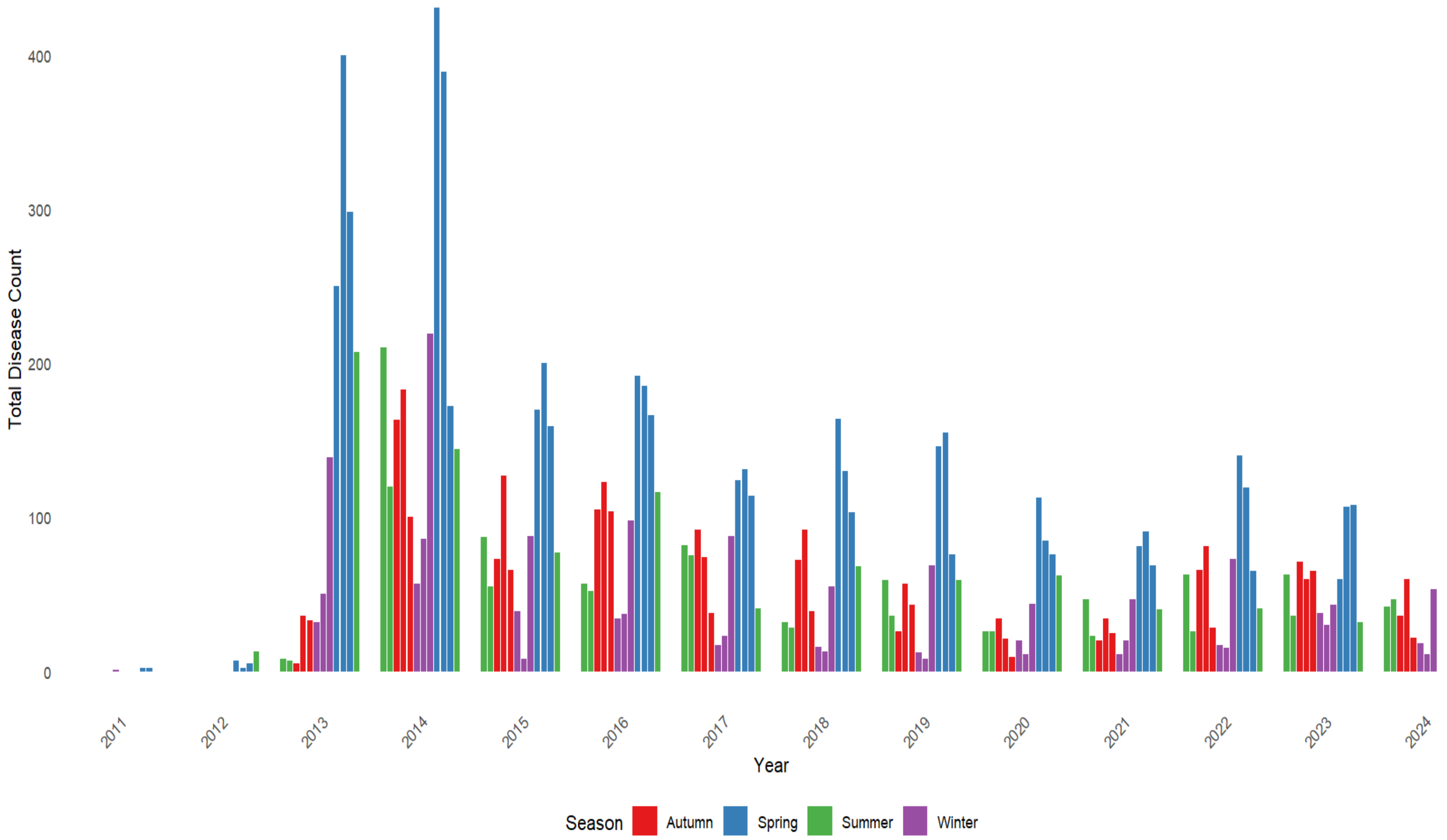

Figure 4: Number of confirmed cases of *Theileria* each month between 2011 and 2024. Bars coloured by seasons.

