Characterising a sarcoptic mange epizootic in quenda (*Isoodon fusciventer*)

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Sarcoptic mange, a parasitic skin disease caused by *Sarcoptes scabiei,* is an emerging conservation threat to some Australian wildlife species. As a zoonotic and multi-host disease, it has the capacity to exploit different hosts, creating management challenges for susceptible wildlife populations that may suffer high rates of morbidity and mortality. Sarcoptic mange was identified in quenda (*Isoodon fusciventer*) in a peri-urban region of Perth, Western Australia in 2019. By mid-2021, reported cases were distributed across 107ha. This retrospective study reviews the spatiotemporal distribution, clinical signs and risk factors for sarcoptic mange in quenda from a metropolitan region. Preliminary epidemiological parameters for the outbreak are described, including period prevalence of infested individuals, spatiotemporal analyses, clinical signs of mange, and preliminary risk factor analyses. The period prevalence of sarcoptic mange between July 1, 2019 and June 30, 2021 was 26.9% (CI 95%; 21.2, 33.5) with a mortality rate of 39.6%, owing to severity of disease or secondary complications. Sarcoptic mange was detected more frequently in adult quenda than juveniles (OR: 176.8, CI 95%: 10.7, 2930.1), with adult males more affected than adult females (OR: 3.5, CI 95%: 1.5, 8.4). Clinical signs of disease presented on the rump and tail (100%), followed by the limbs and digits (61.5%). The most common clinical signs recorded were alopecia (92.3%), erythema (46.2%) and open wounds (42.3%). This is the first documented example of a geographically expanding and propagating epizootic of sarcoptic mange in quenda, with implicit welfare and conservation concerns for the species, alongside potential for cases in humans and domestic species that cohabit with or handle quenda in the urban environment. Further, the detection of cases through wildlife rehabilitation centres highlights the critical role such organisations play in conservation and passive surveillance for wildlife diseases of conservation or public and domestic animal health importance.

Abstract

1. Introduction

Sarcoptic mange, caused by the *Sarcoptes scabiei* mite, is a globally present and emerging parasitic skin disease (Escobar et al., 2021), noted to have profound impacts on some Australian wildlife (Fraser et al., 2016). Sarcoptic mange has been identified as a threatening process in bare-nosed and southern hairy-nosed wombats (*Vombatus ursinus* and *Lasiorhinus latifrons*) where it has caused localised extirpations (Fraser et al., 2016; Martin et al., 2018), and has also become emergent in populations of koalas and wallabies (Skerratt, 2005; Speight et al., 2017). The ongoing impact of *S. scabiei* on wildlife in the south-eastern region of Australia highlights the need to investigate epizootics in their early stages, to determine the scale of welfare and conservation impacts, and whether management intervention is warranted. Given the synergistic impacts of climate change mechanisms (species redistribution, extreme weather events, changing resources), ongoing habitat modification, urban expansion, and other stressors on population health, we

must be ready for further emergence of multi-host diseases that are exacerbated by naivety or host immune compromise.

Sarcoptic mange in quenda (*Isoodon fusciventer*), a bandicoot species endemic to Western Australia, was first reported in 2007 (Wicks et al., 2007). However, this publication was based on the presentation of sarcoptic mange in a single animal. With no cases of sarcoptic mange reported in quenda in the literature since, and an absence of any spike in anecdotal reports from those handling quenda regularly (wildlife centres and wildlife officers), it is likely this case was a sporadic spillover event from a sympatric and endemically affected reservoir species, such as the introduced European fox (*Vulpes vulpes*) (Skerratt et al., 1998). However, between September 2019 and June 2021, 53 quenda from a localised area of Perth, Western Australia, were admitted to a local wildlife rehabilitation centre for treatment of a skin disease, which was confirmed by microscopy as sarcoptic mange. In contrast to the former published literature and data held in rehabilitation records, this seemed a propagating event unlike any seen before in quenda.

Quenda are currently classified as a Priority 4 species under Western Australian legislation, which indicates that they are rare or near

List of abbreviations

BPCV2	Bandicoot Papilloma-Carcinomatosis Virus (Type 2)
CI	Confidence interval
DPIRD	Department of Primary Industries and Resource Development
DRWS	Darling Range Wildlife Shelter
GIS	Geographic Information System
KDE	Kernel Density Estimation
KWRC	Kanyana Wildlife Rehabilitation Centre

threatened and require regular monitoring (Ottewell et al., 2019). Despite this, there is limited health surveillance data available for the species in the region. The emergence of sarcoptic mange in a host species where epizootics have not previously been detected is concerning given the multiple threats already faced by native mammals in this region (Hillman, 2016). The aetiology and pathogenicity of sarcoptic mange in an individual can vary depending on host species, immunological status, environmental stressors and physiological attributes (Pence and Ueck-ermann, 2002; Sarasa et al., 2010). This makes it challenging to assess the potential population impacts of an outbreak such as this in the absence of formal outbreak investigation and follow-up monitoring of both disease status and population parameters.

