

Abstract

Taenia species of domestic dogs can cause cysticercosis and coenurosis in a wide range of intermediate hosts including humans. Most taeniids of dogs are globally distributed, but some wildlife-transmitted species can be specific for certain regions. Generally, little information exists on the species composition and frequency in most regions of the world, which impairs risk assessment and control strategies. This study determined the range of taeniid species in dogs in four widely spaced areas of Kenya by genetic identification of eggs in faeces collected from the environment. Individual taeniid eggs were characterised by nested polymerase chain reaction of NADH dehydrogenase subunit 1 and cytochrome C oxidase 1 genes, restriction fragment length polymorphism and partial sequencing. Overall 79/1621 (4.9%) faecal samples contained eggs of *Taenia* or *Hydatigera* (8.0% in Turkana, 4.8% in Isiolo, 3.8% in Maasai Mara and 1.3% in Meru). *Taenia hydatigena* and *T. multiceps* were the most frequent, found in 36 and 15 samples, respectively. Other eggs found in the faeces belonged to *T. serialis* (sensu lato), *T. madoquae* (the first record in domestic dogs), *T. ovis*, *T. saginata* and *Hydatigera taeniaeformis*. Polymorphism of *nad1* sequences revealed 22 and 8 haplotypes of *T. hydatigena* and *T. multiceps*, respectively. The results show the involvement of dogs in both domestic and sylvatic transmission cycles. In addition to the species range, this study provides data on the intraspecific diversity of *T. hydatigena* and *T. multiceps* in Kenya, which will serve as baseline information for further studies into cysticercosis and coenurosis in livestock and humans in the region