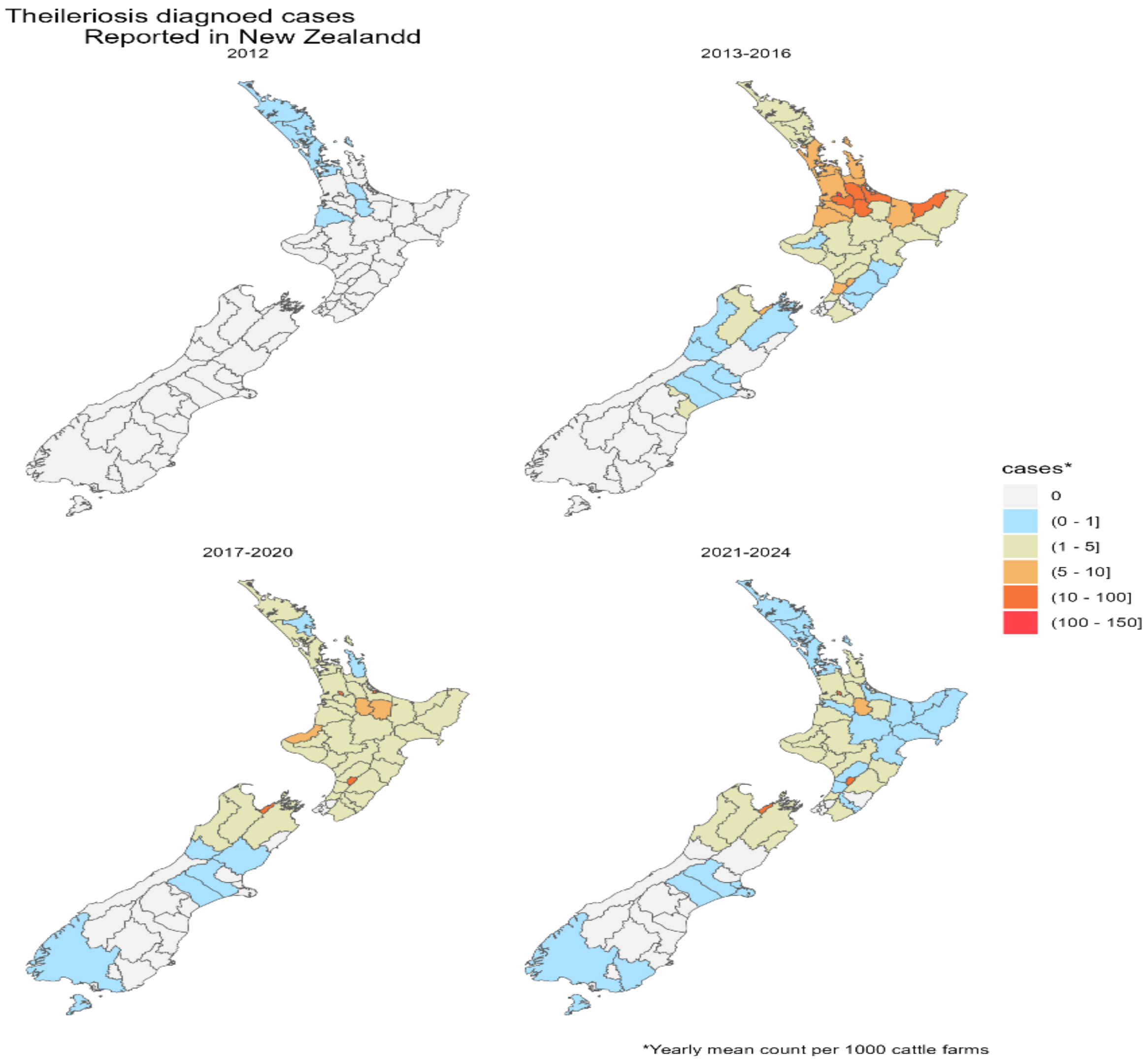

Figure 5: Maps illustrating the number of confirmed laboratory-diagnosed cases of theileriosis in each region of New Zealand from 2012, 2013-2018, 2017-2020, and 2021-2024.