A retrospective study of opportunistic data from cases and non-cases of sarcoptic mange in quenda admitted to wildlife care centres was conducted, with the aim to a) characterise the spatiotemporal patterns of disease including period prevalence, b) describe the clinical signs and distribution of lesions in this species, c) establish risk factors for clinical disease, and d) determine the mortality rate of quenda admitted to wildlife care facilities with sarcoptic mange. Collectively, these aims contribute to our understanding of the individual welfare impacts of disease, as well as inferring potential population scale impacts that can inform future research hypotheses and management objectives. Importantly, they provide a baseline for ongoing surveillance of this apparently emerging disease in this species and region.

2. Materials and methods

Quenda admission records from two wildlife rehabilitation centres, Darling Range Wildlife Shelter (DRWS) and Kanyana Wildlife Rehabilitation Centre (KWRC) over a two-year period from July 1, 2019 to June 30, 2021, were collated, incorporating variables such as location found, weight, sex, clinical presentation, and outcome. A case definition for sarcoptic mange was established based on presence of one or more characteristic clinical signs (pruritis, alopecia, erythema, epidermal hyperkeratosis or deep skin fissures), and evidence of sarcoptiform mites on light microscopy from skin scrapings.

DRWS and KWRC are both located in the Perth hills region and most commonly receive quenda from the suburb of Roleystone and its surrounding areas. Data was reviewed for accuracy and completeness. Incomplete or inconsistent records that could not be corrected for the purpose of an analysis were excluded from that analysis, except where indicated. Where quenda had been transferred between the two shelters for care, records were pooled into a single admission to prevent duplication.

The records identified age on admission as 'pinkie', 'pouched young', 'juvenile' or 'adult'. To reduce the risk of misclassification bias using a subjective measure, standardised criteria were applied for age class. In previous studies, classification between juvenile and adult quenda was determined by scrotal size in males and the presence or absence of a parous pouch in females (Hillman et al., 2017), however this information was not routinely collected for admissions. Instead, age class was allocated against age-weight thresholds (Read, 2016), with additional information from clinical observations included to reclassify each quenda into the age class of joey, juvenile or adult (Supplementary Table 1).

2.1. Prevalence and risk factor analysis

Epitools (Sergeant, 2018) was used to perform statistical analyses including odds ratios with 95%CI for univariate risk factor analyses (age, sex, presence of pouched young). Prevalence was determined with 95%CI using the Wilson score interval. Due to the differing reporting formats and database limitations between both wildlife rehabilitation facilities, a subset of the full dataset was used for risk factors of interest.

2.2. Diagnostics and molecular analysis

Crusted skin sections were collected from a deceased quenda with advanced sarcoptic mange and provided to Murdoch University to confirm the presence of *S. scabiei* by microscopic and molecular methods in order to provide rigorous confirmatory evidence of the disease. Individual mites were extracted from a crusted skin section taken from a deceased Quenda and observed under light microscopy for taxonomic identification. Pooled mites extracted from a single crusted skin section were digested in proteinase K for 48 h at 56 °C before DNA extraction using a Qiagen DNeasy blood and tissue kit (Qiagen, Hilden, Germany). Extracted DNA was then amplified by PCR at the cox1 gene as per published protocols (Andriantsoanirina et al., 2015; Fournier et al., 1994). Purified amplicons were sequenced in both directions using an ABI Prism Dye Terminator Cycle Sequencing Kit (Applied Biosystems, Foster city, CA, USA) as per manufacturer's instructions. Resultant cox1 sequences were compared with available published sequences on Gen-Bank using the basic local alignment search tool (BLAST) (http://www.ncbi.nlmn.nih.gov/BLAST) with further analysis of sequence alignments using ClustalW in MEGA X (Kumar et al., 2018). Published sequences for Australian human and animal hosts were sourced from Fraser et al. (2017) and used for phylogenetic analysis conducted in MEGA X (Kumar et al., 2018). Phylogenetic relationships were inferred with the neighbour-joining method, with a bootstrapping of 1000 replicates and evolutionary distances calculated using the Kimura 2-parameter method (Kimura, 1980; Saitou and Nei, 1987).

