



## The diversity and impact of hookworm infections in wildlife



Mauricio Seguel\*, Nicole Gottdenker

Department of Pathology, College of Veterinary Medicine, University of Georgia, 501 DW Brooks Dr, Athens, GA 30602, USA

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### ABSTRACT

Hookworms are blood-feeding nematodes that parasitize the alimentary system of mammals. Despite their high pathogenic potential, little is known about their diversity and impact in wildlife populations. We conducted a systematic review of the literature on hookworm infections of wildlife and analyzed 218 studies qualitative and quantitatively. At least 68 hookworm species have been described in 9 orders, 24 families, and 111 species of wild mammals. Black bears, red foxes, and bobcats harbored the highest diversity of hookworm species and *Ancylostoma pluridentatum*, *A. tubaeforme*, *Uncinaria stenocephala* and *Necator americanus* were the hookworm species with the highest host diversity index. Hookworm infections cause anemia, retarded growth, tissue damage, inflammation and significant mortality in several wildlife species. Anemia has been documented more commonly in canids, felids and otariids, and retarded growth only in otariids. Population-level mortality has been documented through controlled studies only in canines and eared seals although sporadic mortality has been noticed in felines, bears and elephants. The main driver of hookworm pathogenic effects was the hookworm biomass in a population, measured as prevalence, mean burden and hookworm size (length). Many studies recorded significant differences in prevalence and mean intensity among regions related to contrasts in local humidity, temperature, and host population density. These findings, plus the ability of hookworms to perpetuate in different host species, create a dynamic scenario where changes in climate and the domestic animal-human-wildlife interface will potentially affect the dynamics and consequences of hookworm infections in wildlife.

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\* Corresponding author.

E-mail address: [mseguel@uga.edu](mailto:mseguel@uga.edu) (M. Seguel).

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## 1. Introduction

Hookworms (Nematoda: Strongylida: Ancylostomatoidae) are blood-feeding nematodes that parasitize the mammalian alimentary system (Popova, 1964). Regardless of the large diversity within this parasitic group, all Ancylostomatoidae species share basic morphologic, physiologic and life history traits that translate into similar consequences for their host. In humans and domestic animals, the deleterious effects of hookworms are well documented at the individual and population level, being one of the most significant neglected tropical diseases of humans (Bartsch et al., 2016), and an important cause or contributory factor of anemia and neonatal mortality in domestic dogs and cats (Traversa, 2012). Despite the potential deleterious impact in their hosts, there is no currently available summary on the number of hookworm species described and the significance of hookworm infection in free-ranging wild mammals.

The modification of landscapes and climate change create additional challenges for wildlife disease study, and it is predicted that these phenomena will modify the dynamics of nematode infections (Weaver et al., 2010; Weinstein and Lafferty, 2015). Therefore, improved description, analysis, and understanding of hookworm infections in wildlife are necessary to direct future research efforts and understand host-parasite relationships in a regional and global scale.

In this context, the objectives of this review are to i) provide a systematic summary of the literature available on hookworm infections of wildlife, ii) evaluate the reported hookworm diversity in wildlife corrected for sampling effort, iii) identify significant pathologic features of these infections and the potential drivers of the deleterious effects of hookworms on wildlife hosts.

## 2. Materials and methods

### 2.1. Searching methods and inclusion criteria

A systematic literature review of Ancylostomatoidae nematodes of wildlife was performed using Google scholar, Web of Science and Biosis search engines on April 27th, 2016; following recommended practices for systematic reviews in the field of parasitology (Haddaway and Watson, 2016). The initial term searched was “hookworm(s)” AND “wildlife”. The abstracts of the papers retrieved were reviewed and included in the study if they met the

following criteria: i) The parasitic nematode found belonged to a genus within the Ancylostomatoidae family. (Studies describing the presence of eggs or nematodes as “hookworms” or “strongyles” without genus identification were excluded). ii) The host species was any free-ranging non-domesticated (wild) animal. Captive wild animals were only included if they were taken from the wild soon before the study, and therefore, transmission of parasites was assumed to occur in the wild. In the case of domestic animal-wildlife hybrids, these were included if they were free-ranging. Additional searches were performed using the preliminary list of genera identified in the initial search plus the word “wildlife” (e.g. “Ancylostoma wildlife”). The studies selected based on abstract screening (N = 216) were fully reviewed and the most significant findings summarized into a master spreadsheet (supplementary material).

### 2.2. Data analyses

To identify host species with high hookworm diversity, an index penalized for sampling effort was calculated based on previously published methods (Nunn et al., 2003; Ezenwa et al., 2006). Briefly; the citations for each host species were extracted from the databases and after factor analyses condensed into one variable, citation-principal component (citation-PC). Additional sampling effort measures included the number of animals sampled in the reviewed studies and the number of studies in our review for each host species. Negative binomial regression models were fitted for each measure of sampling effort and the residuals were used as a penalized index of hookworm diversity. To assess which hookworm species parasitized higher number of wildlife species a similar approach was used with the difference that citation-PC was not used because of “too high” penalization for highly studied hookworm species infecting humans or domestic animals (e.g. *Necator americanus*). We used instead, the total number of mammalian species screened in the studies where that hookworm species was found, since in many studies several host species were assessed. The penalized measurements of host diversity were calculated as previously described.

To assess which factors influenced the likelihood of finding a mammalian-hookworm species relationship that had detrimental effects for the host, the paired mammalian-hookworm species were categorized as 1 if there was at least one study describing adverse health effects at the individual or population level and as

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