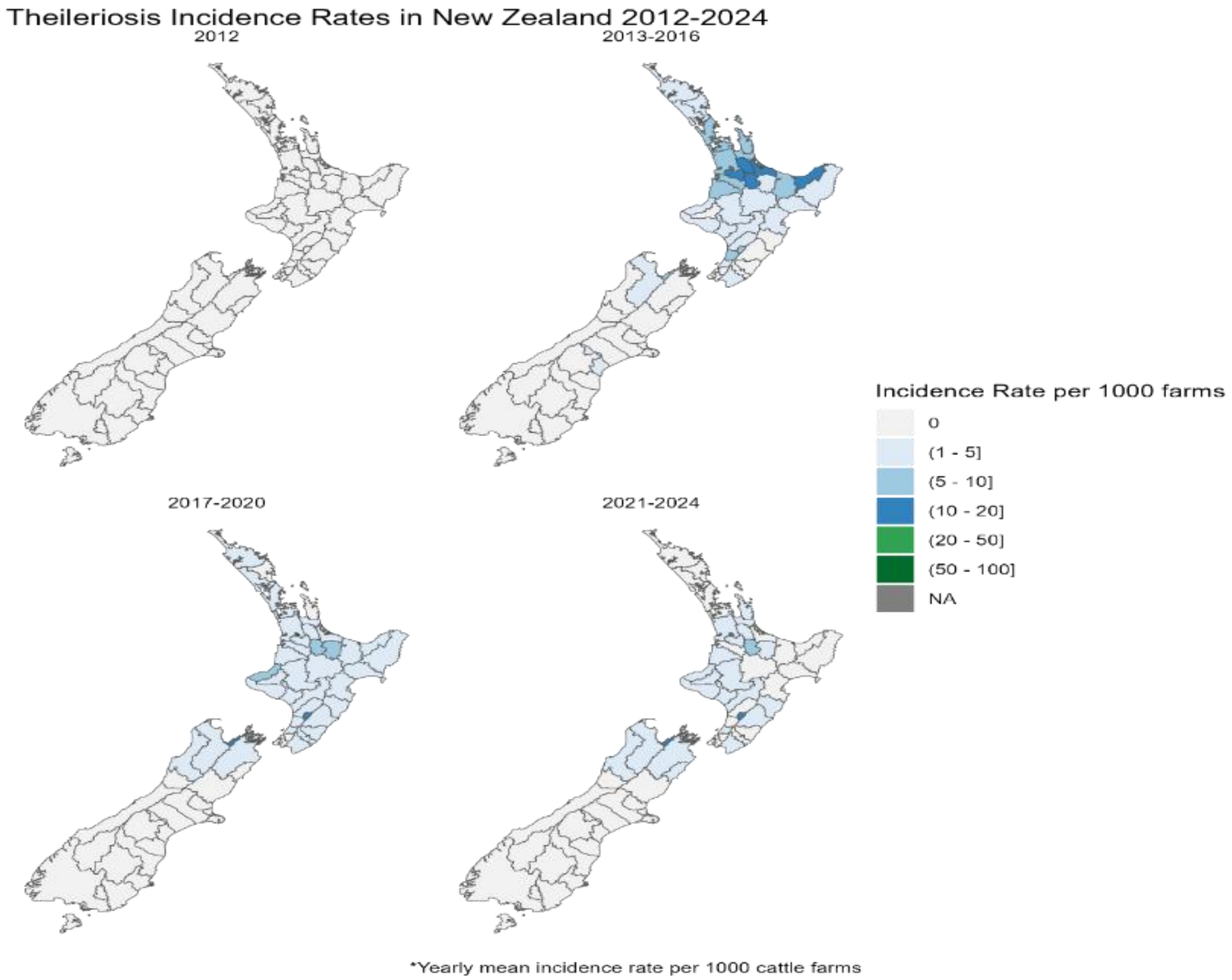

Figure 6: Maps illustrating the spatial distribution of theileriosis incidence rates across New Zealand from 2012 to 2024.

