

Sarcoptic Mange in a Tasmanian Devil (*Sarcophilus harrisii*) and Bennett's Wallaby (*Notamacropus rufogriseus*)

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ABSTRACT: *Sarcoptes scabiei* mites and skin lesions consistent with severe sarcoptic mange were identified in a Tasmanian devil (*Sarcophilus harrisii*) and Bennett's wallaby (*Notamacropus rufogriseus*) from Tasmania, Australia. The devil and wallaby both had severe hyperkeratotic skin lesions. All stages of mite development were identified in the devil, suggesting parasite reproduction on the host. The devil was also affected by devil facial tumor disease and several other parasites. This expands the global host range of species susceptible to this panzootic mange disease.

Key words: *Cylicospiura*, *Demodex*, devil facial tumor disease, *Macropus*, marsupial.

Sarcoptic mange, caused by infestation with the parasitic mite *Sarcoptes scabiei*, is a highly contagious disease affecting humans (in which it is known as scabies), wildlife, and domestic animals. *Sarcoptes scabiei* is one of the most widely distributed and burdensome mammalian parasites, having been reported in 148 species including both placental and marsupial mammals (Escobar et al. 2022). Its dissemination has been associated with European colonialism, and its host and geographic range are continually expanding (Fraser et al. 2017). Here, we document the first reported cases of severe sarcoptic mange in a Tasmanian devil (*Sarcophilus harrisii*) and a Bennett's wallaby (*Notamacropus rufogriseus*) in the island state of Tasmania, Australia.

In March 2023, an adult male Tasmanian devil was reported near Magra, Tasmania, Australia with crusted skin lesions and multiple ulcerated masses in the mouth and ventral neck consistent with devil facial tumor disease (DFTD; Fig. 1a–c). The devil was euthanized

at Bonorong Wildlife Hospital, Brighton, Tasmania, Australia and stored at 4 C. A necropsy was performed at the Tasmanian Animal Health Laboratory, Prospect, Tasmania, Australia (submission # 3-23-1806). Severe hyperkeratotic skin lesions were identified, extending from the nasal planum caudally along the dorsal midline, lateral trunk, and bilaterally on front and hind limbs. Epaxial muscle atrophy and absence of subcutaneous fat confirmed emaciation.

Histopathologic examination of formalin-fixed tissues confirmed that nodules were composed of tissues consistent with the clonally transmissible devil facial tumor 1 (DFT1) cells (Pearse and Swift 2006). Live DFT1 cells were isolated in culture more than 14 h after euthanasia of the devil and were confirmed to be DFT1.

Additionally, variable mild acanthosis and spongiosis with marked para- and orthokeratotic hyperkeratosis were observed in sections of haired skin. There was moderate infiltration of the dermis with lymphocytes and mast cells, large arthropod profiles with cuticles and spines, and chitinized appendages with striated muscle and coelom. Within multiple hair follicles, there were small cuticularized elongated arthropod profiles without chitin. Evaluation of deep skin scrapings under light microscopy showed morphologic profiles consistent with *Sarcoptes scabiei* and *Demodex* sp. (Fig 1e–i). Skin sections were subjected to DNA sequencing.

In September 2021, a 10.5-kg adult male Bennett's wallaby with severe skin disease (Fig 1d) was captured in Glamorgan-Spring Bay, Tasmania, Australia and euthanized at

