

Sarcoptic Mange in a South American Gray Fox (Chilla Fox; *Lycalopex griseus*), Chile

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ABSTRACT: Mange, a prevalent disease of dogs in Chile, is also a serious threat to wildlife. We report a case of sarcoptic mange in a South American gray fox or chilla fox (*Lycalopex griseus*). Further research is needed to understand the impact of mange in wildlife populations.

Mange, caused by *Sarcoptes scabiei*, is a highly contagious disease that may severely affect wildlife worldwide. A wide range of hosts are affected, including camelids, ungulates, and carnivores, among others (Oleaga et al. 2012; Gomez-Puerta et al. 2013). In South America, mange associated with *S. scabiei* has been described affecting domestic animals, such as rabbits (*Oryctolagus cuniculus*), dogs (*Canis familiaris*), cats (*Felis catus*), pigs (*Sus domesticus*), cattle (*Bos taurus*), llamas (*Lama glama*), and alpacas (*Vicugna pacos*; Alcaino and Gorman 1999; López et al. 2009). Wildlife cases have been sporadically reported in guanacos (*Lama guanicoe*) and vicuñas (*Vicugna vicugna*; Alvarado et al. 2004; Gomez-Puerta et al. 2013), brown-throated sloth (*Bradypus variegatus*; Oliveira et al. 2000), and capybaras (*Hydrochoerus hydrochaeris*; Cueto 2013) and peccaries (*Pecari tajacu*; Neta et al. 2012) held in captivity. A few cases of sarcoptic mange affecting wild South American carnivores are reported in the literature affecting pampas foxes (*Lycalopex gymnocercuin*; Deem et al. 2002) and a nonconfirmed case in a maned wolf (*Chrysocyon brachyurus*; Díaz Luque et al. 2014).

Although sarcoptic mange is one of the most prevalent diseases in domestic dogs in Chile (López et al. 2009), the disease is rarely reported in wildlife and is mainly conveyed by

park rangers as accidental sightings in protected areas. The South American gray fox or chilla fox (*Lycalopex griseus*) is the most abundant of the three foxes in Chile, inhabiting steppes, grasslands, and scrublands from Atacama to Tierra del Fuego (González del Solar and Rau 2004). The chilla fox is considered of least concern by the International Union for Conservation of Nature and seems not to be decreasing in number (González del Solar and Rau 2004). Here, we report a severe case of a hyperkeratotic form of sarcoptic mange, the histopathologic lesions, and the molecular identification of mites in a wild chilla fox in Chile.

In June 2014, an 8-mo-old juvenile, 3.04 kg male chilla fox was presented to the wildlife rehabilitation center at the Universidad Austral de Chile, Valdivia, Chile. The animal came from the surrounding rural area of the city of Osorno, Los Lagos Region, southern Chile. On clinical examination, the fox was dehydrated (10%), hypothermic (35.7 C), with poor body condition (1.5/5), and generalized skin lesions consistent with hyperkeratotic mange (Oleaga et al. 2012). These lesions had crusts of variable thickness, with skin fissures, alopecia, and hyperpigmentation mostly on the muzzle and ears, fore and hind legs, ischial region, and tail (Fig. 1). The complete blood count and plasma biochemistry profile were unremarkable. Skin scrapings were collected from the affected area for microscopy and molecular identification. The animal died minutes after the clinical procedures, and a full necropsy was performed. Postmortem examination revealed marked



FIGURE 1. Macroscopic skin lesions in a wild South American gray fox (chilla fox; *Lycalopex griseus*) from Chile with *Sarcoptes scabiei* (insert). Affected areas included the face, limbs, ischial region and tail.

lichenification on the surface of the sacral region and dorsal tail. Skin lesions on the muzzle and ischial region showed focal dermatitis associated with moderate alopecia (Fig. 1). An absence of subcutaneous and abdominal fat with generalized muscle atrophy confirmed that the carcass was emaciated. No other gross abnormalities were found in the remaining organs examined. Histopathologic examination of skin sections (Fig. 2) showed severe hyperkeratosis and parakeratosis of the epidermis. A large infiltration of polymorphonuclear neutrophils associated with numerous cocci bacteria was present on the surface of the stratum corneum. Large numbers of eggs in oviposition tunnels, nymphs, mites, and evidence of burrowing activity were present in the parakeratotic stratum corneum and stratum granulosum, reaching the stratum spinosum associated with a transmigration of mixed mononuclear and polymorphonuclear inflammatory cells (Fig. 2). Sections of multiple oval to irregular arthropod parasites, characterized by a chitinous cuticle, striated muscle, and a body cavity, were observed with mouthparts facing the

