Molecular Characteristics of *Echinococcus granulosus* Strains Isolated from Iranian Camel Using High Resolution Melting Analysis of *atp6* and *cox1* Genes

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Abstract

**Background:** Cystic echinococcosis (CE) also known as hydatid disease, is a zoonotic helminthic disease caused by infection with the larval stage of a tapeworm *Echinococcus granulosus*. It is an important parasite regarding human health and is categorized into different genotypes. The present study aimed to identify different genotypes of *E. granulosus* metacestode isolated from Iranian camel.

**Methods:** In this cross-sectional study, 54 hydatid cysts were isolated from slaughtered Iranian camels (*Camelus dromedarius*) in Isfahan (33 samples) and Yazd (21 samples) province's slaughterhouses. The DNA was extracted from the isolated hydatid cysts and high resolution melting analysis (HRM) was performed. The curves were confirmed by sequencing and aligning with previously deposited sequences.

**Results:** Based on the results of the present study, 94.4%, 3.7%, and 1.9% of the studied isolates were identified as *E. granulosus* (G1), *E. granulosus* (G2), and *E. intermedius* (G6) in the two studied regions, respectively. Moreover, 85.18% of the cysts were isolated from lung and 5.82% of them were also isolated from the liver of the camels.

**Conclusion:** Based on the HRM analysis of *cox1* and *atp6* genes, *E. granulosus* (G1) accounts for the most cases of camelid cystic echinococcosis, and demonstrates camels as a source of human cystic echinococcosis.

**Keywords:** *Echinococcus granulosus*, genotype, real-time polymerase chain reaction, Iran, high resolution melting analysis

Background

Cystic echinococcosis (CE), also known as hydatid disease, is a zoonotic helminthic disease caused by infection with the larval stage of a tapeworm belonging to the family of Taeniidae, *Echinococcus granulosus*. The tapeworm is common in certain parts of the globe; with the exception of Antarctica, it is found on every continent. Thus, a large number of people are affected by CE. The prevalence rates are as high as 5%–10% in the endemic areas and the relatively silent clinical aspect of CE causes challenges for accurate and early diagnoses. Cyst formation upon the infection mainly, about 70%, occurs in the liver (1,2).

Four species of the tapeworm have been recognized to cause public health problems. The most common species that causes the human disease is *E. granulosus*, the cause of CE in human and some animals. Although *Echinococcus multilocularis* is fairly rare, it is the most virulent one and causes alveolar echinococcosis in human and some animals. The 2 other species, *Echinococcus vogeli* and *Echinococcus oligarthus* cause polycystic echinococcosis (2,3).

The CE is a major zoonotic disease with substantial public health and economic concerns (2, 4). It is endemic in many regions of the globe, especially the Mediterranean areas, Australia, Central Asia and the Tibetan Plateau, South America as well as Northern and Eastern Africa (5). There is the enormous socioeconomic impact of CE on the human populations, which is calculated as the global burden as 1009662 DALYs (disability-adjusted life years). It also stands for US$763980979 (2,6).

*Echinococcus granulosus* is grouped in different genotypes or strains. In recent years, the usage of mitochondrial phylogenetic analysis allowed statistis to classify some of the genotypes as new species (7). The latest classification indicates that *E. granulosus* includes the G1, G2, and G3 genotypes. The G1 strain is the most frequently reported genotype all over the globe, which produces fertile hydatid cysts mostly in sheep and it is also frequently isolated.
from human cases. Lately, *E. granulosus* (G1) has been also identified in cats as well (7, 8).

*Echinococcus equinus* (G4) has notable morphological and developmental differences compared to the G1 genotype and has only been reported in equines, yet no human cases have been reported (9). *E. ortleppi* (G5) produces fertile cysts most of the times in cattle and has been reported in few human cases (7, 10). The *E. intermedius* groups the G6 as well as G7, and *E. canadensis* relates to G8 and G10 genotypes. The main intermediate hosts for the G6 genotype are camels and goats; pigs are also the main intermediate hosts for G7. Besides, for the genotypes G8 and G10, cervids are considered as the main intermediate hosts. The G6, G7, and G8 genotypes have been isolated from humans as well. The human cases with the G9 genotype that was described in 1997 are now considered to be the G7 genotype (7, 11).

Camels are important regarding the epidemiology *E. intermedius* (G6), which can be transmitted to humans (9). In Iranian context, few studies have been performed regarding the genetic characteristics of camelid echinococcosis (12, 13). Molecular studies on the *E. granulosus* genotypes in different parts of the world can produce a useful set of data about the parasites epidemiological, ecological and transmission as well as the sources of human infection. These data can be used for public health, prevention, and control programs for the disease not only in humans, but also in animals, in order to minimize its socio-economic impacts.

The high resolution melting analysis (HRM) is a new approach by a single step with the closed tube method. It is reported to be appropriate especially for fast screening of a large number of isolates. The method is also fast, simple, accurate, and cost-effective, especially considering that it does not need post-PCR processes, thus it eliminates the hazards of ethidium bromide staining on the gel electrophoresis. In human research, this method has been vastly used for identification of single nucleotide polymorphisms in genetic disorders and also for detection of some infectious germs (14-17).