2.3. Clinical presentation

Cases of sarcoptic mange were diagnosed through clinical examination of each animal on admission and, when the disease was suspected, the collection of diagnostic skin scrapings and microscopy. The positive visual identification of *Sarcoptes* sp. to genus level provided confirmation of the disease in the animal and treatment was commenced. This diagnostic method combining clinical examination with microscopy provides confidence of diagnosis with a specificity of 100% and sensitivity of 87% (Moog et al., 2021; Valldeperes et al., 2019). The clinical records for a subset of these cases were reviewed to determine common clinical signs in sarcoptic mange-affected quenda in the current outbreak.

2.4. Spatiotemporal analysis

All quenda admissions to DRWS and KWRC from the study period were categorised into the suburb from which they were received and analysed for the presence or absence of the disease. Confidence of freedom (or likelihood of detecting one infected individual) was calculated based on sample size by suburb in Epitools (Sergeant, 2018) using the following assumptions: diagnostic test sensitivity of 87%, specificity of 100% and prior or expected prevalence of 26.9% (reflecting the prevalence of disease found in the Roleystone population).

Quenda home ranges vary based on sex, resource availability and population density (Broughton and Dickman, 1991; Paull et al., 2008)

and are reported to be between 2 and 7 ha for males and 1–3 ha for females (DEC, 2012). Therefore, the potential geographic extent of an outbreak will lie beyond the boundary of case locations. To account for the possibility that quenda were located at the edge of their home range upon capture, a radius of double their maximum home range radius was used to determine the maximum extent to which they would likely transmit the disease. This was 298 m and 196 m for males and females respectively.

Case density and potential geographical extent over time was determined using Kernel Density Estimation (KDE) and the Time Slider tool in ArcGIS (Silverman, 1986). This analysis can provide an effective visualisation of the clustering or dispersal of a disease in an area through contoured hotspots (Murad and Khashoggi, 2020). Case density contour maps were created using the location data of *S. scabiei* infested quenda and a defined search radius (bandwidth) of 298 m.

3. Results

During the study period (September 2019–June 2021), 754 quenda from across Perth, ranging in age from pouched joey to adult, were admitted to DRWS or KWRC. A total of 26.1% (197/754) were from the suburb of Roleystone, of which 26.9% (CI 95%; 21.2, 33.5) were diagnosed with sarcoptic mange. The initial case in the current outbreak was identified in September 2019.

3.1. Prevalence and risk factor analysis

There were 53 cases of sarcoptic mange in quenda during the outbreak from a total of 197 admissions of quenda from the Roleystone area (Fig. 1). The overall prevalence of sarcoptic mange in quenda admissions was 26.9% (CI 95%; 21.2, 33.5). There were no records of juveniles or pouched joeys diagnosed with sarcoptic mange, thus adults were significantly more likely to present with the disease (OR: 176.8, CI 95%: 10.7, 2930.1, p=<0.0001). The age of 19 of the admitted quenda was unknown, however none of these individuals were diagnosed with the disease. Of the 53 adult quenda that were diagnosed with sarcoptic mange, 21 were female, 31 were male and the sex of one animal was

unknown. Male quenda were significantly more likely than females to be admitted with sarcoptic mange (OR: 3.5, CI 95%: 1.5, 8.4, p = 0.0003). The sex of four of the adult admissions was not specified. Nine of the 21 females admitted with sarcoptic mange were carrying pouched young, however this was not a significant risk factor for disease (OR: 2.6, CI 95%: 0.8, 8.6, p = 0.11).

Of the 53 recorded cases of sarcoptic mange, 21 quenda died or were humanely euthanised due to disease progression or severe secondary complications, such as infected wounds or respiratory disease that did not respond to treatment, resulting in a mortality rate of 39.6%. The remaining 32 quenda were successfully treated, rehabilitated, and returned to their environment.

3.2. Diagnostics and molecular analysis

Skin scrapings from all clinically affected individuals contained sarcoptiform mites based on identification at DRWS. The skin sample from the affected individual submitted to Murdoch University contained a high load of mites which were all morphologically identified as *Sarcoptes* sp. with molecular characterisation of a single representative sample confirming these to be *Sarcoptes scabiei* (GenBank accession no. OM349485). The phylogenetic analysis of the Quenda *Sarcoptes* sequence with published *Sarcoptes* sequences obtained from a range of Australian human and animal hosts placed the Quenda mite with wombat mites sourced from NSW (Supplementary Fig. 1). Nodal support for this specific placement was not strong, however overall support for placement within *Sarcoptes scabiei* was provided.