stratum spinosum (Fig. 2). Epidermal pegs and hyperplastic sebaceous glands were observed deep into the dermis. A mononuclear inflammatory cell response was present in areas of the dermis associated with mites and tunnels in the epidermis. Skin scrapings revealed adult *Sarcoptes* sp. after soaking samples with 10% potassium hydroxide (Fig. 1). For further identification, DNA was extracted from individual mites by using the HotSHOT Plus ThermalSHOCK technique (Alasaad et al. 2008) and a commercial kit (DNeasy Blood and Tissue Kit, Qiagen, Valencia, California, USA). The second internal transcribed spacer (~440 base pairs [bp]), internal transcribed spacer-2 (ITS-2), and a fragment of the 16S rRNA gene (~360 bp) were amplified by using RIB-18/RIB-3 and 16SD1/16SD2 primers, respectively, as described by Walton et al. (2004). The PCR products were purified and directly sequenced in both directions by using standard methods. Sequences were aligned after edition and deposited in GenBank (accession no. KT223563–KT223564). Sequence analyses revealed a 99% of identity of ITS-2 and 16S

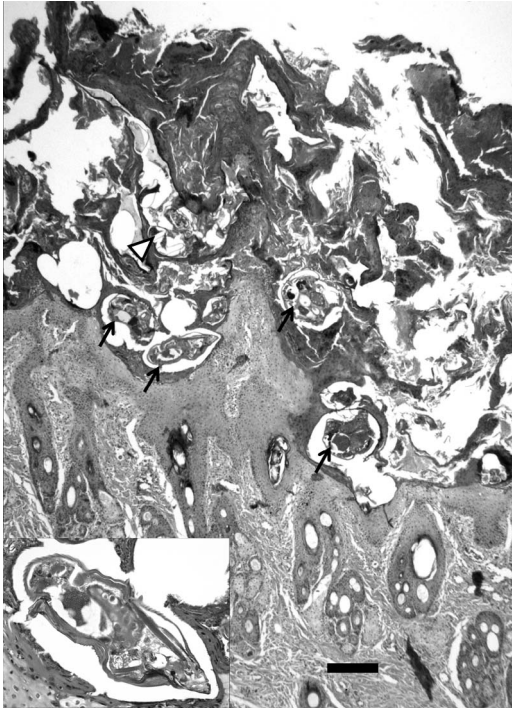


FIGURE 2. Photomicrograph of the skin of a wild South American gray fox (chilla fox; *Lycalopex griseus*) from Chile with *Sarcoptes scabiei*. Severe hyperkeratosis and parakeratosis associated with infiltration of mixed inflammatory cells and bacteria in the stratum corneum. Eggs in oviposition tunnels (open arrowhead) and multiple mites between stratum granulosum and spinosum (black arrows). Insert: section of a mite characterized by a chitinous cuticle, striated muscle, and a body cavity, with mouthparts facing toward the stratum spinosum. H&E stain. 4X. Bar=100 μ m.

genes of *S. scabiei* after comparing sequences with those available in the database by using the Basic Local Alignment Search Tool (National Center for Biotechnology Information 2015). The highest similarity of each sequence was with *S. scabiei* isolated from the European rabbit (*Oryctolagus cuniculus*; AB778905.1 for ITS-2 and AB779577.1 for 16S). The European rabbit is widely distributed in Chile and is occasionally preyed upon by chilla foxes in southern Chile (González del Solar and Rau 2004). Parasite demands may severely affect the host condition. The alopecia and intense pruritus induced by chronic mange infections may increase the energy demands for thermoregulation, cause scratch-

ing, and trigger the induced immune response. These energetic demands may lead to reduced mass and fat reserves with symptoms of chronic undernourishment (Newman et al. 2002), as may have occurred in this chilla fox.

Although sarcoptic mange is highly prevalent in domestic dogs in Chile, other host interactions, such as predator-prey, may also play an important role in the transmission of mites. Further research into reservoir hosts is required to understand the role of sympatric hosts and domestic animals on the persistence and transmission of *S. scabiei* and the impact of mange in populations of wild foxes in Chile.

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