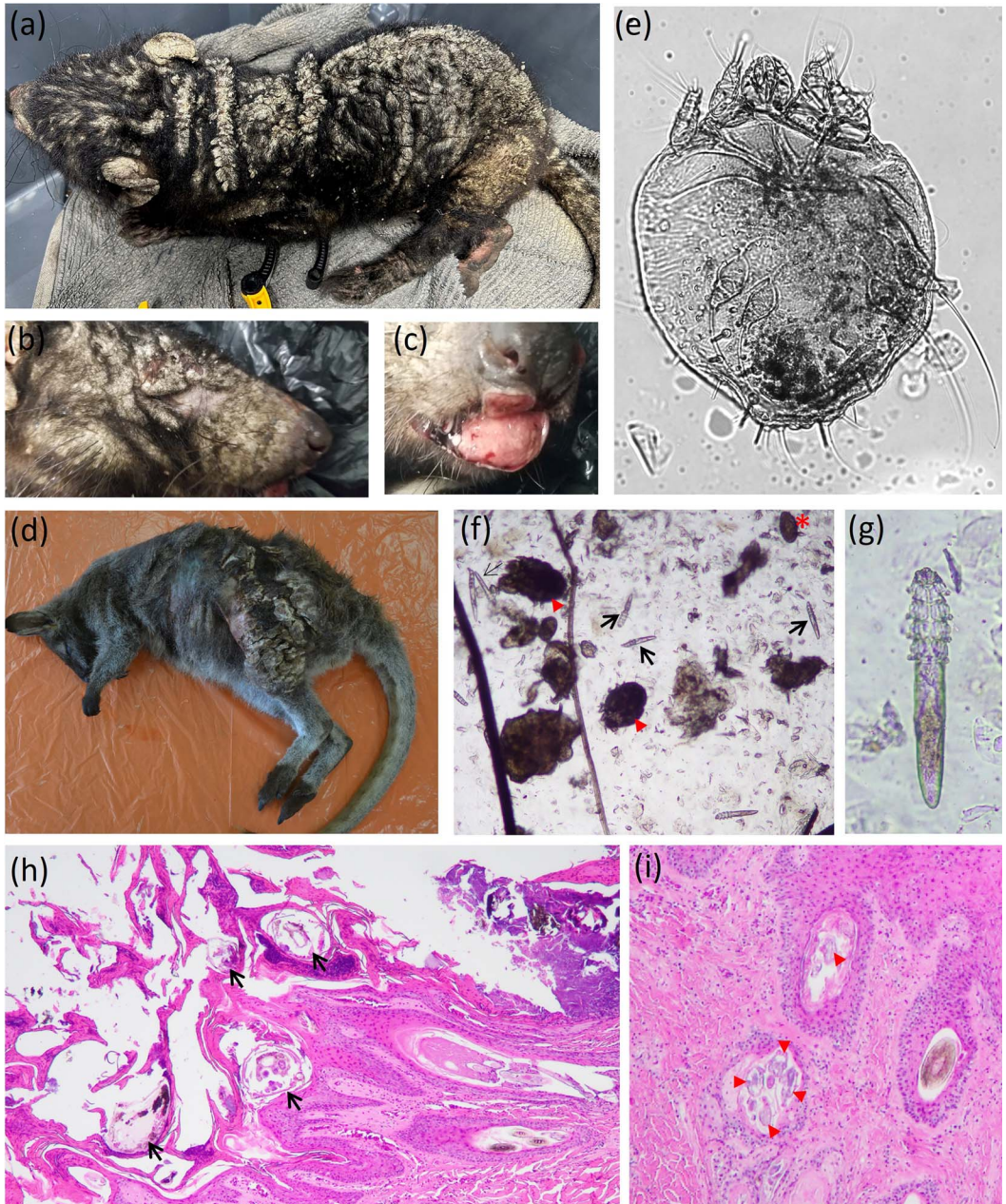


FIGURE 1. Generalized severe hyperkeratotic lesions in an adult Tasmanian devil (*Sarcophilus harrisii*) and Bennett's wallaby (*Notamacropus rufogriseus*). (a) Lesions consistent with sarcoptic mange were present on the trunk and (b) face of the devil. (c) Devil facial tumor 1 on the mucosal surface of the upper and lower lips. (d) Lesions on the lateral trunk and hind leg of an adult Bennett's wallaby. (e) Adult, female, nonpregnant *Sarcoptes scabiei* mite. (f) Red arrowheads show multiple *S. scabiei* and black arrows show *Demodex* sp. identified in skin scrapings from the devil; red star shows a *S. scabiei* egg. (g) Enlarged view of *Demodex* mites. (h) Skin biopsy from the Tasmanian devil showed hyperkeratosis with nymph and adult stages of *S. scabiei* identified by black arrows. (i) Red arrows show multiple *Demodex* sp. within the hair follicles. Image credits: (a–d) Bonorong Wildlife Sanctuary, Brighton, Tasmania, Australia; (e) Grace G. Russell; (f–i) Animal Health Laboratory, Mount Pleasant, Tasmania, Australia.

Bonorong Wildlife Hospital. Necropsy, undertaken at The University of Tasmania, Hobart, Tasmania, Australia, revealed marked hyperkeratosis and erythema, with deep skin fissures, hemorrhage, and exudative lesions on the trunk, legs, thorax, and tail. Generalized lymphadenopathy was identified, with petechial hemorrhage on external surfaces of brachial lymph nodes. The lungs were bilaterally congested, with multifocal bullae on the surface. Perirenal and pericardial fat were absent, confirming emaciation. Histopathology was not performed, although mites with features characteristic of *S. scabiei* were identified in deep skin scrapings examined under light microscopy. Tissue sections in RNAlater (Invitrogen, Waltham, Massachusetts, USA) were stored at $-80\text{ }^{\circ}\text{C}$ until molecular analysis. No significant pathogens were isolated from bacterial and fungal culture of skin, lung, liver, and kidney swabs.