3.3. Clinical presentation

A subset of 26 clinical records was reviewed to determine common clinical signs in sarcoptic mange-affected quenda. In these cases, clinical signs of sarcoptic mange were found most frequently on the rump and tail (100%), followed by the limbs and digits (61.5%) (Fig. 2). In quenda that were exhibiting clinical signs of sarcoptic mange, the disease appeared to progress from the tail or rump to the flanks and limbs, body and face. The frequency of key clinical signs has been detailed in Table 1
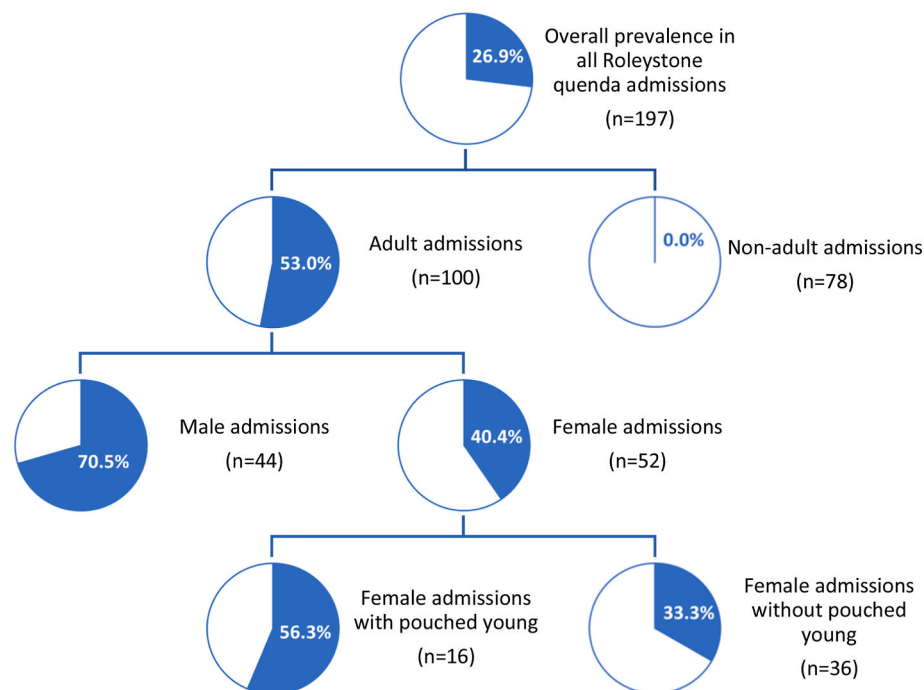

Fig. 1. Prevalence of sarcoptic mange in population groups of quenda (*Isoodon fusciventer*) admitted to care from Roleystone, Western Australia between July 1, 2019 and June 30, 2021.
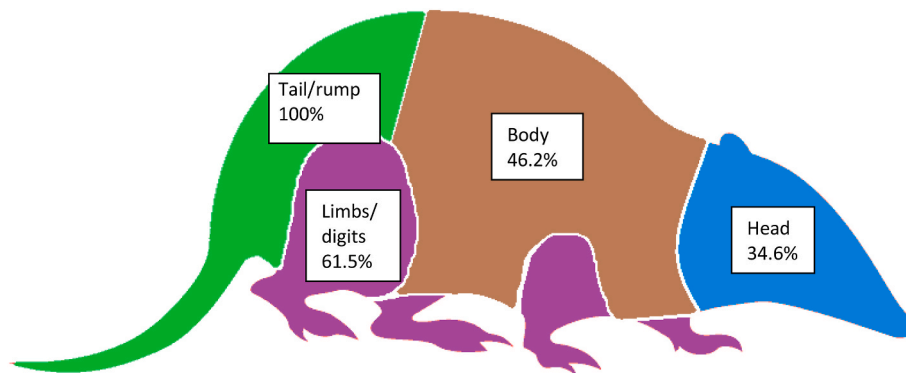
Fig. 2. Frequency of infestation by location on the body recorded from 26 quenda (*Isoodon fusciventer*) with sarcoptic mange admitted to care at Darling Range Wildlife Shelter from Roleystone, Perth, Western Australia from July 1, 2019 to June 30, 2021. (Image: Katerina Ryabtseva).

Table 1

Frequency of clinical signs and comorbidities recorded in 26 quenda (*Isoodon fusciventer*) with sarcoptic mange admitted to care at Darling Range Wildlife Shelter from Roleystone, Perth, Western Australia from July 1, 2019 to June 30, 2021.