**Objective**
The present study aimed at identifying different molecular characteristics of *E. granulosus* metacestode using HRM.

**Methods**

**Sampling and Sample Preservation**
In the present cross-sectional study, 54 hydatid cysts were isolated from slaughtered Iranian camels (*Camelus dromedarius*) in Isfahan (33 samples) and Yazd (21 samples) provinces’ slaughterhouses; the involved organ was recorded as well. The studied regions (Yazd and Isfahan) are located in the central part of Iran. The samples were transferred to the Applied Physiology Research Center, Isfahan University of Medical Sciences. The hydatid fluid was examined for the presence of protoscoleces, centrifuged at 800 rpm for 1 minute. The sedated protoscoleces and a piece of hydatid cysts wall were preserved in 70% ethyl alcohol for DNA extraction.

**DNA Extraction**
Samples were washed in phosphate-buffered saline (PBS) prior to DNA extraction in order to remove residual ethanol from the parasite tissue. DNA extraction kit from tissue (PrimePrepTM, Genet Bio, Korea) was used for genomic DNA extraction. The procedure of the DNA extracting was performed according to the manufacturer’s manual. The extracted DNA samples were preserved at -20°C for later application.

**Real-Time Polymerase Chain Reaction and High Resolution Melting Analysis**
The 2 pairs of primers, *cox1*: F: TTTTTTGGG-CATCCTGAGGTTAT, R: TAAAGAAAGACATA-ATGAAAAATG (18) and *ap6*: F: GCATCTATTGAA-GAGTTGGGATAAC, R: CCAAAATCTATCAAC-TACACAAAC (19) were applied for the real-time implication of partial sequence of *cox1* and *ap6* genes. The real-time PCR detection system (Rotor-Gene 6000, Germany) was used for 25 µL reactions. The master mix contained, 10 µL master mix premix (Type-it® HRM®, Qiagen, Germany), 10 µL distilled nuclease-free water, 1 µL from each primer (10 pmol/µL), and 4 µL template DNA.

The reaction condition was as follows, *cox1*: 10 minutes at 95°C (initial denaturation) followed by 40 cycles of 95°C for 10 seconds (denaturation), 55°C for 40 seconds (annealing) and 72°C for 27 seconds (extension), and a final extension step at 72°C for 5 min, *ap6*: 10 minutes at 95°C (initial denaturation) followed by 40 cycles of 95°C for 17 seconds (denaturation), 60°C for 30 seconds (annealing) and 72°C for 28 seconds (extension), and a final extension step at 72°C for 5 minutes. The melting curve was drawn by increasing the temperature from 65°C to 90°C at intervals of 0.2°C/2 seconds (20). The curves were interpreted according to the simultaneously tested known genotypes.

Three previously known isolates regarding genotypes with the identical sequences to the accession numbers, namely, G1: KC660075, G3: KU697314, and G6: KC415063 were obtained from the first author of the previous study in the same laboratory (20). Control and sample isolate were tested simultaneously. The identity of the curves was confirmed by sequencing of the amplified genes. From each distinct curve of the 2 studied genes, the amplicons of 3 isolates were purified and directly sequenced by ABI 3730x DNA analyzer (Applied Biosystem*, USA). The sequences were compared to GenBank using basic local alignment search tool (BLAST). Melting curves were interpreted according to the control and sequenced isolates.
Results

Totally, 54 hydatid cyst samples (8 from liver and 46 from lungs) were collected and analyzed. The results illustrated that, 32 out of 33 (97%) isolates from Isfahan province were E. granulosus (G1) and one out of 33 (3%) was E. intermedius (G6). In Yazd province, 2 out of 21 (9.6%) isolates were E. granulosus (G3) and 19 out of 21(90.4%) isolates were E. granulosus (G1). The involved organ and city distribution of the 54 studied E. granulosus isolates are available in Table 1. The mean temperature (°C), SD, as well as intra- and inter-assay coefficient of variations calculated for E. granulosus G1, G3, and G6 genotype are available in Table 2. The normalized HRM curves of the standard known genotypes and the studied samples are available in Figure 1 and 2.

Based on the results of the present study, 94.4%, 3.7%, and 1.9% of the studied isolates were identified as E. granulosus (G1), E. granulosus (G3), and E. intermedius (G6) in the 2 studied regions, respectively.


Discussion

The results of the present study showed that \textit{E. granulosus}.