Molecular diagnostics on mites from both the Tasmanian devil and the Bennett's wallaby was performed at Biosecurity Tasmania Plant Diagnostic Services Laboratory, New Town, Tasmania, Australia (enquiry numbers EN18303 and EN19775). The DNA was extracted in duplicate using the Monarch genomic DNA purification kit (New England Biolabs, Ipswich, Massachusetts, USA) following the protocol for genomic DNA purification from insects from the kit's instruction manual. The internal transcribed spacer 2 (ITS2) amplicon was generated following Fraser et al. (2018) using the F3/B3 primers from a loop-mediated isothermal amplification (LAMP) assay (Fraser et al. 2018). The LAMP assay was also performed and was positive for both samples. Sequencing was performed using Oxford Nanopore MinION (Oxford Nanopore Technologies, Littlemore, Oxford, UK) and analyzed via Geneious Prime 2024.0.2 (Geneious, Auckland, New Zealand) following the amplicon metagenomic analysis workflow. The ITS2 sequences for the mites isolated from the Tasmanian devil (GenBank PP827363.1) and Bennett's wallaby (GenBank PP827364) were both a 100% match for 217 nucleic acids in the *S.*

scabiei ITS2 gene (Genbank AB820972.1; Makouloutou et al. 2015).

Marsupials are known to be susceptible to *S. scabiei* infestation, with previous reports in wombat (*Vombatus ursinus*, *Lasiiorhinus latifrons*), koala (*Phascolarctos cinereus*), possum (*Pseudocheirus peregrinus*, *Trichosurus vulpecula*), bandicoot (*Isodon* spp.), wallabies (*Wallabia bicolor*, *Macropus agilis*; Fraser et al. 2016), and potoroo (*Potorous tridactylus tridactylus*; Wildlife Health Australia 2021). They generally develop characteristic clinical signs of erythema, alopecia, pruritis, and hyperkeratotic dermatitis (Holz et al. 2011; Speight et al. 2017; Botten et al. 2022). The observed clinical signs, such as hyperkeratotic dermatitis, findings in deep skin scrapings, and pathologic findings were consistent with sarcoptic mange in other species, including marsupials. All stages of mite development were identified in the devil, suggesting parasite reproduction on the host. The sarcoptiform mites *Diaboliocoptes sarcophilus* and *Sataniocoptes armatus* have caused outbreaks of alopecia, erythema, and hyperkeratosis in captive devils but these are usually mild in comparison with clinical signs caused by *Sarcoptes scabiei* (Fain and Laurence 1975; Obendorf 1993).

