

## **Molecular epidemiology of ascariasis in East Africa.**

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The Autumn Meeting  
British Society for Parasitology  
Durham University  
UK  
September 23-24; 2010

### **ABSTRACT**

It is estimated that more than 1 billion people are infected with the giant intestinal roundworm, *Ascaris lumbricoides*. Although the greatest numbers of infected individuals are found in Asia and sub-Saharan Africa, ascariasis shows a cosmopolitan distribution and is found in many deprived communities in temperate and tropical areas.

We are using molecular epidemiology techniques to study the population structure of *Ascaris*. Ascarid worms were obtained from human hosts on Zanzibar and in Uganda. Additionally, worms were collected from pigs in Uganda and Tanzania. Genomic DNA was extracted from all worms. A 383 base pair region of the mitochondrial cytochrome c oxidase I gene (CO1) was sequenced for each worm. Sequences were aligned to identify non-synonymous substitutions, and phylogenetic analysis and assessment of genetic diversity was undertaken. In addition, 4 microsatellite loci were amplified for all Tanzanian samples and a subset of the Ugandan samples. *Ascaris* populations from different areas and hosts were compared by calculating pairwise  $F_{ST}$  and testing for genetic differentiation.

So far 40 different CO1 haplotypes have been detected in *A. lumbricoides* from humans and pigs. There is near complete segregation of CO1 haplotypes between pig and human worms but little obvious geographical structuring. In contrast, based on the microsatellite analysis there is evidence for genetic differences between populations from different countries and different hosts. Further analysis should provide insights into the transmission dynamics of *Ascaris* in East Africa.