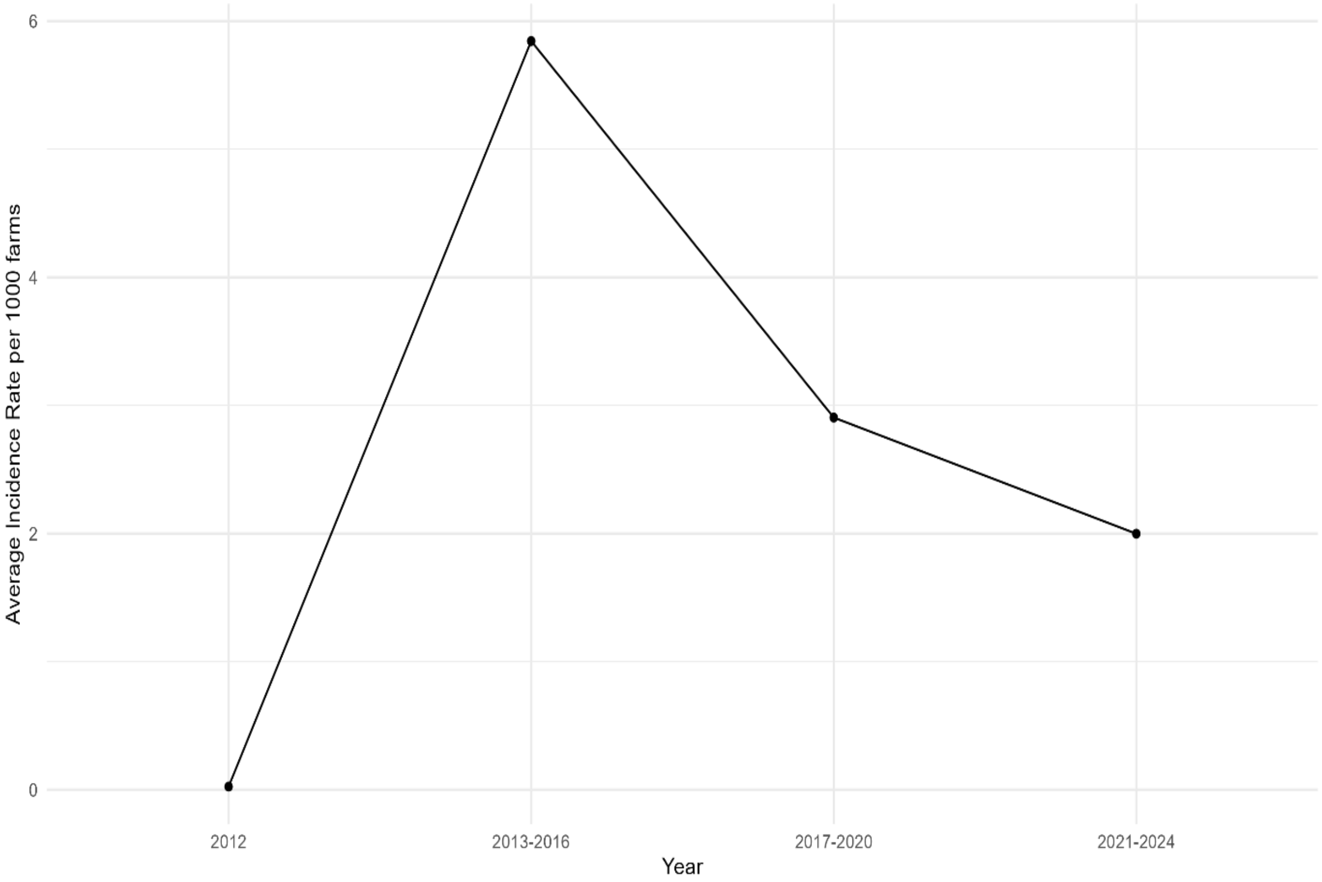

Figure 7: Timeline of the theileriosis incidence rates per 1000 farms in New Zealand from 2012 to 2024.

Table 8: Results of univariable negative binomial models for each climatic variable with the most significant variables with individual P-Values, Risk Ratios and the 95% Confidence Intervals.' 1.

Climate variable	Risk Ratio (RR)	95% Confidence Interval (CI)	P-Value
Annual mean rainfall (mm/year)	0.876	(0.813, 0.943)	< 0.001
Atmospheric pressure (hPa): 0-month lag	0.966	(3.844, 3.876)	< 0.001
Beef	1.006	(1.005, 1.008)	< 0.001
Dairy	1.004	(1.003, 1.006)	< 0.001
Latitude	2.205	(1.869, 2.602)	< 0.001
Longitude	2.230	(1.744, 2.852)	< 0.001
Maximum temperature (°C): 0-month lag	0.988	(0.973, 1.003)	0.1
Maximum Temperature (°C): -1-month lag	0.937	(0.924, 0.949)	< 0.001
Maximum Temperature (°C): -2-month lag	0.910	(0.898, 0.921)	< 0.001
Maximum Temperature (°C): -3-month lag	0.893	(0.882, 0.904)	< 0.001
Mean Annual Temperature (min/max °C)	1.272	(1.094, 1.479)	<0.01
Mean July maximum temperature (°C)	0.873	(0.801, 0.952)	<0.01
Mean July minimum temperature (°C)	0.869	(0.815, 0.926)	< 0.001
Median soil deficit (mm) January.	0.989	(0.987, 0.994)	< 0.001
Median Vapour Pressure from Feb-April (hPa)	1.446	(1.351, 1.548)	< 0.001
Minimum temperature (°C): 0-month lag	0.990	(0.9726, 1.008)	0.3
Minimum temperature (°C): 1-month lag	0.931	(0.916, 0.946)	< 0.001
Minimum temperature (°C): 2-month lag	0.898	(0.885, 0.912)	< 0.001
Minimum temperature (°C): 3-month lag	0.880	(0.867, 0.893)	< 0.001
Potential Evapotranspiration (mm): 0-month lag	1.149	(1.103, 1.197)	< 0.001
Potential evapotranspiration (mm): -1-month lag	0.948	(0.911, 0.986)	<0.01
Potential evapotranspiration (mm): -2-month lag	0.831	(0.801, 0.861)	< 0.001
Potential evapotranspiration (mm): -3-month lag	0.773	(0.747, 0.710)	< 0.001
Rainfall (mm): 0-month lag	0.987	(0.965, 1.010)	0.3
Rainfall (mm): -1-month lag	1.015	(0.992, 1.039)	0.2
Rainfall (mm): -2 months lag	1.042	(1.019,1.066)	< 0.001