Bare-nosed wombats seem the most likely source of *S. scabiei* for the devil and wallaby. Mange is common in wombats throughout Tasmania (Ringwaldt et al. 2023) but is not frequently reported in other species (e.g., domestic dogs, *Canis familiaris*) in the state. Wombat burrows provide a stable temperature and humidity profile, ideal for the environmental transmission of *S. scabiei* (Browne et al. 2021). Devils regularly inhabit wombat burrows and scavenge on wombat carcasses (Owen and Pemberton 2005). Transmission of *S. scabiei* therefore may have occurred via fomites in burrows or via scavenging on infested wombats.

The devil was coinfecting with DFT1 cells, *Demodex* sp., and gastrointestinal helminths. *Demodex* sp., not previously reported in Tasmanian devils, was confirmed (Fig 1g) by its characteristic morphology consisting of an elongated, cigar-like idiosoma (trunk) with eight short legs attached to the cranial portion (Saari et al.

2019). More than 100 host-specific species of demodecid mites have been described, including in dasyurid species such as the agile antechinus (*Antechinus agilis*; Desch and Holz 2006) and brown antechinus (*Antechinus stuartii*; Nutting and Woolley 1965). In contrast to *S. scabiei* infestations, demodecid mites do not readily transmit between adults and are often commensal with the host. Nevertheless, clinical demodicosis does occur and may be associated with compromised host immunity or malnutrition or both (Izdebska and Rolbiecki 2020).

The duodenum of the devil contained a moderate parasite burden with cestode and ascarid profiles. Multiple spirurid nematodes without median lobes to the buccal capsule, with six sharply pointed teeth, four pairs of precloacal papilla, three adcloacal papillae, two pairs of postcloacal papillae, and spicules 2.2–2.8 mm (left) and 0.6–0.7 mm (right) long consistent with *Cylicospirura heydoni* were identified in the rectum and colon (Mawson 1968). This parasite has not been reported previously in Tasmanian devils, and nematode specimens were stored at the South Australian Museum, Adelaide, South Australia, Australia (Australian Helminthological Collection 49423).

Metastatic cancer is known to cause immunosuppression (Garner and de Visser 2020), which is a risk factor for crusting scabies in humans (Bhat et al. 2017) and in laboratory mouse models (Bhat et al. 2020). Additionally, *S. scabiei* has shown rapid phenotypic adaptation to an immunosuppressed host (Stingeni et al. 2020). Although causality cannot be inferred in this case, DFTD-induced immunosuppression may be a risk factor associated with susceptibility to parasitism. As DFT1 is widespread in Tasmania (Cunningham et al. 2021) and a second type of DFT (DFT2) is emerging in southern Tasmania (Pye et al. 2016; Stammnitz et al. 2023), opportunistic mite infestations may present a risk for endangered devils. Nonetheless, despite extensive sampling and observations of wild devils across Tasmania, sarcoptic mange has not previously been documented. Enhanced surveillance for mites on devils could help establish

the frequency of exposure and estimate the likelihood of mite adaptation to devils.

No comorbidities were identified in the Bennett's wallaby via gross pathology. Absence of evidence of *S. scabiei* in other macropods in Tasmania, despite co-occurrence with bare-nosed wombats, may reflect the rarity of macropod contact with wombats and their burrows. Alternatively, this may suggest that *S. scabiei* lineages in Tasmania are yet to adapt to colonize macropod hosts. Analogously, *S. scabiei* has been occasionally detected in swamp wallabies on mainland Australia but has not become established (Holz et al. 2011).

Sarcoptes scabiei infestation is one of the most infectious and burdensome mammalian parasitic infections worldwide. The cases reported here, combined with other novel reports since Escobar et al. (2022), increase the number of known affected species to over 150 mammals.

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