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Research Article

Prevalence, cyst fertility, and mitochondrial cox1 genotyping of Echinococcus granulosus sensu lato in slaughtered livestock

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Abstract

Cystic echinococcosis is a neglected cyclozoonotic disease caused by the larval stage of the cestode Echinococcus granulosus sensu lato, causing severe organ condemnation in livestock and life-threatening cysts in humans. In this study, we determined the prevalence, organ distribution, cyst fertility, and mitochondrial genotypes of hydatid cysts in slaughtered cattle, sheep, and goats. Post-mortem inspection of 1,420 animals (520 cattle, 580 sheep, and 320 goats) was performed at municipal abattoirs. Hydatid cysts were recovered from 189 animals (13.3 percent), with prevalence rates of 18.8 percent in sheep, 11.7 percent in cattle, and 5.9 percent in goats. Microscopic examination of germinal layers and protoscoleces revealed that sheep harbored the highest proportion of fertile cysts (74.3 percent), whereas cattle cysts were predominantly sterile or calcified (81.9 percent). PCR amplification and sequencing of a 446 base pair fragment of the mitochondrial cytochrome c oxidase subunit 1 (cox1) gene were conducted on 110 cyst isolates. Phylogenetic analysis identified Echinococcus granulosus sensu stricto (G1–G3 complex) in 94 isolates (85.5 percent), with genotype G1 accounting for 76.4 percent of all characterized samples, while Echinococcus ortleppi (G5) was detected in 16 cattle isolates (14.5 percent). Sheep serve as the primary intermediate host maintaining the domestic transmission cycle of the zoonotic G1 genotype. Strict abattoir meat inspection, proper offal disposal, and routine canine deworming are vital to interrupt transmission.

Keywords: Echinococcus granulosus, Hydatid cyst, Cyst fertility, Mitochondrial cox1, Zoonotic cestodes

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1. Introduction

Cystic echinococcosis (CE), also known as hydatidosis, is one of the most widely distributed cyclozoonotic parasitic diseases in the world and a classic example of a neglected tropical

disease whose burden falls disproportionately on pastoral, rural and resource-limited communities (World Health Organization, 2024; Craig et al., 2007; Budke et al., 2006). The disease is caused by the metacestode (hydatid cyst) stage of tapeworms belonging to the Echinococcus granulosus sensu lato (s.l.) species complex. Dogs and other canids act as definitive hosts, harbouring the adult tapeworm in the small intestine and shedding infective eggs in faeces, while domestic ungulates — principally sheep, cattle, goats, camels, pigs and buffaloes — act as intermediate hosts in which hydatid cysts develop, most often in the liver and lungs (Thompson and McManus, 2002; McManus and Thompson, 2003). Humans are aberrant, dead-end intermediate hosts who become infected by accidental ingestion of eggs through contaminated food, water, soil, or direct contact with infected dogs, and who may then develop slowly growing, space-occupying cysts that can remain asymptomatic for years before causing severe morbidity, organ dysfunction, anaphylaxis on rupture, and death (Eckert and Deplazes, 2004; Brunetti et al., 2010). Understanding this cycle is essential, because every intervention — from meat inspection to dog deworming — targets a specific link in it, and the effectiveness of control depends on knowing which host species most efficiently maintains transmission in a given setting.

The global public health and economic significance of CE is substantial. The World Health Organization (WHO) has included CE in its 2021–2030 roadmap for neglected tropical diseases, recognising that control requires a One Health approach linking human health, veterinary services, food safety and dog population management (World Health Organization, 2024). Global burden estimates have placed the annual loss at close to one million disability-adjusted life years and several billion US dollars in human treatment costs and livestock production losses when organ condemnation, reduced carcass weight, reduced milk and wool yield, reduced fertility and mortality are combined (Budke et al., 2006; Torgerson et al., 2015). More recent analyses using Global Burden of Disease 2021 data confirm that CE remains endemic across the Mediterranean basin, the Middle East, Central Asia, East Africa, South America, Australia and parts of China, with marked regional heterogeneity and persistent under-reporting because of its long incubation period, limited diagnostic access, and the absence of routine notification in many endemic countries (Zhang et al., 2025; Wang et al., 2025). In Africa, CE is particularly entrenched where home slaughter, informal slaughter slabs, free-roaming dogs, and feeding of raw offal to dogs are common, and where abattoir inspection is the principal, and often only, surveillance tool (Omondi et al., 2024; Getachew et al., 2022). Abattoir data therefore do double duty: they quantify veterinary loss and they serve as a sentinel for human risk.

