



Sarcoptic mange in wild quichua porcupines (*Coendou quichua* Thomas, 1899) in Colombia

Viviana Gonzalez-Astudillo^{a,*}, Omar D. Leon-Alvarado^b, Paula Andrea Ossa-Lopez^c,
Fredy Arvey Rivera-Paez^c, Héctor E. Ramírez-Chaves^c

^a School of Veterinary Science, Building 8114, The University of Queensland, Gatton Campus, Queensland, Australia, 4343

^b Laboratorio de Sistemática y Biogeografía, Escuela de Biología, Facultad de Ciencias, Universidad Industrial de Santander, Cra. 27 Calle 9 A.A. 678, Bucaramanga, Colombia

^c Departamento de Ciencias Biológicas, Universidad de Caldas, Calle 65 # 26-10, Manizales, Colombia



ARTICLE INFO

Keywords:

Alopecia
Andes
Colombia
Rodentia
Sarcoptes scabiei
PCR

ABSTRACT

The Quichua porcupine (*Coendou quichua*) is a neotropical rodent with uncertain taxonomic and conservation status. Two Quichua porcupines with severe hyperkeratosis and alopecia were found in the Magdalena River Basin of Colombia. *Sarcoptes scabiei*, the mite causing mange, a disease carried mainly by domestic animals, was confirmed via parasitological and molecular methods. This is the first report of mange in neotropical porcupines to date. The population-level impact of mange in *Coendou* spp., related mammals and predators in Colombia might represent a threat and needs further investigation.

Mites from the genus *Sarcoptes* (species *scabiei*) cause sarcoptic mange, a highly-contagious disease detected in various hosts ranging from humans, to domestic animals and wildlife (Bornstein et al., 2001). Mange can cause negative economic impacts (Bornstein et al., 2001), particularly in countries lacking effective surveillance systems leading to underreporting of animal cases (Cediel et al., 2013). *Sarcoptes scabiei* appears to be one highly diverse species according to microsatellite analyses (Arlian and Morgan, 2017). Consequently, it is thought that cases of wildlife mange are the result of an infection by a single highly variable species displaying physiological specificity across many hosts (Pence et al., 1975). The main morphologic features of *S. scabiei* include tooth-like denticles and club-like setae on the mid-dorsal and posterior idiosoma, respectively (Pence and Ueckermann, 2002). Currently, molecular markers can be used to detect and genetically evaluate the presence of *S. scabiei* in domestic animals, wildlife and humans (Alasaad et al., 2014; Angelone-Alasaad et al., 2015). Clinical manifestations are dictated by the type and magnitude of innate, humoral and cellular responses to mite proteins (Arlian and Morgan, 2017). Two main forms of the disease are recognized depending on the host response, ordinary (protective) and severe crusted mange (pathological). Pathogen 'spillover' to naive hosts can induce marked pathological host responses manifesting in the severe crusted mange form.

Mange is rated as a low priority, emerging zoonosis in Colombia (Rentería, 2008). Because of this, compilation of data regarding prevalence of sarcoptic mange or any other mite infection in the country in

human and domestic animals is challenging. Domestic animal cases are not required to be reported to veterinary authorities, leading to scant availability of official animal health data. Only a few wildlife cases are publicly available, the most recent on a cervid (*Mazama* sp.; ICA., 2012). However, parasitological surveys in Colombia have produced a plethora of mite species records, compiled in a recent systematic literature review (Gonzalez-Astudillo et al., 2016), but primarily restricted to other vertebrate species. From the 11 mammalian taxonomic orders analysed in the report (data not shown), 31 mite species were documented in chiropterans - the most extensively sampled order, and one in primates. In contrast, rodents - the second most extensively sampled order, reported no mite records.

Coendou quichua is a medium-sized porcupine, distributed in western Colombia, Panama and Ecuador, from sea level to 3300 m (Voss, 2015; Ramírez-Chaves et al., 2016). *C. quichua* is classified as Data Deficient according to the International Union for the Conservation of Nature (Delgado, 2016). Although little is known about its natural history in Colombia, *C. quichua* is mostly arboreal but may use natural burrows, is solitary and nocturnal, with a diet mainly of leaves and fruits (Voss, 2015).

A mature male Quichua porcupine was live-trapped in 09/2014 in San Vicente de Chucurí, Eastern Cordillera range (N 6°47'33.27", W 73°28'48.23", 1250m), an area with mixed crops and forest patches. The porcupine was humanely euthanized in the field due to an extremely poor prognosis. The second case involved a mature female

* Corresponding author.

E-mail address: v.gonzalez@uq.edu.au (V. Gonzalez-Astudillo).



