

## Strongyloides infections in humans and other reservoir hosts in Dzanga-Sangha Protected Areas, Central African Republic

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Strongyloidiasis, a parasitic disease of humans caused by the *Strongyloides* nematode, was recently added to the list of neglected tropical diseases requiring control measures in endemic areas<sup>(1)</sup>. According to the recent estimates, 614 million people are infected worldwide<sup>(2)</sup>. Metagenomic analysis of model parasite multihost systems is a key to uncovering the molecular diversity required to understand disease transmission. In our project, we confirmed the transmission of zoonotic *Strongyloides fuelleborni* haplotype between lowland gorillas and humans. In addition, we have detected *Strongyloides stercoralis* in both dogs and humans.

**Key words:** *Strongyloides*, zoonosis, human, dog

### Genetická diverzita hlístic rodu *Strongyloides* u lidí a rezervoárových hostitelů v rezervaci Dzanga-Sangha ve Středoafričské republice

Strongyloidóza byla nedávno přidána na seznam opomíjených tropických chorob vyžadujících kontrolní opatření v endemických oblastech<sup>(1)</sup>. Podle nedávných odhadů je celosvětově nakaženo 614 milionů lidí<sup>(2)</sup>. Metagenomická analýza modelových parazitárních multihostitelských systémů je klíčem k odhalení diverzity potřebné k pochopení přenosu onemocnění. V našem projektu jsme potvrdili přenos zoonotického haplotypu *Strongyloides fuelleborni* mezi gorilami nížinnými a lidmi. Kromě toho jsme detekovali *Strongyloides stercoralis* jak u psů, tak u lidí.

**Klíčová slova:** *Strongyloides*, zoonóza, člověk, pes

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### Introduction

Neglected parasites, such as rhabditid nematodes of the genus *Strongyloides* are among the most common soil-transmitted nematodes in both humans and non-human primates<sup>(3,4)</sup>. Two species, *S. stercoralis* and *S. fuelleborni* have been detected in humans; both are causative agents of strongyloidiasis. *Strongyloides stercoralis* is considered a generalist with a cosmopolitan distribution, infecting a wide range of hosts, including primates (humans and mainly captive NHPs) and carnivores<sup>(5)</sup>. Two lineages have been described within the genus *Strongyloides*: potentially zoonotic lineage A and the likely canine lineage B<sup>(6)</sup>. The specialist *S. fuelleborni* includes two subspecies: *S. fuelleborni fuelleborni* and *S. fuelleborni kellyi*. *Strongyloides f. fuelleborni* occurs in African and Asian NHPs, with occasional spread to humans, while *S. f. kellyi* appears to be endemic to humans in New Guinea<sup>(5,7)</sup>. In our project, we explored the genetic diversity of *Strongyloides* species in humans, lowland gorillas and dogs sharing the same habitat in the rainforest ecosystem of Dzanga-Sangha Protected Areas (DSPA), Central African Republic (CAR).

### Material and methods

Individual samples from humans (N=50), lowland gorillas (N=100) and dogs (N=48) were collected in the Dzanga-Sangha Protected Areas in the Central African Republic. Total DNA was extracted and analyzed by qPCR for detection *Strongyloides*<sup>(8)</sup>. Selected positive samples for *Strongyloides* were amplified and high-throughput sequenced (HTS) on the Illumina MiSeq platform. The hypervariable region (HVR-IV) of the 18S rDNA gene and a portion of the mitochondrial cytochrome c oxidase subunit 1 gene (*cox1*) were selected for *Strongyloides* amplification for samples processed by HTS<sup>(9)</sup>.

### Results

The prevalence of *Strongyloides* based on qPCR was high in all species studied (76 %, 57 %, and 60 % in humans, gorillas and dogs, respectively). *Strongyloides stercoralis* was detected in both human and canine samples. In addition, haplotype L of *S. fuelleborni* was detected in humans and gorillas, confirming interspecies transmission.

## Discussion

Regular surveillance of *Strongyloides* infections, including molecular identification and genotyping, should be an important component of health management. Close contact between humans, NHPs, and dogs poses a risk for transmission<sup>(5,6,10)</sup>. Based on our findings, we propose that dogs may be a reservoir of *Strongyloides stercoralis* to humans and potentially NHPs. However, NHPs may also be a source of *Strongyloides fuelleborni* infection to humans and vice versa.

Strongyloidiasis remains a major veterinary and human public health challenge globally and both dogs and NHPs should be recognised as a possible source of *Strongyloides* infections in *Strongyloides* control programs.

## Conflict of interest statement

The authors declare no conflict of interest. The conference paper has not been published.

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