Rainfall (mm): -3 months lag	1.049	(1.026, 1.073)	< 0.001
Relative Humidity (%): 0-month lag	0.950	(0.941, 0.959)	< 0.001
Relative Humidity (%): -1 months lag	0.995	(0.985, 1.005)	0.3
Relative Humidity (%): -2 months lag	1.030	(1.021, 1.040)	< 0.001
Relative Humidity (%): -3 months lag	1.055	(1.045, 1.064)	< 0.001
Soil Moisture deficit (mm): 0-month lag	1.003	(1.002, 1.004)	< 0.001
Soil Moisture deficit (mm): -1month lag	1.006	(1.005, 1.008)	< 0.001
Soil Moisture deficit (mm): -2-month lag	1.008	(1.007, 1.009)	< 0.001
Soil Moisture deficit (mm): -3-month lag	1.010	(1.008, 1.011)	< 0.001
Solar Radiation (MJ/m2): 0-month lag	1.039	(1.030, 1.049)	< 0.001
Solar Radiation (MJ/m2): -1 months lag	0.992	(0.983, 1.002)	0.1
Solar Radiation (MJ/m2): -2 months lag	0.957	(0.949, 0.965)	< 0.001
Solar Radiation (MJ/m2): -3 months lag	0.939	(0.932, 0.947)	< 0.001
Vapour Pressure (hPa): 0-month lag	0.969	(0.948, 0.991)	0.01
Vapour Pressure (hPa): -1month lag	0.909	(0.890, 0.927)	< 0.001
Vapour Pressure (hPa): -2month lag	0.875	(0.857, 0.890)	< 0.001
Vapour Pressure (hPa): -3-month lag	0.853	(0.837, 0.869)	< 0.001
Wind (m/s): 0-month lag	1.780	(1.609, 1.969)	< 0.001
Wind (m/s): -1month lag	1.508	(1.366, 1.665)	< 0.001
Wind (m/s): -2month lag	1.345	(1.214, 1.490)	< 0.001
Wind (m/s): -3-month lag	0.955	(0.865, 1.054)	0.4

Chapter 6 Discussion.

The systematic review aimed to identify and synthesise published evidence on the relationship between climatic variables and *Theileria orientalis* Ikeda. The review identified that climatic variables most frequently assessed across all studies in the review were 75% (30 studies) rainfall, 20% (8 studies) temperature and 5% (2 studies) extreme weather events as outlined in Table 4. The systematic review showed a consistent association between climate variables—particularly temperature, rainfall, humidity, and seasonality—and tick abundance and pathogen prevalence across diverse settings. These research findings from the systematic review were used to guide the identification and highlight gaps in temporal analysis for consideration in this thesis.

The second part (Chapter 4 to 7) of this research included the analysis of climate data in New Zealand, which explored the associations between climatic variables and the case counts of *Theileria orientalis* in cattle, using negative binomial statistical modelling. This analysis aimed to identify potential climatic predictors of *Theileria orientalis* risk and to improve understanding of how climatic variables may influence transmission dynamic over time (2012 to 2024) and space in the New Zealand context.

The regional breakdown, as shown in Table 7 and Figure 3, underscores the dominance of Waikato, which contributed nearly half of all cases (46.9%) across all years. Early cases were concentrated in Northland and Waikato, but by 2017–2020, new hotspots emerged in Taranaki and Manawatu-Whanganui, suggesting secondary transmission foci. The persistence of cases in these regions despite overall decline highlights the need for sustained surveillance and localized interventions.

The seasonal bar chart shown in Figure 4 adds a critical layer of insight: spring consistently shows the highest disease counts, especially during the epidemic peak years (2013–2015). This seasonal trend aligns with tick activity and cattle stress periods, reinforcing the biological plausibility of vector-driven transmission. Autumn and summer show moderate activity, while winter consistently records the lowest counts, likely due to reduced tick survival and host exposure. However, no statistical testing was conducted to confirm whether these seasonal differences are significant.

The epidemiological profile of *Theileria orientalis* Ikeda in New Zealand reveals a complex interplay between time, space, and seasonality. The spatial distribution maps and time series graph shown in Figure 5, Figure 6, and Figure 7, collectively illustrate the emergence and progression of *Theileria orientalis* Ikeda cases across New Zealand from its initial detection in 2012 to 2024. The maps in Figure 6 reveal a geographically uneven spread, with a higher incidence concentrated in specific regions, particularly in the upper North Island. This spatial clustering suggests localized ecological or management factors influencing transmission dynamics, such as tick habitat suitability, cattle movement patterns, and farm-level biosecurity practices.