Disease phase (León-Vizcaíno et al., 1999)	Clinical Signs and comorbidities	Frequency of detection (%) (number of cases)
Developmental	Erythema	46.2 (12)
Consolidation	Alopecia	92.3 (24)
	Epidermal hyperkeratosis	26.9 (7)
	Open wounds	42.3 (11)
	Lethargy	38.5 (10)
Chronic	Deep dermal fissures	7.7 (2)
	Emaciated	7.7 (2)
Other	Cellulitis	11.5 (3)
	Papilloma-type lesions	15.4 (4)
	Respiratory tract infection	7.7 (2)
	Dental disease	11.5 (3)
	Other ectoparasites	61.5 (16)
	Endoparasites	38.5 (10)

and classified into the three main phases of the disease: developmental, consolidation, and chronic (León-Vizcaíno et al., 1999). The most common clinical signs recorded were alopecia (92.3%), erythema (46.2%) and open wounds (42.3%). Images of these clinical signs occurring in quenda have been provided in Fig. 3. Clinical signs associated with the consolidation phase of the disease were evident from September 2019 and admissions of quenda experiencing evidence of the chronic disease phase commenced in April 2020. Ectoparasites other than *S. scabiei* were present in 61.5% of quenda with sarcoptic mange and 38.5% were diagnosed with endoparasites. Papillomatous lesions were observed in 15.4% of the reviewed cases. These lesions were only observed in quenda with sarcoptic mange, with next generation sequencing and BPCV-1 PCR screening by the WA Department of Primary Industries and Resource Development (DPIRD) unable to identify a papilloma virus, nor any histopathological evidence of papilloma-virus in a single set of tissues examined. Investigation is ongoing to determine whether these lesions are a nodular manifestation of the disease.

3.4. Spatiotemporal analysis

Confidence of freedom from disease (the probability of finding disease if it were present, based on a given sample size) was determined for areas beyond the known case locations in the study area for the outbreak period, using data on quenda admissions from surrounding suburbs. Data were not available for all suburbs in the Perth region, however neighbouring suburbs of Roleystone had a high confidence of freedom

from sarcoptic mange, given the sample sizes of admitted quenda, and the specified prevalence of 26.9%. Other suburbs that are known to have high populations of quenda (Howard et al., 2014) also had sufficient sample sizes to provide a high confidence of freedom from disease during the period of the study (Supplementary Fig. 2).

A potential home range was determined for each quenda diagnosed with sarcoptic mange based on the known home range extent for their sex. Thirty-one males, 21 females and one quenda of unknown sex were admitted for sarcoptic mange. The quenda of unknown sex was allocated a male home range to represent the maximum potential area that an individual quenda may spread the disease. The combined buffer area of all cumulative sarcoptic mange cases has identified spatial connectivity between all mange cases recorded since September 2019, forming a potential outbreak area of 297 ha (Supplementary Fig. 3). Over the two-year study period, the disease has spread a linear distance of approximately 1 km from the first reported case.

The spatiotemporal review of sarcoptic mange cases identifies a linear increase in spatial distribution of cases during the outbreak period, indicating that the potential extent of the outbreak increased by 760% over an 18-month period. Maximum case densities also increased from 0.5 to 2.6 cases per hectare as additional animals from the area were diagnosed with the disease (Fig. 4).

4. Discussion

This study provides the first documented evidence of a sustained epizootic of sarcoptic mange in quenda (*Isodoon fusciventer*) of Western Australia, in contrast to prior reports of sporadic cases in this species. Case admissions suggest that quenda are highly susceptible to the disease, presenting with severe and chronic forms of the disease during the study period, with a high mortality rate (39.6%) for animals receiving care and treatment. Based on the retrospective wildlife care data, the outbreak appears to be spreading steadily through a peri-urban area towards bushland. Age and sex correlated with a significantly higher likelihood of sarcoptic mange in the study area, with adult males most likely to be admitted with the disease. To develop an appropriate management strategy for this emerging disease with marked welfare implications, targeted epidemiological investigations are required to determine key elements such as the reservoir source for the outbreak, cross-species transmission capacity, and the extent of spread into surrounding regions. Given the multi-host nature of sarcoptic mange, this study highlights the value of wildlife rehabilitation centres as early detection tools for emerging infectious diseases at the wildlife-human-domestic animal interface.

