

### ***Ascaris lumbricoides*, *Ascaris suum*, or “*Ascaris lumbricum*”?**

TO THE EDITOR—For decades, there has been a discussion about the zoonotic potential of the 2 species *Ascaris lumbricoides* and *Ascaris suum* or whether these should be a single species [1–3]. It has been demonstrated that the biological cycle of *Ascaris* organisms originating from humans or from pigs can be completed in both hosts, that cross-transmission occurs, that gene flow and hybridization events occur, that there are genotypes of *Ascaris* that are common to both hosts, and that, when found, there are few differences in their nucleotides. As more *Ascaris* organisms are isolated from different hosts and geographic localities and with different methods, increased evidence will be generated to clarify this question. Progress regarding this matter was recently demonstrated by Betson et al in this journal [4].

We previously demonstrated that, in developing countries where there is a close relationship between these hosts, it is also not uncommon to find *Ascaris* genotypes typical of pigs in humans [5]. This might be interpreted as an indication that cross-transmission also occurs in these regions and that, therefore, there is zoonotic potential among these organisms. We recently conducted a study in the municipality of Guapimirim in the state of Rio de Janeiro and found that, among the subjects with ascariasis, most of the worms genotyped for the target *cox1* had the genotype of *Ascaris* organisms typical in pigs, known as P3 [6].

This result might lead us to think that the infection was acquired from a pig. However, in this population, the majority of the individuals had not had contact with pigs. Therefore, this suggests that the infection was acquired from another human and that it was this other human who had had contact with a pig. Will we reach this so-called mitochondrial Eve someday in the future?

Are we faced with a single species, a more troublesome notion for scientists? Studies have provided new evidence that this is a single species, through comparing the complete mitochondrial genome and, most recently, through analysis of the microRNA of *A. suum* and *A. lumbricoides* [7, 8]. It seems that it is not possible to differentiate them even by using additional molecular targets for genotyping. Perhaps this is simply because these differences do not exist.

In most of the isolates that we have genotyped, independent of the molecular target used, the differences in the nucleotides (when they exist) are small and almost always result in synonymous mutations in the translation to amino acids. This also applies to other *Ascaris* sequences that have been deposited in GenBank by other research groups. This is despite what is seen with so many other parasites that are zoonotic or have genotypes that are considered to be zoonotic, yet are not classified as distinct species, as exemplified by *Giardia duodenalis*.

#### **Notes**

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### ***Ascaris lumbricoides* or *Ascaris suum*: What's in a Name?**

TO THE EDITOR—We thank da Silva Alves et al [1] for their comments. As they rightly point out, the species status of *Ascaris lumbricoides* and *Ascaris suum* has been a matter of debate for some years [2]. We welcome widening the discussion and draw attention to another important milestone in the study of this parasite, the publication of a book about *Ascaris*, edited by Celia Holland [3]. In this volume, we elaborated on this question, concluding that it all depends on the species definition used [4]. For example, based on a phenetic species concept, *A. lumbricoides* and *A. suum* would belong to the same species.

In contrast, based on a biological species concept, it could be argued that they comprise 2 separate species. Confirmation of this would entail experimental crosses, but what experimental infections, hosts, and parental isolates should be used?

As discussed by a number of authors, including da Silva Alves et al and ourselves, the use of mitochondrial markers or DNA barcoding approaches to infer species relationships and transmission dynamics for *Ascaris* is controversial [5]. We have also found pig-associated haplotypes among *Ascaris* worms collected from humans who live in areas where there are no pigs, suggesting retention of ancestral haplotypes. In contrast, based on nuclear markers (microsatellites), these parasites looked like human-associated *Ascaris* [6]. This is an interesting puzzle in Zanzibar, where porcine transmission could have taken place, although hundreds of years ago. We firmly believe that our African-focused sampling has unveiled an important genetic legacy and diversity of ascarids in this region, where it might have first parasitized early hominids. Hopefully, future archaeological studies of parasites will expand and elaborate on this.

This debate on *Ascaris* can, of course, be expanded into the zoonotic transmission of other soil-transmitted helminthiasis, with a new spotlight on *Trichuris trichiura*. Although it is generally accepted that *T. trichiura* (in humans) is a separate species from *Trichuris suis* (in pigs) [7], until recently it was thought that *Trichuris* in humans and nonhuman primates composed a single species (*T. trichiura*). However, ongoing molecular studies of *Trichuris* in samples obtained from humans and nonhuman primates have revealed the evolutionary history of *T. trichiura* to be

more complicated than originally thought. It may comprise a number of species or subspecies, some of which are specific to particular host species and others that are shared between humans and nonhuman primates [8].

To play devil's advocate, does the species status of soil-transmitted helminths really matter? From a public health perspective, it does. With the drive to control and eliminate these parasites from humans, as exemplified by the new initiative of Deworm3 [9], uncovering any zoonotic potential or other natural environmental refugia is important for alternative intervention strategies that may be required. Additionally, any gene flow between worms infecting different hosts could favor the spread of anthelmintic resistance, and, as yet, it is not clear whether the newly described (sub)species of *T. trichiura* shows any significant biological differences in factors such as pathogenesis or response to treatment. This calls for further research.

Our current understanding is lacking. Even though future molecular appraisals will continue to shed new light on parts of the problem, a bottleneck will remain in obtaining sufficient worm material from humans and animals at a level truly representative of natural transmission cycles. We are sure that da Silva Alves et al would agree that better integration of studies in humans and animals and adoption of a One Health approach is a sensible way forward.

#### Notes

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