Veterinary Parasitology 202 (2014) 69–94

Contents lists available at ScienceDirect

Veterinary Parasitology

journal homepage: www.elsevier.com/locate/vetpar

Review

Echinococcosis in wild carnivorous species: Epidemiology, genotypic diversity, and implications for veterinary public health

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ARTICLE INFO

Article history:
Received 13 January 2014
Received in revised form 25 February 2014
Accepted 2 March 2014

Keywords:
Echinococcus
Wildlife
Epidemiology
Molecular characterization
Zoonoses
Veterinary public health

ABSTRACT

Echinococcosis is a zoonosis caused by helminths of the genus *Echinococcus*. The infection, one of the 17 neglected tropical diseases listed by the World Health Organization, has a cosmopolitan distribution and can be transmitted through a variety of domestic, synanthropic, and sylvatic cycles. Wildlife has been increasingly regarded as a relevant source of infection to humans, as demonstrated by the fact that a significant proportion of human emerging infectious diseases have a wildlife origin. Based on available epidemiological and molecular evidence, of the nine *Echinococcus* species currently recognized as valid taxa, *E. canadensis* G8–G10, *E. felidis*, *E. multilocularis*, *E. oligarthrus*, *E. shiquicus*, and *E. vogeli* are primarily transmitted in the wild. *E. canadensis* G6–G7, *E. equinus*, *E. granulosus* s.s., and *E. ortleppi* are considered to be transmitted mainly through domestic cycles. We summarize here current knowledge on the global epidemiology, geographical distribution and genotype frequency of *Echinococcus* spp. in wild carnivorous species. Topics addressed include the significance of the wildlife/livestock/human interface, the sympatric occurrence of different *Echinococcus* species in a given epidemiological scenario, and the role of wildlife as natural reservoir of disease to human and domestic animal populations. We have also discussed the impact that human activity and intervention may cause in the transmission dynamics of echinococcosis, including the human population expansion an encroachment on shrinking natural habitats, the increasing urbanization of wildlife carnivorous species and the related establishment of synanthropic cycles of *Echinococcus* spp., the land use (*e.g.* deforestation and agricultural practices), and the unsupervised international trade and translocation of wildlife animals. Following the 'One Health' approach, we have also emphasized that successful veterinary public health interventions in the field of echinococcosis requires an holistic approach to integrate current knowledge on human medicine, veterinary medicine and environmental sciences.

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http://dx.doi.org/10.1016/j.vetpar.2014.03.009
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Contents

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1. Introduction

Zoonoses are defined as infectious diseases that are naturally transmitted between vertebrate animal species and humans (WHO, 1951). Overall, 61% (868/1415) of the species of infectious organisms known to be pathogenic to humans are zoonotic (Taylor et al., 2001). Among them, helminths are especially likely to be associated with zoonoses, as 95% (274/287) of the members of this parasite group have wild and/or domestic animals acting as natural reservoirs (Taylor et al., 2001). Furthermore, 60% of human emerging infectious diseases can also be catalogued as zoonoses, the majority of these (71.8%) being originated in wildlife (Jones et al., 2008). Not surprisingly, wildlife has received increasing attention in recent years not only as potential reservoir of disease to domestic animals and humans (Kruse et al., 2004; Chomel et al., 2007), but also as recipient of pathogenic agents resulting from spill-over from domestic hosts (Thompson, 2013). This scenario has contributed to the establishment of the "One Health" concept, which has been defined as 'the collaborative effort of multiple disciplines—working locally, nationally, and globally—to attain optimal health for people, animals and the environment' (American Veterinary Medical Association, 2008). Under this approach, animal and environmental health is thought to be mutual and dynamically intersected, and therefore should be considered as a whole (Alexander et al., 2012; Thompson, 2013). Characterization of zoonotic disease transmission with a wildlife reservoir is a complex task which is usually hindered by limited knowledge regarding pathogen diversity and susceptibility (MacPhee and Greenwood, 2013). In addition, a number of natural (size and density of wildlife host populations) or anthropogenic (human population expansion and encroachment, changes in agricultural practices, reforestation, wildlife translocation, and climatic changes) factors may have a marked influence on the epidemiology of these zoonoses (Kruse et al., 2004; Chomel et al., 2007).

Members of the genus *Echinococcus* are zoonotic helminth parasites (phylum Platyhelminthes, class Cestoda) with a worldwide distribution. The adult worm lives in the small intestine of suitable canids (domestic and bush dogs, wolves, foxes, jackals, racoon dogs, and coyotes), felids (lions, cougars, jaguars, and jaguarundis), and hyenids (hyenas) laying eggs that are excreted with the faeces of the animal and contaminating the environment. Susceptible intermediate host (ungulate and rodent) species that accidentally ingest infective eggs will develop the parasite's larval stage or metacestode. Humans are an aberrant, dead-end host that do not play a role in the natural cycle of the parasite. Based on recent molecular and phylogenetic evidence, the *Echinococcus* genus comprises nine valid species including *E. granulosus* sensu stricto (*E. granulosus* s.s., genotypes G1–G3), *E. equinus* (G4), *E. ortleppi* (G5), *E. canadensis* (G6–G10), *E. felidis*, *E. multilocularis*, *E. oligarthrus*, *E. shiquicus*, and *E. vogeli* (Thompson and McManus, 2002; Xiao et al., 2005; Nakao et al., 2007, 2013a,b; Huttner et al., 2008; Thompson, 2008). In addition, intraspecific phylogeny and geographical variations have also been reported in *E. multilocularis* and the Neotropical species *E. vogeli* (Knapp et al., 2009; Nakao et al., 2009; Santos et al., 2012).

E. granulosus s.s., *E. equinus*, and *E. ortleppi* are essentially maintained in domestic cycles involving dogs and a number of livestock species (see Cardona and Carmena, 2013; Carmena and Cardona, 2013). *E. canadensis* can be transmitted through both domestic and sylvatic life cycles, whereas *E. felidis*, *E. multilocularis*, *E. shiquicus*, *E. oligarthrus*, and *E. vogeli* are primarily circulating in wildlife cycles,

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