Table 1. The Involved Organ and City Distribution of the 54 Studied \textit{Echinococcus granulosus} Isolates

<table>
<thead>
<tr>
<th>Organ</th>
<th>Isfahan No. (%)</th>
<th>Yazd No. (%)</th>
<th>Total No. (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Lungs</td>
<td>28 (84.8)</td>
<td>18 (85.7)</td>
<td>46 (85.18)</td>
</tr>
<tr>
<td>Liver</td>
<td>5 (15.2)</td>
<td>3 (14.3)</td>
<td>8 (14.82)</td>
</tr>
</tbody>
</table>

Fertility

<table>
<thead>
<tr>
<th></th>
<th>Fertile</th>
<th>Non-fertile</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>25 (75.8)</td>
<td>8 (24.2)</td>
</tr>
<tr>
<td></td>
<td>19 (90.5)</td>
<td>2 (9.5)</td>
</tr>
<tr>
<td></td>
<td>44 (81.48)</td>
<td>10 (18.52)</td>
</tr>
</tbody>
</table>

Table 2. Mean Temperature (°C), SD and Intra- and Inter-assay Coefficient Of Variations Calculated for \textit{Echinococcus granulosus} G1, G3, and, G6 Genotypes

<table>
<thead>
<tr>
<th></th>
<th>\textit{G1}</th>
<th>\textit{G3}</th>
<th>\textit{G6}</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>\textit{Cox1}</td>
<td>\textit{Atp6}</td>
<td>\textit{Cox1}</td>
</tr>
<tr>
<td>N</td>
<td>51</td>
<td>51</td>
<td>2</td>
</tr>
<tr>
<td>Mean</td>
<td>79.83</td>
<td>77.95</td>
<td>80.31</td>
</tr>
<tr>
<td>SD</td>
<td>0.077</td>
<td>0.1698</td>
<td>0.046</td>
</tr>
<tr>
<td>Coefficient of variation%</td>
<td>Inter-assay</td>
<td>0.097</td>
<td>0.21</td>
</tr>
<tr>
<td></td>
<td>Intera-assay</td>
<td>0.090</td>
<td>0.2</td>
</tr>
<tr>
<td>Minimum</td>
<td>Temperature</td>
<td>79.7</td>
<td>77.63</td>
</tr>
<tr>
<td>Maximum</td>
<td>Temperature</td>
<td>80</td>
<td>78.25</td>
</tr>
<tr>
<td>Total</td>
<td>54</td>
<td></td>
<td></td>
</tr>
<tr>
<td>%</td>
<td>94.45</td>
<td>94.45</td>
<td>3.7</td>
</tr>
</tbody>
</table>
often associated with sheep as intermediate hosts (11). In the present study using HRM approach, 94.4% of the camel isolates of *E. granulosus* were identified as G1 genotype, which shows that even in camel, G1 is the most frequent strain. There are quite a few studies on the genetic characteristics of camelid CE in Iran, some of which are mentioned below.

Sharbatkhori et al studied the genotypes of *E. granulosus* in sheep, cattle, camels, and humans in Golestan province, Iran, using *cox1* and *nad1* gene analyses (13). They found 4 *E. granulosus* genotypes among the 74 studied CE isolates. Their reported isolates from animals and humans were G1 (78.3%), G2 (2.7%), G3 (15%), and G6 (4%). Considering camel as an intermediate host, 44.5%, 22.5%, and 33.3% were reported to be G1, G3, and G6, respectively. Similar to the results of the present study, G1 was the most prevalently found genotype. The G1-G3 complex was reported to be found in all of the sheep, goat, cattle, and buffalo isolates of their study. All those four human CE isolates belonged to *E. granulosus* G1. Sharbatkhori et al found more *E. intermedius* (G6) in camels (3 out of nine isolates, 33.3%) compared to the findings of the present study (one out of 54 isolates, 1.9%). Similar to the findings of the present study, they identified G1, G3, and G6 genotypes from the camel CE in Golestan province.

Moghaddas et al studied the molecular characteristics of 50 *E. granulosus* isolates from the camel in eastern Iran, using PCR-restriction fragment length polymorphism (PCR-RFLP) analysis of *cox1* and *ITS1* genes. Their results showed that 27 out of 50 (54%) *E. granulosus* isolates belonged to G1 strain and 46% were of G6 genotype (12). They reported the fairly high prevalence of G6 genotype compared to the findings of the present study. Their results indicate the high rate of G6 genotype in eastern Iran, yet not in central part of Iran.

Sharifiyazdi et al explored the genotypic characterization of camel isolates of *E. granulosus* using *cox1* and *nad1* gene sequencing in Mashhad, North West of Iran. Similar to the findings of the present study, they reported G3 and G6 genotypes, yet not G1 strain among 85 studied camels. They also reported the lungs as the most-affected organs (95.0%) followed by the liver (26.5%) and spleen (2.4%); these results are in line with the findings of the present study in which 85.18% of the cysts were isolated from the lung and 5.82% from the liver (28).

In a recent study, Jafari et al investigated the genetic characteristics of the human isolates of *E. granulosus* by the *cox1* and *nad1* gene analyses in Isfahan. The same genotypes from human cases of CE (86% G1, 6% G3, and 8% G6) were reported by the researchers in Isfahan (24).

In the present study, the three previously reported genotypes were isolated from Iranian camel and the results indicated that *E. granulosus* (G1) was the predominant genotype in camels in central parts of Iran and considering the high rate of human infections with G1 strain, camel can be one of the major sources of human infections in Iran.
this area.

Conclusions

Based on the HRM analysis of oox1 and atp6 genes, E. granulosus (G1) accounts for the most cases of camelid CE, which represents camels as a source of human CE.

Conflict of interest

The authors declare that they have no conflict of interest

Funding

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