The relative visibility of quenda in urban environments through opportunistic sightings and targeted biodiversity surveys, alongside the limited awareness of mange cases in anecdote or published literature since 2007 (Wicks et al., 2007), suggests the events in Roleystone are an
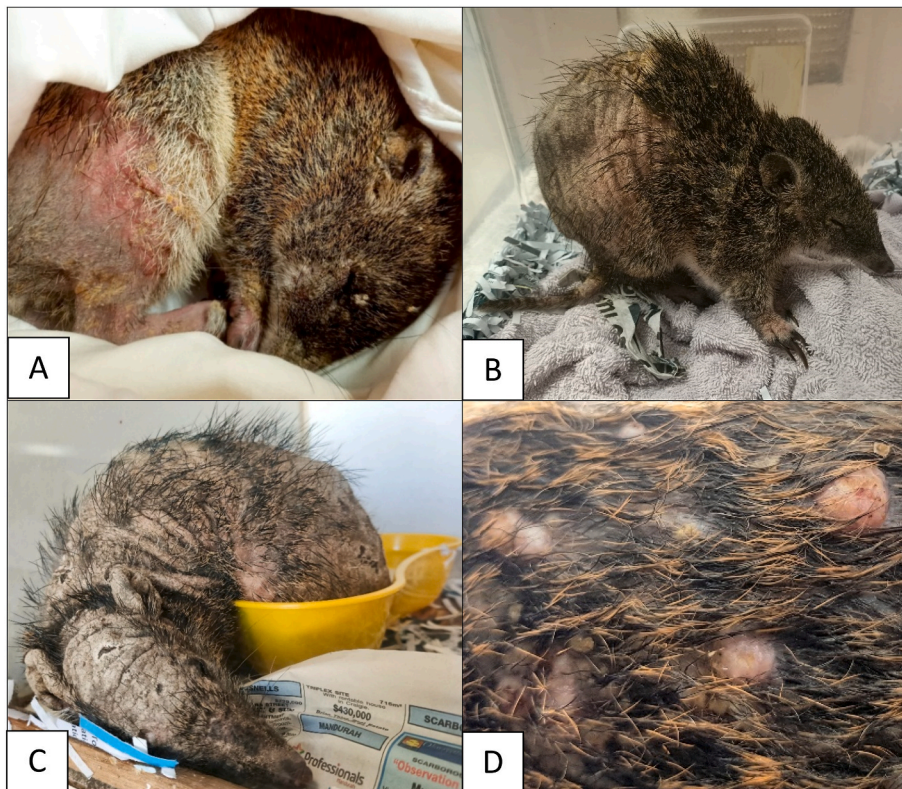
Fig. 3. Common clinical signs of sarcoptic mange in quenda (*Isoodon fusciventer*) from Roleystone, Perth, Western Australia in animals admitted to Darling Range Wildlife Shelter between July 1, 2019 and June 30, 2021. A: The early consolidation phase of the disease, with visible erythema and alopecia on rump, flanks and paws and lesions developing on the face; B: Alopecia and emaciation in a quenda undergoing treatment; C: Severe chronic disease evident by extensive deep fissures throughout the epidermis, emaciation, hyperkeratosis, alopecia and lethargy; D: Papillomatous lesions on the posterior dorsal region of a quenda undergoing treatment for sarcoptic mange. (Images: Darling Range Wildlife Shelter).

outbreak identified in real-time, potentially following a spillover event from a reservoir species. The consistent presentation of sarcoptic mange on the tail and rump area of quenda contrasts with bare-nosed wombats (*Vombatus ursinus*) and the Spanish ibex (*Capra pyrenaica hispanica*) where mite loads are lowest in rump and flank areas and highest on the head (León-Vizcaíno et al., 1999; Skerratt et al., 1999). Whilst quenda also presented with disease in ventral areas of thin, soft skin, the posterior region was most consistently affected by sarcoptic mange. Direct contact between quenda can occur through mating and fighting and indirect contact can occur through rubbing or scratching on fomites, which are all activities that may result in *S. scabiei* contacting the posterior region of an animal (Browne et al., 2022). Fomites may include rocks or tree trunks or the soil within dens or burrows that have been created by reservoir species such as foxes or rabbits, and have been established as a potential transmission source for *S. scabiei* in wombats (Browne et al., 2021; Skerratt et al., 1998).

Several comorbidities were observed in quenda affected by sarcoptic mange, such as respiratory tract infections, characteristic papillomatous lesions, dental disease, and the presence of endoparasites and other ectoparasites. Unfortunately, specific detail on parasite burdens was not obtained in this study. While healthy quenda are known to host a range of parasites (Hillman et al., 2017) the intensity and prevalence of parasites is often increased in immunocompromised hosts. Without further characterisation of the species and burdens of these various parasites, it is not possible to determine any specific associations. However, the growth of papillomatous lesions in some individuals appears to be either a unique clinical sign or a comorbidity to sarcoptic mange. Nodular lesions have been observed in *S. scabiei* infestations of other species including gazelle (*Gazella subguttarosa*) (Bazargani et al., 2007) and one-humped camels (*Camelus dromedarius*) (Ahmed et al., 2020), and can present in humans with nodular scabies (Hengge et al., 2006). If these lesions are identified in quenda in the future, histopathology and further targeted PCR testing as well as next generation sequencing to identify novel agents of disease should be undertaken on tissue samples. Alongside quantitative measures of health (e.g. haematology, body condition scoring, endo and ectoparasitic burdens), such investigations will help clarify whether papillomatous lesions are a manifestation of mange in quenda, or related to co-existing infectious disease and poor health.