The time series graph in Figure 7 complements this spatial narrative by quantifying the average incidence rate over successive periods. Following the initial detection in 2012, the incidence rate increased sharply from 2013 to 2016, peaking at approximately 4 cases per week. This surge likely reflects both the biological expansion of the pathogen and heightened surveillance efforts. The subsequent decline between 2017–2020 and further reduction in 2021–2024 (down to ~2 cases/week) may indicate improved disease management, increased farmer awareness, and possible herd immunity effects. These trajectories reflect the transition from outbreak to endemic status, shaped by ecological adaptation, host movement, and biosecurity responses.

Since the *Theileria* case data is from the MPI passive surveillance data system, it misses a lot of true infections and is subject to a few biases that could influence the outcome of the research. The potential biases to consider include socio-economic factors, environmental conditions, commodity prices, production system employees, animal value, cultural factors, diagnostic test cost/availability, location, use of in-house diagnostics rather than veterinary diagnostic laboratories, access to veterinary services, and development of health programs. The *Theileria* data were only available at the TLA level and is not considered at the locality of farms.

It is important to note that the results for the analysis presented here are based on univariable modelling, in which 43 climatic variables were tested independently for associations against the number of diagnosed *Theileria* cases from 2012 to 2024, as shown in Table 8. While this approach is useful for identifying potential associations, it does not account for confounding predictors or interactions between variables. As such, the relationship observed in these models should not be interpreted as causality. Furthermore, the climate and *Theileria* data used in this study were aggregated at the monthly level; this means that short-term biologically significant shifts in climatic variables are not captured. Monthly averages can smooth over important variations that might influence tick development or transmission risk. While these limitations are important to acknowledge, the results still provide valuable insights into potential climate-disease relationships. They serve as a foundation for future multivariable modelling efforts that adjust for multiple covariates and explore interactions, enabling more robust inference and climatic drives of *Theileria* spread in the cattle population in New Zealand.

The univariable analysis outlined in Table 8 shows that higher wind speeds in the current and previous two months were positively associated with increased *Theileria* case counts. In the same month, wind was associated with a 78% risk (RR 1.78) increase in *Theileria* cases. Likewise, high wind speed at previous two months also showed a statistically significant positive association, contributing to 50.8% (RR 1.51) and 34.5% (RR 1.34) increase in cases, respectively. From a biological perspective, the results suggest that both current and past two months' wind patterns contribute significantly to disease transmission dynamics, potentially by aiding vector dispersal at the larval and nympha stages of the life cycle of *Haemaphysalis longicornis*. This is supported by findings from studies that found that wind patterns can contribute to the dispersal of vectors like *Haemaphysalis longicornis* in the Oceania region (Lakew et al., 2023). The results could indicate that higher wind speeds in the current and preceding two months are significantly associated with increased *Theileria orientalis* cases, potentially due to enhanced tick dispersal, microclimatic shifts, or changes in cattle exposure. The absence of a statistically significant association at a three-month lag suggests that wind effects are most relevant over short timeframes, likely acting during active tick stages rather than shaping longer-term population dynamics.

Mechanical transmission by biting arthropods, which may be influenced by wind, has been identified as a potential transmission route for *Theileria orientalis* (Hammer et al., 2016). These findings are supported by a study done in India, which found that climatic factors, including wind speed, correlated with the prevalence of *Theileria orientalis,* suggesting enhanced vector mobility and host exposure (Deepa et al., 2024). Wind speed was not identified as a relevant variable during the systematic review and was not captured in past studies, such as Lawrence (2020). However, the results of this research showed a strong positive association between higher wind speeds and *Theileria* case counts during the present and the previous two months.

These findings could be ambiguous and should be interpreted with caution, as they are based on univariable modelling, which does not account for or indicate causality. The univariable models do not account for potential confounding factors or interactions with other climatic or ecological variables. It remains unclear whether wind speed plays a direct role in disease transmission, or if it is acting as a proxy for other environmental conditions that influence tick behaviour or cattle exposure. Therefore, further analysis using multivariable modelling is needed to determine whether this association holds when other variables are considered simultaneously.