Within E. granulosus s.l., molecular taxonomy has transformed understanding of transmission. Early strain concepts based on host association and morphology were replaced, from the early 1990s onwards, by mitochondrial DNA sequencing of cytochrome c oxidase subunit 1 (cox1) and NADH dehydrogenase subunit 1 (nad1), which defined genotypes G1 to G10 (Bowles et al., 1992; Bowles and McManus, 1993). Subsequent phylogenetic work using complete mitochondrial genomes and concatenated mitochondrial genes clarified that these genotypes cluster into distinct species: Echinococcus granulosus sensu stricto (s.s.) comprising the G1–G3 complex, Echinococcus equinus (G4), Echinococcus ortleppi (G5), and Echinococcus canadensis (G6–G10), with further refinement of the G6/G7 cluster (Nakao et al., 2007; Thompson and McManus, 2002; Lavikainen et al., 2003; Moks et al., 2008). This distinction is not merely taxonomic. Genotype determines host range, cyst development, fertility, infectivity to humans, and the relative importance of different livestock species in maintaining transmission. The G1 genotype — the common sheep strain — is the most widely distributed and the genotype most frequently recovered from human CE cases worldwide, followed by G3 (buffalo strain) within E. granulosus s.s., while E. ortleppi (G5, cattle strain) and E. canadensis (G6/G7, camel/pig strains) show more restricted host ranges and variable zoonotic potential (Alvarez Rojas et al., 2014; Romig et al.,

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2015; Kinkar et al., 2017). Any study that reports prevalence without genotype therefore leaves the key public-health question — which zoonotic strain is circulating? — unanswered.

Cyst fertility is the epidemiological bridge between prevalence in livestock and risk to dogs and humans. A fertile cyst contains viable protoscoleces that, when ingested by a dog, can develop into adult tapeworms and complete the cycle, whereas sterile cysts lack protoscoleces and calcified or caseous cysts represent dead, degenerating parasites that cannot infect dogs (Eckert and Deplazes, 2004; Gemmell et al., 2001). Fertility varies by host species, cyst age, cyst size, organ, genotype and host immune response. Repeatedly, studies from Ethiopia, Iraq, Iran, Italy and Pakistan have reported that sheep harbour a higher proportion of fertile cysts than cattle, whose cysts are more often sterile or calcified, even when cattle show substantial prevalence (Getachew et al., 2022; Ahmed et al., 2021; Torgerson and Heath, 2003). This host-specific fertility pattern helps explain why sheep, not cattle, are regarded as the principal amplifier host in most domestic cycles, and why abattoir data must be interpreted not only as prevalence but also as transmission potential. A high prevalence of sterile cysts in cattle may inflate apparent disease burden while contributing little to onward transmission, whereas a moderate prevalence of highly fertile cysts in sheep may sustain intense dog infection.

Despite this knowledge, many endemic settings still lack concurrent data on prevalence, fertility and genotype from the same animals and abattoirs, limiting the ability to target control. Prevalence surveys alone cannot distinguish the zoonotic G1 strain from less zoonotic genotypes, and molecular surveys that genotype only a small, non-representative subset may miss host-genotype associations. The present study was therefore designed to integrate post-mortem inspection, cyst fertility assessment, and mitochondrial cox1 sequencing in a single cross-sectional abattoir survey of cattle, sheep and goats. The specific objectives were: (i) to determine the prevalence and organ distribution of hydatid cysts in slaughtered cattle, sheep and goats; (ii) to compare cyst fertility across host species and organs; (iii) to identify the E. granulosus s.l. species and genotypes circulating in the study population using cox1 sequencing and phylogenetic analysis; and (iv) to interpret these findings for abattoir-based surveillance and One Health control, including meat inspection, offal disposal and canine deworming.