The spatiotemporal review of sarcoptic mange cases has shown that the extent of the outbreak and case densities have steadily increased over time. The high confidence of freedom from sarcoptic mange in the peri-urban suburbs surrounding Roleystone indicate that despite the same human-animal-environment interface, the disease has not yet established beyond the known outbreak area. It is unlikely that this localised outbreak has dispersed into quenda in other areas of the Perth region, although surveillance in other areas would provide a larger sample size and confirm the absence of sarcoptic mange of any origin in quenda. The extent of the outbreak may be greater in bushland areas with lower human population densities, as this may reduce the likelihood of unwell animals being observed and subsequently admitted to wildlife shelters. The urban areas within Roleystone to the southwest and northeast of the outbreak area consistently received admissions that were free of disease, suggesting the outbreak had not yet extended into those areas at that time. A targeted surveillance program, alongside education and extension work to raise awareness in those living or working with quenda, would provide additional data to inform the true and current extent of sarcoptic mange in quenda in the area and increase certainty in determining the potential extent of this outbreak within and beyond the suburb.

The rate of spread of approximately 1 km over two years is moving more rapidly than the movement of the mange front reported in a wombat population in Tasmania, which spread a similar distance over a period 1.5 times greater and resulted in a 94% decline in wombat population in the area (Martin et al., 2018). Exponential spread of the disease is possible, as has occurred in wild mammals across Europe over the last 30 years (Pisano et al., 2019). However, a steady, linear dispersal has been observed instead, which may be partially attributed to the success of the treatment program at DRWS, with proactive trapping and treatment conducted on properties where diseased animals
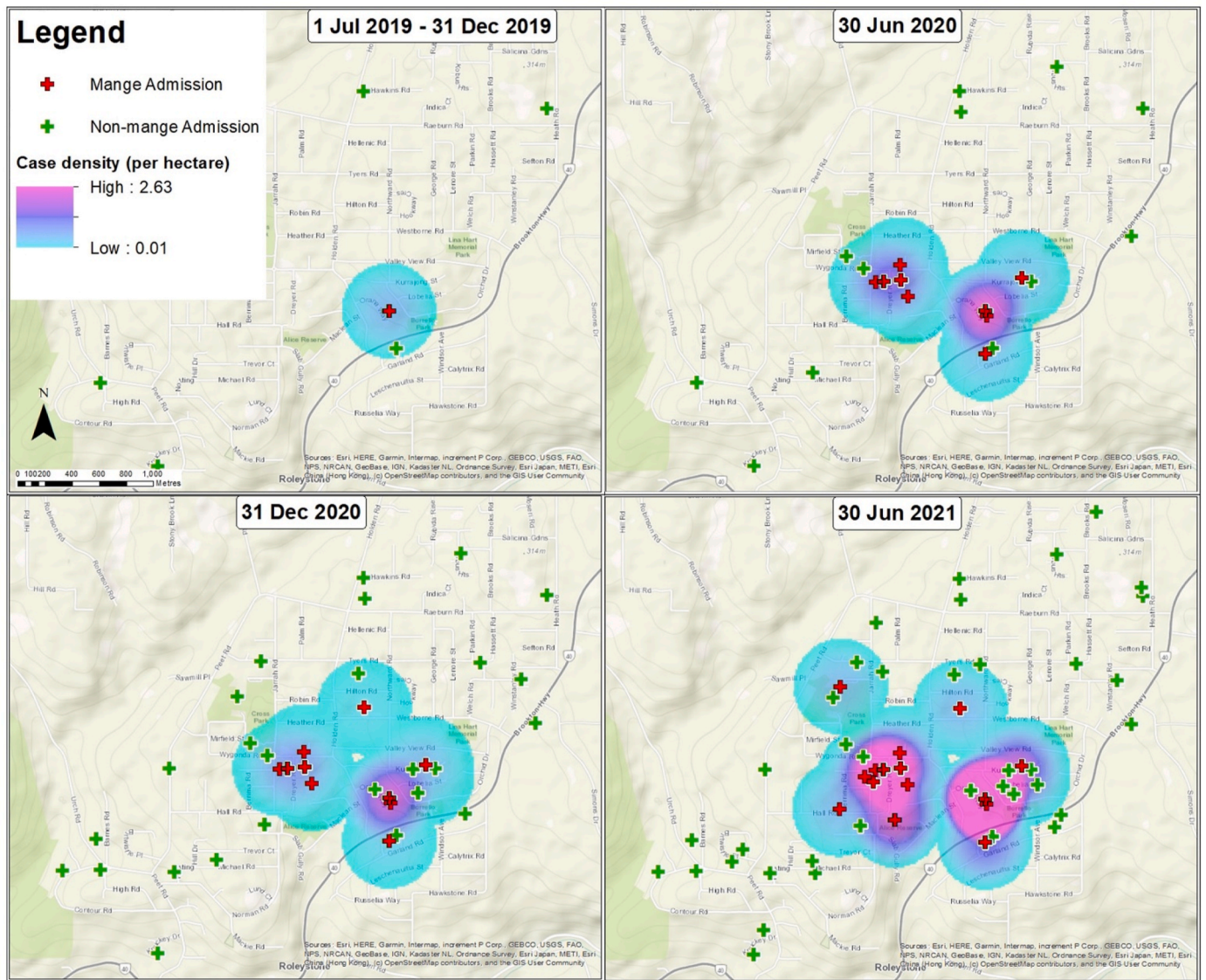
Fig. 4. Density of sarcoptic mange cases in quenda (*Isoodon fusciventer*) and potential outbreak extent in Roleystone, Perth, Western Australia from July 2019 to June 2021.

