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Genetic characterization of *Strongyloides* spp. from captive, semi-captive and wild Bornean orangutans (*Pongo pygmaeus*) in Central and East Kalimantan, Borneo, Indonesia

Labes, E M ; Wijayanti, Nurcahyo ; Deplazes, P ; Mathis, A

Abstract: Orangutans (*Pongo* spp.), Asia's only great apes, are threatened in their survival due to habitat loss, hunting and infections. Nematodes of the genus *Strongyloides* may represent a severe cause of death in wild and captive individuals. In order to better understand which *Strongyloides* species/subspecies infect orangutans under different conditions, larvae were isolated from fecal material collected in Indonesia from 9 captive, 2 semi-captive and 9 wild individuals, 18 captive groups of Bornean orangutans and from 1 human working with wild orangutans. Genotyping was done at the genomic rDNA locus (part of the 18S rRNA gene and internal transcribed spacer 1, ITS1) by sequencing amplicons. Thirty isolates, including the one from the human, could be identified as *S. fuelleborni fuelleborni* with 18S rRNA gene identities of 98·5–100%, with a corresponding published sequence. The ITS1 sequences could be determined for 17 of these isolates revealing a huge variability and 2 main clusters without obvious pattern with regard to attributes of the hosts. The ITS1 amplicons of 2 isolates were cloned and sequenced, revealing considerable variability indicative of mixed infections. One isolate from a captive individual was identified as *S. stercoralis* (18S rRNA) and showed 99% identity (ITS1) with *S. stercoralis* sequences from geographically distinct locations and host species. The findings are significant with regard to the zoonotic nature of these parasites and might contribute to the conservation of remaining orangutan populations.

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CORRIGENDUM

Genetic characterization of *Strongyloides* spp. from captive, semi-captive and wild Bornean orangutans (*Pongo pygmaeus*) in Central and East Kalimantan, Borneo, Indonesia – CORRIGENDUM

E. M. LABES, N. WIJAYANTI, P. DEPLAZES *and* A. MATHIS

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The author's name N. WIJAYANTI should be replaced by W. NURCAHYO and the address of this author should be written as University Gadjah Mada, Faculty of Veterinary Medicine, Department of Veterinary Parasitology, Jalan Fauna 2, 55281 Yogyakarta, Indonesia.

REFERENCE

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