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A MOLECULAR METHOD TO DIFFERENTIATE BETWEEN THREE GENOTYPES OF *TRICHURIS* RECOVERED FROM HUMANS AND PIGS

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Abstract

The whipworms *Trichuris trichiura* and *T. suis* in humans and pigs, respectively, are believed to be closely related but different species. Despite several attempts no reliable morphological characters have been identified which can discriminate worms from the two hosts. Recent sequence analysis has suggested that 3 major ITS-2 genotypes are present in *Trichuris* obtained from human and pigs; namely a type 1 and 2 and a heterozygote. We have used this information to develop a PCR-linked Restriction Fragment Length Polymorphism (PCR-RFLP) that can identify the three genotypes. The method was applied on worms obtained from pigs collected in Uganda, USA, Tanzania, Jamaica and Denmark and worms obtained from humans collected in Uganda, Jamaica and China. The distribution of the three genotypes (type 1, type 2 and heterozygote) was 2, 0 and 57, respectively, in 59 worms recovered from pigs and 26, 2 and 1, respectively in 29 worms recovered from human. The results clearly suggest that *Trichuris* in humans and pigs belong to two different populations ($\chi^2 = 49.5$; $P < 0.001$). However, we have also found evidence for a few cases of cross-infections and the existence of heterozygote worms, the latter suggesting cases of hybridization or retention of ancestral polymorphism.