Fig. 1. a-b. Macroscopic lesions of severe sarcoptic mange in two Quichua porcupines (*Coendou quichua*) from central Colombia with a microphotograph of *Sarcoptes scabiei* (inset). a) Mature male with extensive alopecia affecting ventral, inguinal region, and limbs. b) Mature female with severe hyperkeratosis and alopecia covering 80% of the body.

trapped in the city of Bucaramanga (N 7°08', W 73°00', 959 m) which died under veterinary care and was submitted to the local School of Biology on 06/2016.

In both specimens, gross lesions corresponded to hyperkeratosis, and extended ventrally from the cervical region and caudally towards the proximal portion of the tail and above the tarsal and carpal regions; the skin presented regionally extensive alopecia with broken quills. The alopecic area appeared thickened, wrinkled, and with multifocal white to straw-coloured encrustations. The skin covering articulated regions presented cracks exposing the dermis (Fig. 1a–b). Skin sections and scrapings were submitted to the Universidad Nacional de Colombia (Bogotá) and to Universidad del Valle (Cali) for histopathological assessment and parasitological identification. In the first porcupine, severe changes resembled a moderately lymphoplasmacytic dermatitis with severe hyperkeratosis and pustules. The epidermis was moderately hyperplastic with orthokeratotic and parakeratotic hyperkeratosis. Epidermal crusting with intralesional bacterial erosion and sloughing with intra- and subcorneal epidermal pustules were also observed. Dermal lesions were mild and corresponded to hydroptic change, spongiosis, lymphoplasmacytic and mast cell infiltrate and lymphatic dilation. The histopathological findings of the second porcupine paralleled the description of the first individual, but were more severe, and included a marked epidermal necrosis and epidermolysis with embedded quill and keratin fragments. In both porcupines, evidence of multiple intralesional mite structures were found, characterised by a cuticle with peripheral and dorsal horns, hatched egg fragments and intraepidermal coalescing tunnels (Fig. 2a–b). Secondary infection by cocci is considered common in severe mange (Verdugo et al., 2016), likely incited by the excessive epidermal sloughing and other disturbances caused by the mite invasion which can also debilitate the host. Mites were identified as *S. scabiei* using amplification and sequencing of fragments of mitochondrial 16S rDNA, using universal primers for the amplification of *S. scabiei* with an estimated size of 135

bp (Angelone-Alasaad et al., 2015). Both samples were individually submitted for DNA extraction, using the DNeasy Blood and Tissue kit (Qiagen), following the manufacturer's protocol. Extracted DNA samples were tested by PCR, using the forward primer SSUDF (5'-GGGTC TTTTGTCTTGGATAAAA-3') and reverse primer SSUDR (5'-CTAAGG TAGCGAAATCATTAGC-3'). PCR products were purified with the QIAquick PCR purification kit (Qiagen) and sent to the Universidad de Los Andes (Bogotá, Colombia) for DNA sequencing. GenBank nucleotide sequence accession numbers for the partial sequences generated in the present study are **MG645006** (San Vicente) and **MG645007** (Bucaramanga). The sequences were analyzed using Basic Local Alignment Search Tool (BLAST; Altschul et al., 1990) to determine the closest similarities with other mite species.

The partial sequences of 16S were 100% and 98% (San Vicente de Chucurí and Bucaramanga, respectively) identical to the corresponding sequences available for *S. scabiei* in GenBank isolated from the domestic dog (*Canis lupus familiaris*; KJ781373.1), the Argentine Gray fox (*Lycalopex griseus*; KT223563.1), the European rabbit (*Oryctolagus cuniculus*; AB779577.1), and the buffalo (*Bubalus bubalis*; AB779569.1). Of these, *L. griseus* is not present in Colombia and it is restricted to Patagonia (Hunter, 2011) whereas the others are domestic and/or feral species in the country (Ramírez-Chaves et al., 2011). In particular, domestic dogs are distributed throughout Colombia (Baptiste et al., 2010), where they overlap with *C. quichua* habitat. Dogs have high urban and rural densities (Hughes-David and Macdonald, 2013), and are currently recognized nationally as wildlife predators, disease carriers and competitors (Manjarres-Rodríguez, 2013). Despite the wide host range of *Sarcoptes*, there are no records of mange in neotropical porcupines, likely due to underreporting (Gonzalez-Astudillo et al., 2016; Verdugo et al., 2016). Other arachnids have been reported in Colombian porcupines; specifically, *Amblyomma longirostre* in *Coendou* spp. and *C. prehensilis* (Osorno-Mesa, 1940, Wells et al., 1981), *A. longirostre*, and *A. goeji* in *Coendou* spp. (CIAT, 1973). The only records

Download English Version:

<https://daneshyari.com/en/article/8386596>

Download Persian Version:

<https://daneshyari.com/article/8386596>

[Daneshyari.com](https://daneshyari.com)