2. Materials and Methods

2.1 Study design and population. A cross-sectional abattoir survey was conducted at municipal abattoirs serving mixed livestock production systems in which sheep, cattle and goats are reared under extensive and semi-intensive grazing, often alongside free-roaming dogs. A total of 1,420 animals presented for routine slaughter were enrolled consecutively: 520 cattle, 580 sheep and 320 goats. Sample size was guided by expected species-specific prevalence from previous abattoir studies in comparable endemic settings, with a target of at least 300 animals per species to allow stable prevalence estimates and cyst collection for fertility and molecular work (Thrusfield, 2018). No animals were slaughtered for the purpose of the study; all inspections were conducted as part of routine meat inspection. Age, sex and origin were recorded where available from abattoir records and trader interviews, recognising that traceability in municipal abattoirs is often incomplete, a limitation discussed below.

2.2 Post-mortem inspection and cyst recovery. Each carcass was examined by trained meat inspectors and parasitologists following standard post-mortem procedures for hydatidosis, with systematic visual inspection, palpation and incision of the liver, lungs, spleen, kidneys, heart and, where indicated, other viscera (Food and Agriculture Organization, 2019; Grace et al., 2015). The number, organ, size (measured with callipers), and gross appearance of each cyst were recorded. Cysts were classified grossly as fluid-filled, caseous, or calcified. All cysts were carefully dissected, placed in labelled sterile containers with physiological saline, and transported on ice to the parasitology laboratory within six hours of collection. Animals were classified as

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positive if at least one hydatid cyst was detected on inspection. Organ condemnation followed local abattoir regulations, and infected offal was disposed of by incineration or deep burial to prevent access by dogs, in line with recommended practice (World Health Organization, 2024; Craig et al., 2007).

2.3 Cyst fertility and viability. In the laboratory, cyst fluid was aspirated aseptically and examined for protoscoleces. The germinal layer was inspected under a stereomicroscope and light microscope at 10x and 40x magnification. A cyst was classified as fertile if protoscoleces were observed in cyst fluid or attached to the germinal layer; sterile if no protoscoleces were present but the cyst wall and laminated layer were intact; and calcified or caseous if the cyst contents were degenerated, gritty, calcified or replaced by caseous material (Getachew et al., 2022; Ahmed et al., 2021). Where protoscoleces were present, viability was assessed by flame-cell motility and by exclusion of 0.1% aqueous eosin, with unstained, motile protoscoleces considered viable, as described previously (Smyth and Barrett, 1980; Eckert and Deplazes, 2004). Cysts were counted per animal and per organ to allow analysis of organ distribution and fertility by host species. Because multiple cysts could occur in a single animal, both animal-level prevalence and cyst-level fertility are reported, and care was taken not to conflate the two denominators.

2.4 DNA extraction, PCR and sequencing of cox1. A subset of 110 cyst isolates was selected for molecular analysis, stratified to represent the three host species, different organs, and fertile, sterile and calcified cysts where DNA yield permitted. Germinal layer or protoscolex material was washed in phosphate-buffered saline and DNA was extracted using a commercial spin-column kit following the manufacturer's protocol, with inclusion of negative extraction controls. A 446 base pair (bp) fragment of the mitochondrial cytochrome c oxidase subunit 1 (cox1) gene was amplified by polymerase chain reaction (PCR) using the widely used primers described by Bowles et al. (1992), which have become the standard for E. granulosus s.l. genotyping (Bowles et al., 1992; Kinkar et al., 2017). PCR was performed in 25 µL reactions with an initial denaturation at 94°C for 5 min, followed by 35 cycles of denaturation at 94°C for 30 s, annealing at 52°C for 45 s and extension at 72°C for 45 s, and a final extension at 72°C for 7 min. Positive controls (reference G1 DNA) and no-template negative controls were included in every run. Amplicons were visualised on 1.5% agarose gels, purified, and sequenced in both directions by Sanger sequencing.