have been observed. At the very least, these actions have resolved the debilitating symptoms of dozens of quenda since this outbreak began.

Adult quenda may be more susceptible to sarcoptic mange than pouched joeys and juveniles due to an increased risk of exposure to *S. scabiei* through contact with other quenda and fomites within their home range (Browne et al. 2022). Adults also have greater exposure to environmental stressors, which may result in compromised immunity and greater susceptibility to disease (Bradley and Altizer, 2007). Despite the close and prolonged contact of joeys with infested mothers and the detection of sarcoptic mange in joeys at foot in other marsupial species such as bare-nosed wombats (Hartley and English, 2005), quenda joeys appear to be less susceptible to the disease in this study, although we note the small sample sizes from which to infer this. There is also a possibility that joeys contract the disease and it progresses rapidly to death, however as quenda mothers are known to cannibalise their young it is unlikely such a scenario would be easily detected (Jackson, 2003).

It is likely the mortality rate (39.6%) is higher in the natural environment, as this value reflects animals that have been targeted in known mange hotspots, admitted to care and undergone treatment. These methods do not capture moribund animals that are too unwell to emerge, are not in an observable location (e.g. residential properties), or

are unable to be trapped. Diagnosed animals are provided with effective treatment to resolve the disease, which improves outcomes compared to those remaining in the wild that would otherwise receive no medical interventions. The mortality rate of quenda in the wild due to sarcoptic mange cannot be accurately estimated without further prospective survival studies using either tracking devices, or mark-recapture trapping events. However, the severe clinical signs and disease progression observed suggests that morbidity and mortality is likely high in quenda, suggesting relative naivety to the disease, and the need to evaluate effective management options from a welfare perspective if not population viability.

Although infested quenda are a potential transmission source, the reservoir species responsible for this spillover event may still be in the area and seeding further infestations through direct contact or fomites that remain in the environment. European foxes are present in the region (Fleming et al., 2021) and are a known reservoir for *S. scabiei* (Pisano et al., 2019). Opportunistic or targeted access to fox carcasses (e.g. from pest control work), as well as tissue from any other mammals diagnosed with sarcoptic mange in the region, will help provide molecular and spatial data on the mite that may help determine the epidemiological role of other mammals in the region for sarcoptic mange persistence and

spread.

5. Conclusions

This disease event is the first sarcoptic mange epizootic reported in quenda, with ongoing transmission of the disease likely to have been seeded by a spillover event from a reservoir species. There is a risk of population impacts in the short to medium term and the potential risk of a larger epizootic if transmission continues unabated, which could have an impact on neighbouring populations of quenda, wildlife, domestic animals and humans. There are also welfare and conservation implications of allowing *S. scabiei* to continue to spread through the population, as diseased animals that do not receive treatment and supportive care are likely to experience more severe presentation of the disease and have higher mortality rates. Wildlife shelters are a critical partner in the management of this issue, providing positive outcomes for human health, animal welfare and wildlife conservation. In the absence of active or targeted surveillance, the use of spatial and epidemiological analysis has provided a preliminary insight into the extent and severity of this outbreak. These findings have established greater confidence in our understanding of the current situation, which will provide guidance on the resources and level of investigation required to minimise further risk to the local quenda population and other animals and humans in the region.

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Declaration of competing interest

None.

Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.ijppaw.2022.04.010.

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