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Published

2010

Conference Title

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Genetic characterization of *Giardia duodenalis* from Australian sheep - zoonotic implications ?

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Giardia duodenalis is one of the commonest non-bacterial causes of diarrhoea worldwide. Of the seven known genetic assemblages (A-G) of *G. duodenalis*, A and B are usually associated with human infections, although some wild and domestic animals can harbour the same genotypes as those found in humans. Here, we explored the genetic composition of *G. duodenalis* from lambs from farms in south-eastern Australia, employing PCR-coupled targeted sequencing and restriction endonuclease fingerprinting (REF) analysis of part of the triose-phosphate isomerase gene (designated *tpi*). *G. duodenalis* was detected by PCR in 15% of 284 sheep. The analysis of all *tpi* amplicons identified 14 distinct sequences (half of which had 1-5 polymorphic positions) which were linked to assemblages A and E based on phylogenetic inference. These sequences differed by up to 12.5%, equating to a maximum of 63 mutations over 504 nucleotide positions. The nucleotide polymorphisms detected in *tpi* were inferred not to be a consequence of mixed-assemblage infection, or PCR- or sequencing-induced errors. With one exception, none of the polymorphisms recorded was inferred to exert a change to the conformation or functionality of the encoded protein, suggesting that some populations of *G. duodenalis* (assemblages A and E) in individual sheep harboured distinct alleles encoding distinct isoforms of triose-phosphate isomerase. Of the 14 sequence variants detected, 13 are new records. One dominant variant (representing assemblage A) has been detected previously in humans and is thus suggested to be zoonotic. Future investigations, using *tpi* and other loci, should assess the zoonotic potential of *G. duodenalis* from a wide range of yet unstudied animals.