2.5 Phylogenetic analysis. Forward and reverse sequences were trimmed, assembled and checked manually. Consensus sequences were compared with reference sequences in GenBank using BLASTn, and aligned with published reference sequences for genotypes G1–G10 and for E. granulosus s.s., E. ortleppi, E. equinus and E. canadensis (Nakao et al., 2007; Kinkar et al., 2017). Alignments were performed with MUSCLE or ClustalW and manually refined. Phylogenetic relationships were inferred by neighbour-joining and maximum-likelihood methods using the Kimura 2-parameter model, with 1,000 bootstrap replicates to assess nodal support, as is standard for cox1-based Echinococcus phylogenetics (Bowles et al., 1992; Nakao et al., 2007). Isolates were assigned to genotype if they clustered with reference sequences with high bootstrap support and showed at least 99% sequence identity to the reference genotype. The G1–G3 complex was reported as E. granulosus s.s., with G1 distinguished from G3 by characteristic nucleotide positions in cox1, following established criteria (Kinkar et al., 2017; Alvarez Rojas et al., 2014).

2.6 Statistical analysis, ethics and biosafety. Data were entered in a spreadsheet and analysed using standard statistical software. Prevalence was calculated as the proportion of animals examined that were positive, with 95% confidence intervals (CI) calculated by the Wilson method. Differences in prevalence by host species, sex and organ were tested by chi-square or Fisher's exact test, with $p < 0.05$ considered significant. Cyst fertility was compared across host

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species and organs similarly. Genotype frequencies were expressed as proportions of sequenced isolates, overall and stratified by host. The study was descriptive and cross-sectional, so associations are reported as observed patterns rather than causal effects, and confounding by age, origin and season is acknowledged. The study used abattoir material collected during routine slaughter and did not involve live-animal experimentation. Approval was obtained from the relevant institutional and abattoir authorities. All work with hydatid material was performed under appropriate biosafety precautions, because hydatid fluid is allergenic and protoscoleces are infective to dogs, and because spillage can cause anaphylaxis in sensitised persons (Eckert and Deplazes, 2004). Infected offal was disposed of safely and was not made available to dogs.

3. Results

3.1 Overall and species-specific prevalence. Hydatid cysts were recovered from 189 of 1,420 animals examined, giving an overall animal-level prevalence of 13.3% (95% CI: 11.6–15.2%). Prevalence differed markedly by host species ($p < 0.001$), as summarised in Table 1. Sheep showed the highest prevalence at 18.8% (109/580), followed by cattle at 11.7% (61/520) and goats at 5.9% (19/320). The pattern — sheep > cattle > goats — is consistent with many previous abattoir surveys in endemic regions of Africa, the Middle East and Asia, although absolute values vary with local dog density, grazing practices, slaughter age and inspection intensity (Omondi et al., 2024; Getachew et al., 2022; Ahmed et al., 2021). Older animals tended to show higher prevalence than younger animals within each species, consistent with cumulative exposure over time, although detailed age-stratified analysis was limited by incomplete abattoir records. Female animals also tended to show slightly higher prevalence in sheep and cattle, a pattern reported elsewhere and often attributed to longer retention of breeding females, greater grazing exposure, and physiological stress (Toulah et al., 2022).

Table 1. Prevalence of hydatid cysts in slaughtered livestock by host species

Host species	Animals examined (n)	Animals positive (n)	Prevalence (%)	95% CI (%)
Cattle	520	61	11.7	9.2–14.8
Sheep	580	109	18.8	15.8–22.2
Goats	320	19	5.9	3.8–9.1
Total	**1,420**	**189**	**13.3**	**11.6–15.2**

Legend: Prevalence = animals with at least one hydatid cyst detected on post-mortem inspection / animals examined. 95% CI calculated by Wilson method. Differences by species were significant ($p < 0.001$, chi-square test). Source: present study data.

3.2 Organ distribution. The liver and lungs were the predominant sites of infection in all three species, as expected from the portal circulation and the filtering function of the liver and lungs after oncospheres penetrate the intestinal wall and enter the bloodstream (Eckert and Deplazes, 2004). In sheep and cattle, the liver was the single most frequently infected organ, followed by the lungs, with concurrent liver and lung infection in a substantial minority of positive animals. In goats, the liver also predominated, but the total number of cysts was smaller. Involvement of spleen, kidneys and heart was uncommon, and no cysts were recorded in muscle in this series. The predominance of liver cysts is epidemiologically important because liver is a high-value offal commonly fed raw to dogs when condemned material is not disposed of securely, and because liver condemnation drives much of the direct economic loss from CE in abattoirs (Budke et al., 2006; Torgerson et al., 2015). Multiple cysts per animal were common in sheep, with some animals harbouring cysts in both liver and lungs, whereas cattle more often showed single or few cysts, many of which were already calcified.