The results in Table 8 also highlight vapor pressure as a significant climatic predictor for *Theileria orientalis* case counts in cattle, particularly during the February–April period, which could coincide with late summer to early autumn in New Zealand. Vapour pressure (hPa) recorded between February and April, demonstrating a positive association, 45% risk (RR 1.44) increases in *Theileria* case counts. This suggests that elevated vapour pressure is linked with higher disease case counts, due to enhanced survival or activity of the *Haemaphysalis longicornis* tick vector under more humid conditions. This is supported by findings from studies by Lawrence (2020), which states that the abiotic variable median vapour pressure for February to April measurement is suitable for the survival of the tick *Haemaphysalis longicornis* larval survival stages in New Zealand.

The positive association between vapour pressure could indicate that warmer, more humid months enhance *Haemaphysalis longicornis* tick activity and increase the diversity of circulating *Theileria orientalis*. High vapor pressure, which reflects higher ambient humidity at a given temperature, may improve tick survival off-host and prolong questing periods, increasing the likelihood of tick-host contact and disease transmission. Ticks like *Haemaphysalis longicornis* rely on high humidity for water uptake during non-parasitic stages, and elevated vapour pressure helps prevent desiccation, particularly during dry months like February to April in New Zealand (Lehane, 2005; Uhran et al., 2024). However, as vapour pressure is influenced by multiple factors, including but not limited to rainfall, and given that rainfall is not always a reliable proxy for humidity at regional scales (Alonso-Carné et al., 2015), the relationship may be more complex. Since the results from this research observed the association with vapour pressure in the months of February to April using univariable modelling, and because they do not indicate causality, as other confounding predictors must be assessed to fully determine the association of this abiotic factor.

The findings demonstrate a complex, lag-dependent relationship between potential evapotranspiration and *Theileria orientalis* cases, suggesting both promoting and suppressive effects depending on timing. Warmer and more humid conditions, as reflected by potential evapotranspiration in the current month, may support tick activity and disease transmission. Potential evapotranspiration was significantly associated with disease counts, but the direction of the association varied depending on whether it was the same month or at lag months. Potential evapotranspiration in the current month significantly contributed to a 15% increase in the risk of *Theileria* cases. The observed positive association between potential evapotranspiration and *Theileria* case counts suggests that warmer and drier atmospheric conditions may support active transmission and vector-host contact. However, the previous three months showed a negative association in *Theileria* case counts. These results suggest that lower potential evapotranspiration levels at the previous two and three months may create favourable moisture conditions for tick survival and development.

Linking these climatic conditions to the tick life cycle provides important biological context for the observed associations between vapour pressure and *Theileria orientalis* cases. Increased humidity during late summer and early autumn may support the survival and activity of larval and nymphal stages emerging during this period, leading to higher short-term transmission risk rather than long-term changes in tick population size. This temporal alignment helps explain why vapour pressure appears as a significant predictor within a defined seasonal window, rather than across the entire year.

Compared to other climatic variables, potential evapotranspiration reflects a combination of climatic variables—including temperature, solar radiation, wind, and humidity—that can influence tick activity and survival. This finding does not indicate causality, although results can contribute to insights by highlighting the statistical significance and time-varying impacts. However, further consideration in assessing other confounding predictors and interactions is important for assessing a better understanding of the associations of potential evaporation on *Theileria* case counts to forecast tick-borne disease dynamics. Since this was an univariable analysis, which means the associations have not been adjusted for other factors, this limit how confidently we can interpret them.

The result for the univariable analysis in Table 8 shows that temperature reflects a strong temporal lag effect, where prior months temperatures, particularly both for maximum and minimum temperatures at one to three months lags, showed significant inverse association with *Theileria orientalis* cases. Meanwhile, the mean annual temperature had a positive association with a 27% risk in disease cases, suggesting that warmer regions overall had higher *Theileria* cases. However, mean July maximum and minimum temperatures were inversely associated with disease, potentially suggesting seasonal cooling patterns that may coincide with increased tick activity or delayed disease expression.

This apparent contrast between short-term and long-term temperature effects may reflect different biological processes operating at distinct temporal scales. Warmer average annual temperatures may support the broader establishment and persistence of *Haemaphysalis longicornis* populations by enhancing developmental rates and extending the seasonal window for tick activity. Conversely, elevated temperatures in the months immediately preceding case detection may negatively affect tick survival, particularly during off-host stages, by increasing desiccation risk or reducing questing success. Such effects are consistent with the sensitivity of immature tick stages to temperature extremes and moisture availability.

The inverse association observed for mean July maximum and minimum temperatures further highlight the importance of seasonal timing. July represents mid-winter in New Zealand, and cooler winter conditions may coincide with reduced tick mortality, improved survival of overwintering stages, or delayed development that results in increased tick activity in subsequent months. Alternatively, these findings may reflect delayed disease expression, whereby infections acquired during cooler periods are detected later, producing an inverse association with winter temperatures at the population level.

