

## Investigating the possible cross-transmission between humans and animals of *Giardia lamblia* and *Ascaris* parasites in Ecuador

Ascariasis, caused by the helminth *Ascaris lumbricoides*, and giardiasis, caused by the protozoan *Giardia lamblia*, are considered neglected tropical diseases and are common in developing countries (Savioli et al. 2006). Ascariasis usually affects the poorest communities (de Silva et al. 2003; Hotez et al. 2009) and has broad societal impacts, namely on decreasing productivity and employment, adding to the precarious situation of these communities (Brooker and Pullan 2013). These diseases have a faecal-oral transmission and *Ascaris* eggs and *Giardia lamblia* cysts can contaminate water, food and soil, and can be associated with poor sanitary conditions.

Infections with both parasites can range from asymptomatic to people presenting diarrhoea, stomach pain and distension, and malabsorption, stunting and wasting in children ((Berkman et al. 2002; Eckmann 2003; Bethony et al. 2006; Cacciò and Ryan 2008).

Both species of parasites can also be found in animals. *Ascaris suum*, the swine counterpart, mostly causes subclinical infections (Thamsborg et al., 2013), but can also generate respiratory difficulties and diarrhoea in pigs (Bowman, 2014). Most importantly, economic losses can arise from the condemnation of livers due to the presence of white spots, i.e. fibrotic lesions caused by larval migration, and from an influence upon weight gain and growth rate (Kipper et al. 2011; Knecht et al. 2011; Roepstorff et al. 2011).

*Giardia lamblia* has been identified in a variety of mammals and birds (Sprong et al. 2009) and it has been genetically divided into 8 assemblages (Monis et al. 2003). Assemblages A and B are found both in humans and in other mammalian and avian species (Ryan and Cacciò 2013). Assemblages C and D are found in canids, E in cattle, sheep and goats, F in cats, G in rodents and H in marine mammals (Cacciò and Ryan 2008; Lasek-Nesselquist et al. 2010). This parasite is mostly asymptomatic in animals (Thompson et al. 2008). Nonetheless, dogs, cats (mostly in animal shelters), calves and lambs can present with diarrhoea (Thompson et al., 2008; Bowman, 2014).

Evidence suggests that in some settings transmission of *Ascaris* and *Giardia lamblia* parasites between humans and animals takes place. *Ascaris* and *Giardia* parasites deriving from humans cannot be distinguished from those coming from swine and/or other animals based on their shape, size or other visible characteristics. Nonetheless, several DNA-based markers can help distinguish human parasites from animal parasites.

The aim of this project was to conduct a pilot study to investigate the possible cross-transmission of *Giardia lamblia* and *Ascaris* between animals and people living in the Quinindé district, a rural and poor tropical area of Ecuador. This district is found in the province of Esmeraldas, one of the poorest regions in Ecuador, with a per capita income of less than US\$5,000 in 2012 (Foros del Ecuador 2013).



**Figure 1** Location of the Quinindé district

A compound located in a rural area outside of Quinindé, where only 10% of the population have access to electricity and none have access to other services (Cooper et al. 2011) and one household (located in an isolated area in the outskirts of Quinindé), for a total of 32 households, accepted to participate in the study.



**Figure 2 Part of the compound**

A single faecal sample was collected from each consenting member of participating households and from dogs, cats, pigs, chickens and ducks belonging to the household, for a total of 139 human (out of 157 total household members) and 153 animal (out of 203 total animals present in the households) samples.





**Figure 3 Animal sampling**

Animal and human samples were firstly analysed by microscopy (wet mount and Kato-Katz). The most prevalent parasite diagnosed through this analysis in humans was *Trichuris trichiura*, arriving to almost 50%, followed by *Ascaris* and *Entamoeba histolytica*. The most prevalent parasite in dogs was *Ancylostoma caninum*, 3 out of the 6 pigs were infected with either *Trichuris suis* or *Ascaris*, while few parasites were found in duck and chicken flocks.

People and swine positive to *Ascaris* were subsequently treated to chemo-expel whole adult parasites, needed for the genotyping. Polymerase chain reaction (PCR)-Restriction Fragment Length Polymorphism (RFLP) analysis of the internal transcribed spacer (ITS) region (Nejsun et al. 2005) was chosen for genotyping, as this is the best single marker to distinguish *Ascaris suum* from *Ascaris lumbricoides*. 23 adult parasites were collected from 7 humans and none from swine. All of these parasites were identified as *Ascaris lumbricoides*.

*Giardia lamblia* was diagnosed with the use of real time-PCR, being this more sensitive than microscopy (Mejia et al. 2013). 40.3% of humans, 61% of dogs, one pig and 2 chicken flocks were positive to this parasite. Interestingly, multivariate statistical analysis showed that a dog was at higher risk of being *GI* positive if it shared the household with positive humans.

Overall, 20.9% of people had no parasites, 36% one parasite and 43.1% had two or more parasites.

Also epidemiological data was gathered and it was found that more than 80% of the human population had not been dewormed in the last 3 months and 1/6 pigs, 8/26 dogs, 1/9 cats, 1/7 duck flocks and no chicken flock had been dewormed in the last 3 months. The most frequent source of water was well water (84.4%) and 56.3% of households did not treat the drinking water in any manner.

No evidence of transmission from swine to humans was found during this study. Unfortunately, no parasites were obtained from swine, thus, transmission from humans to swine could not be investigated. Therefore, it would be interesting to apply in the future genotyping protocols to human and swine faecal samples to determine the species of *Ascaris* present, as well as for *Trichuris*, which was highly prevalent in the area and has also been reported to be zoonotic (Nejsum et al. 2012). Regarding *Giardia lamblia* genotyping to identify if animals and humans share the same assemblages could be sought in the future. It would also be interesting to conduct more observation and group-focused discussion to investigate hygiene practices and to get a deeper understanding of the population's views on parasitism.

Above all, understanding the different sources of infection for humans and animals can help improve control programmes and monitor possible anthelmintic resistance genes (Anderson 2001) or adaptive markers transfer.

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