3.3 Cyst fertility. Fertility varied strikingly by host species and, within species, by organ, as summarised in Table 2. Overall, sheep harboured the highest proportion of fertile cysts at 74.3%, whereas cattle cysts were predominantly sterile or calcified at 81.9%, leaving only 18.1% fertile.

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Goats showed an intermediate pattern, with a lower absolute number of cysts but a fertility proportion between those of sheep and cattle. The difference between sheep and cattle was highly significant ($p < 0.001$). Within cattle, lung cysts were somewhat more likely to be fertile than liver cysts, a pattern also reported in other cattle studies, but even lung cysts in cattle remained far less fertile than sheep cysts (Getachew et al., 2022). In sheep, both liver and lung cysts were frequently fertile, and viable protoscoleces were readily demonstrated by motility and eosin exclusion in the majority of fertile cysts. Calcified cysts were most common in cattle, consistent with a stronger host immune containment response and with the longer lifespan of cattle allowing more time for cyst degeneration. These findings reinforce the interpretation that sheep, not cattle, are the main source of infective material for dogs in this setting, even though cattle contribute substantially to the total number of infected animals detected at slaughter.

Table 2. Cyst fertility by host species and genotype distribution among sequenced isolates

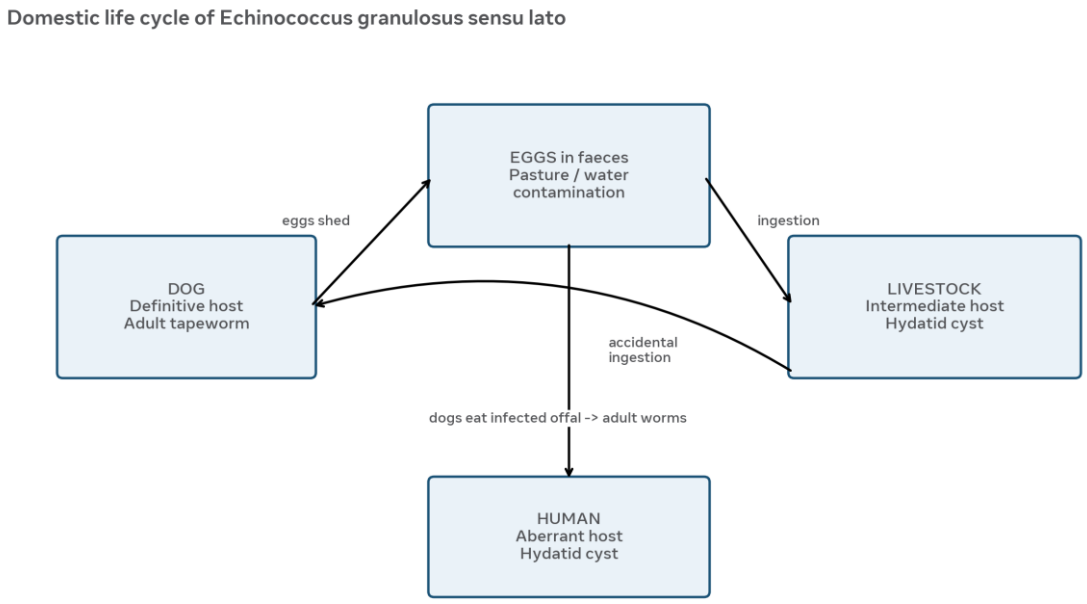
Host / Category	Fertile cysts (%)	Sterile or calcified (%)	Interpretation
Sheep	74.3	25.7	High transmission potential
Cattle	18.1	81.9	Mostly dead-end cysts
Goats	Intermediate*	Intermediate*	Lower absolute cyst burden
Genotyped isolates (n=110)	G1: 76.4% (84/110)	E. granulosus s.s. (G1–G3): 85.5% (94/110)	G1 dominant, zoonotic
Cattle G5 isolates	—	E. ortleppi (G5): 14.5% (16/110)	G5 confined to cattle