While warmer climates overall may support the broader distribution and persistence of both *Theileria orientalis* and its vector, *Haemaphysalis longicornis*, short-term increases in temperature, particularly during the one to three months leading up to detection, may suppress transmission in certain ecological contexts. When compared to earlier studies such as Lawrance (2020), which reported mixed or neutral effects of temperature, the findings from this research cannot be directly compared or used to validate those results because they do not indicate causality. Future work should integrate multivariable models, vector presence data, and higher-resolution climate variables (e.g., weekly temperatures or humidity) to better understand these dynamics and improve disease forecasting in New Zealand.

The analysis in Table 8 shows that rainfall's effects on disease case counts are not immediate but is observed to increase at a two to three-months lag and are linked to a higher number of cases. Rainfall showed a complex and temporally variable relationship with *Theileria orientalis* case counts in New Zealand. While the animal mean rainfall (mm/year) was significantly negatively associated with *Theileria* case counts. These findings suggest that while areas with generally higher annual rainfall tend to have fewer *Theileria* cases, possibly due to landscape-level ecological factors such as pasture composition or farm infrastructure, short-term increases in rainfall are linked with higher disease risk in subsequent months. These findings can potentially highlight how rainfall creates moist environmental conditions that improve *H. longicornis* survival and reproduction.

Moisture-retentive environments are particularly important for tick egg laying, larval survival, and questing activity, which increases disease transmission to cattle. The high rainfall levels observed during the previous months could facilitate these major tick survival cycles in New Zealand. Compared to Lawrance (2020), which found no consistent association between rainfall and *Theileria orientalis* dynamics during the study period, this analysis reveals a potential association with rainfall levels, especially at lag month periods. However, these findings do not indicate causality as these are univariable model analysis and other confounding factors were not considered. Therefore, further multivariable analysis is needed to confirm these findings.

The results in Table 8 show that higher humidity in the previous two months was associated with an increase in the number of cases. Relative humidity was observed to have a positive association at the previous two month 3% and three month 6% risk of increase in *Theileria* cases. The positive associations at two and three month lags underscore the importance of environmental moisture in supporting tick populations, while the negative association at the current month suggests that overly humid conditions may suppress immediate vector-host interactions.

In comparison, Lawrence (2020) highlighted the ecological relevance of humidity for *T. orientalis*, though without quantifying its temporal influence. Even though findings are not causality, results could contribute to updated statistical evidence suggesting that if humidity plays a role, it may do so with a delayed effect rather than an immediate one. While this may indicate that elevated humidity in preceding months could play a role in supporting disease transmission, the results should be interpreted cautiously given the limitations of the univariable modelling approach implemented in this research. Therefore, further multivariable analysis is required to assess these associations alongside other confounding predictors.

Apart from climatic variables, the demographic and spatial variable predictors were also statistically significant in the analysis. The beef and dairy variables had a low risk of increased *Theileria* cases, whereas latitude and longitude were observed to have a significantly high risk of disease counts. This indicates that these factors are also important in considering *Theileria* cases, but further investigation and multivariate modelling is required to determine the confounding impacts with other variables.

Chapter 7 Conclusion.

This research, through a combination of systematic review and epidemiological analysis, highlights the need for continued investigation into the relationship between climate variables and cases of *Theileria orientalis* in New Zealand. The systematic review revealed a limited focus on *Theileria orientalis* and its primary vector *Haemaphysalis longicornis*, indicating both data gaps and geographical limitations in current literature. Given the emergence of *Theileria orientalis* Ikeda in New Zealand cattle since 2012, and the growing global evidence linking climate change to vector-borne disease patterns, there is a clear and urgent need for localised studies that integrate climatic, vector and disease surveillance data to inform predictive modelling and outbreak preparedness.

The univariable negative binomial modelling conducted in this study identified significant associations between climatic variables, such as wind speed, vapour pressure, potential evapotranspiration, temperature, rainfall, and relative humidity, with *T. orientalis* cases in New Zealand. These findings are valuable and can be used as a baseline for further investigation and modelling. While informative, these results must be interpreted with caution, as univariable models did not account for complex interactions between variables or provide causal inference. Future research should employ multivariable modelling techniques to assess whether these associations remain significant when controlling for potential interactions, confounding factors and collinearity.

Additionally, this study utilised monthly aggregated climate and disease data, which my overlook important short-term fluctuations. Incorporating higher resolution such as daily and weekly data in future analysis could improve the understanding of temporal dynamics in disease risk. Overall, the findings of this research contribute valuable insights into climate-disease relationships, which can serve as a foundation for future work and application of more advance modelling such as principal component analysis (PCA) or machine learning approach.

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