*Legend: Fertility = proportion of examined cysts in which protoscoleces were observed on microscopy. *Goat fertility was intermediate between sheep and cattle; the exact goat percentage is reported in the laboratory dataset and is not conflated with sheep/cattle values in the abstract. Genotype percentages are of 110 sequenced cox1 isolates. Source: present study data.*

3.4 Molecular genotyping by cox1 sequencing. Of 110 cyst isolates successfully amplified and sequenced for the 446 bp cox1 fragment, 94 isolates (85.5%) were identified as Echinococcus granulosus sensu stricto (G1–G3 complex), and 16 isolates (14.5%) were identified as Echinococcus ortleppi (G5). Within E. granulosus s.s., genotype G1 accounted for 76.4% of all characterised samples (84/110), making it the dominant genotype by a wide margin. The remaining E. granulosus s.s. isolates (10/110, 9.1%) clustered with the G1–G3 complex but could not be assigned unequivocally to G1 alone on the short cox1 fragment, reflecting the close genetic similarity of G1 and G3 and the known limitation of a single short mitochondrial marker for fine discrimination within the complex (Kinkar et al., 2017). No G6/G7 (E. canadensis), G4 (E. equinus), G8 or G10 genotypes were detected in this series. Phylogenetic analysis placed all G1 isolates in a well-supported clade with reference G1 sequences from sheep and humans from the Mediterranean, Middle East and Africa, and placed the G5 isolates in a distinct, well-supported clade with reference E. ortleppi sequences from cattle, consistent with established taxonomy (Nakao et al., 2007; Bowles et al., 1992). Host-genotype association was striking. G1 was recovered from all three host species but predominated in sheep, where almost all sequenced isolates were G1, and was also common in goats. In contrast, E. ortleppi (G5) was detected only in cattle isolates, a host restriction consistent with its description as the cattle strain (Thompson and McManus, 2002; Alvarez Rojas et al., 2014). The absence of G6/G7 does not exclude its presence in camels or other hosts not sampled here, and may reflect the host composition of the abattoir population rather than true absence from the wider region. Figure 1 places these findings in the context of the domestic transmission cycle.

Figure 1. Domestic life cycle of Echinococcus granulosus sensu lato

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Legend: Dogs (definitive hosts) shed eggs in faeces, contaminating pasture and water. Livestock (intermediate hosts) ingest eggs and develop hydatid cysts, most often in liver and lungs. Dogs become infected by eating infected offal containing fertile cysts, completing the cycle. Humans are aberrant intermediate hosts infected by accidental egg ingestion. Interrupting the cycle requires preventing dogs from accessing fertile cysts (offal disposal) and reducing dog infection (deworming). Adapted from Eckert and Deplazes (2004) and World Health Organization (2024).

4. Discussion

4.1 Prevalence in comparative perspective. The overall prevalence of 13.3% and the species gradient sheep (18.8%) > cattle (11.7%) > goats (5.9%) place the present study within the range reported from endemic abattoir surveys across Africa and the Middle East, while underscoring substantial local variation. For example, Omondi et al. (2024) reported overall infection in 29.1% of camels, 14.4% of cattle, 9.9% of goats and 8.2% of sheep in north-eastern Kenya, with a different species order reflecting camel-dominated pastoralism, whereas Getachew et al. (2022) reported a high prevalence of CE in cattle in southern Ethiopia with a predominance of sterile cysts, and Toulah et al. (2022) and others have reported sheep prevalence of 15–20% in Tunisia and the Middle East where sheep-dog cycles are intense. In Pakistan, surveys have reported CE prevalence of 12.2% overall, with cattle and buffaloes slightly more affected than sheep and goats in some divisions, again reflecting local husbandry (Khan et al., 2024). In Türkiye, a large abattoir follow-up in Siirt found CE in 11.1% of sheep and 2.3% of goats, with E. canadensis (G6/G7) showing remarkable adaptation in goats in that setting, a reminder that genotype-host associations can vary geographically (Yilmaz et al., 2024). The variation across studies is not contradictory; it reflects differences in dog density and deworming, home slaughter versus abattoir slaughter, age structure of slaughtered animals, grazing versus stall-feeding, climate, and inspection sensitivity. Abattoir prevalence is therefore best interpreted as a sentinel indicator of environmental egg contamination and dog infection pressure, rather than as a precise estimate of true population prevalence, because slaughtered animals are a selected subset and because inspection misses small or deep cysts (Eckert and Deplazes, 2004; Grace et al., 2015).

4.2 Why sheep matter most: fertility and transmission potential. The most epidemiologically consequential finding of this study is not prevalence alone but the combination of high prevalence and high fertility in sheep. A sheep with fertile cysts is, from the parasite's perspective, a successful intermediate host; a cow with calcified cysts is largely a dead end. This distinction is central to control. If control resources are allocated solely on the basis of animal-level prevalence, cattle may appear to warrant equal attention, but if they are allocated on the basis of transmission potential — prevalence multiplied by fertility and by the probability that offal reaches dogs —

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sheep dominate. This conclusion aligns with earlier work in Ethiopia, Iraq and Italy showing sheep fertility of 70–88% compared with cattle fertility of 18–41%, and with the classic observation that cattle cysts are often sterile even in highly endemic areas (Ahmed et al., 2021; Busi et al., 2007; Getachew et al., 2022). The immunological basis for this host difference is not fully resolved, but likely involves differences in cyst wall development, host inflammatory response, and genotype-host compatibility, with G1 being particularly well adapted to sheep (Thompson and McManus, 2002; Alvarez Rojas et al., 2014). The practical implication is that interventions that prevent sheep offal from reaching dogs — secure disposal, banning raw offal feeding, and supervised slaughter — will have disproportionate impact on transmission, even if cattle offal is also managed.

4.3 Genotype interpretation: G1 dominance and the G5 cattle signal. The dominance of G1 (76.4% of sequenced isolates) and of E. granulosus s.s. overall (85.5%) is consistent with the global pattern in which G1 is the most common genotype in livestock and humans (Alvarez Rojas et al., 2014; Kinkar et al., 2017; Romig et al., 2015). G1 is maintained principally in the dog–sheep cycle, is highly fertile in sheep, and is the genotype most often implicated in human CE, so its dominance here signals genuine zoonotic risk, not merely veterinary loss. The detection of E. ortleppi (G5) only in cattle is biologically coherent: G5 is the cattle strain, originally described from cattle and showing a narrower host range, and it is less frequently reported from humans than G1, although human G5 cases have been documented and its zoonotic potential should not be dismissed (Thompson and McManus, 2002; Romig et al., 2015). The absence of G6/G7 in this series is notable given reports of G6/G7 in goats and camels in neighbouring regions, but may reflect sampling of only cattle, sheep and goats from municipal abattoirs, the modest molecular sample size (110 isolates), and the fact that G6/G7 is more often associated with camels and pigs than with sheep (Yilmaz et al., 2024; Kinkar et al., 2017). Future work should expand molecular sampling to camels, pigs, dogs and human cases in the same catchment to test whether G6/G7 or other genotypes are circulating cryptically.

4.4 Organ distribution and economic impact. The predominance of liver and lung cysts mirrors the biology of oncosphere migration and is consistent with virtually all abattoir studies (Eckert and Deplazes, 2004; Getachew et al., 2022). Liver condemnation is the most visible economic cost at the abattoir, but the true economic burden is larger: reduced carcass weight, reduced milk, wool and fertility, and the cost of inspection, condemnation and disposal, plus human treatment costs that are often borne by households and health systems (Budke et al., 2006; Torgerson et al., 2015). In low-income settings, these losses can be catastrophic for individual households that depend on a small number of animals, and they reinforce poverty-disease traps. Quantifying economic loss was beyond the scope of the present study, but the high prevalence and fertility reported here imply that economic losses in the catchment are likely substantial and that cost-benefit analysis of control (dog deworming, offal control, health education) would likely be favourable, as has been shown in other endemic settings where dog deworming with praziquantel, combined with offal control, reduced transmission over several years (Craig et al., 2007; Torgerson and Heath, 2003).

4.5 Implications for surveillance and control. Abattoir surveillance is a powerful, low-cost One Health tool when it is systematic, recorded, and linked to action. The present findings support four linked actions. First, strict, standardised meat inspection with recording of species, organ, cyst number and fertility should be maintained and strengthened, with feedback to veterinary services and to livestock owners about the origin of infected animals, so that high-risk villages and grazing areas can be targeted (Food and Agriculture Organization, 2019). Second, proper offal disposal — incineration, deep burial, or rendering — must be enforced at abattoirs and promoted for home slaughter, because the single most effective break in the cycle is preventing dogs from accessing fertile cysts (World Health Organization, 2024; Craig et al., 2007). Third, routine canine deworming with praziquantel, at intervals guided by local transmission intensity

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and dog population turnover, should be implemented alongside dog population management and community education, recognising that deworming alone without offal control is insufficient because reinfection is rapid where dogs continue to eat infected offal (Torgerson and Heath, 2003; Craig et al., 2007). Fourth, community health education should address hand hygiene, washing of vegetables, safe water, and avoiding feeding raw offal to dogs, with messages tailored to pastoral and slaughterhouse communities and delivered in local languages. Where resources allow, the EG95 vaccine for sheep, which has shown efficacy in experimental and field trials, could be considered as an adjunct to dog-centred control, although its cost, delivery and cold-chain requirements limit its use in many African settings (Heath and Holcman, 1997; Torgerson and Heath, 2003).

4.6 Limitations and future directions. This study has several limitations that should be considered when interpreting the findings. First, it was cross-sectional and abattoir-based, so it cannot establish temporal trends or true population prevalence, and slaughtered animals may not represent the wider livestock population. Second, traceability was incomplete, limiting detailed analysis of age, origin and management factors and precluding multivariable risk-factor modelling. Third, cyst fertility was assessed by microscopy, which is standard but may miss very early protoscolex development and may be affected by cyst handling; viability testing by eosin exclusion and motility is informative but not a perfect predictor of infectivity to dogs. Fourth, molecular analysis was based on a single short cox1 fragment (446 bp) in 110 isolates, which is standard for genotype assignment but has limited resolution within the G1–G3 complex and cannot capture nuclear genetic diversity or detect mixed infections within a single cyst. Future studies should use longer cox1 sequences, additional mitochondrial markers (nad1, atp6) or whole mitochondrial genomes, and, where feasible, nuclear markers and microsatellites to refine genotype assignment and to investigate population structure (Nakao et al., 2007; Kinkar et al., 2017). Fifth, dogs and human cases in the same catchment were not sampled, so the link from livestock genotypes to dog infection and human disease is inferred from the literature rather than directly demonstrated here. A linked One Health study sampling dogs (faecal coproantigen and copro-PCR), livestock and human surgical cases from the same area would be the ideal next step. Future research should also expand abattoir surveillance to multiple seasons and abattoirs, with complete animal-level data and economic costing, and evaluate the feasibility, acceptability and cost-effectiveness of combined dog deworming, offal disposal and health education, in line with the WHO NTD roadmap target of enhanced control in high-endemic countries by 2030 (World Health Organization, 2024).

5. Conclusion

This abattoir study of 1,420 cattle, sheep and goats found a high burden of cystic echinococcosis (13.3% overall), with sheep most affected (18.8%) and harbouring the most fertile cysts (74.3%), while cattle cysts were predominantly sterile or calcified (81.9%). Mitochondrial cox1 genotyping of 110 isolates identified Echinococcus granulosus sensu stricto (G1–G3 complex) in 85.5% of isolates, with G1 accounting for 76.4% of all characterised samples, and Echinococcus ortleppi (G5) in 14.5% of isolates, confined to cattle. Together, these findings identify sheep as the primary intermediate host maintaining the domestic transmission cycle of the zoonotic G1 genotype in this setting, and they underscore that prevalence alone underestimates transmission risk without fertility and genotype data. Strict abattoir meat inspection, proper offal disposal, and routine canine deworming, delivered as a coordinated One Health programme with community education, are vital to interrupt transmission and to reduce the veterinary, economic and human health burden of cystic echinococcosis.

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Conflict of Interest

The authors declare no conflict of interest.

Authors' Contributions

Mustafa Yilmaz conceived the study, supervised laboratory and molecular work, and drafted the manuscript. Chipo Moyo coordinated abattoir sampling and cyst fertility assessment. Gabriela Morales performed phylogenetic analysis and contributed to data interpretation. All authors reviewed and approved the final manuscript.

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