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Original Article

Genotyping of *Echinococcus granulosus* Isolates from Human Clinical Samples Based on Sequencing of Mitochondrial Genes in Iran, Tehran

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Abstract

**Background:** The present study was aimed to investigate molecular diversity of *Echinococcus granulosus* isolates collected from human clinical samples using two mitochondrial genes cox1 and nad1 in Iran.

**Methods:** Forty seven human hydatid cysts were collected through surgery from two hospitals in Tehran during 2010-2012. To determine the fertility of protoscoleces, the cyst fluids were subjected to morphological microscopic examinations. Protoscoleces were removed from each cyst and their total genomic DNAs were extracted. PCR was performed to amplify fragments of 450 and 400 base pair (bp) for cox1 and nad1 genes, respectively. Genotype diversity and sequence variation of the strains were studied by bioinformatics software and in comparison with those mtDNA sequences already deposited in GenBank.

**Results:** Sixteen, (53.3%), 13 (43.3%), and 1 (3.3%) samples were related to lung, liver, and spleen, respectively. The remained 17 unfertile samples were excluded from the study. From the 29 isolates, 86.7% (n=26) and 10% (n=3) were related to G1, and G3 genotypes, respectively. The sole isolate with G6 genotype was obtained from lung sample. Analysis of concatenated sequences of cox1+nad1 indicated the presence of 11 haplotypes among our strains that were related to genotypes G1 (n=9), G3 (n=1) and G6 (n=1).

**Conclusion:** In consistent to other reports from Iran, genotypes G1, G3, and G6 were observed in our human isolates. The rate of G3 genotype was however higher than other studies implying that human can be considered as a new appropriate host for G3 genotype. Further studies with more sample size from different geographic areas of Iran are needed for *E. granulosus* mapping.

Keywords

*Echinococcus granulosus, Genotyping, cox1, nad1, Iran*

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Introduction

Human cystic echinococcosis (CE) is a chronic zoonotic infection caused by the larval stage of the canid tapeworm, Echinococcus granulosus (1). Both cystic and alveolar echinococcosis were reported from Middle East countries, which cystic echinococcosis was assumed as the predominant type (2-5). E. granulosus is one of the most important parasites in different parts of Iran (6). Although sheep, camels, cattle and goats are considered as commonly intermediate hosts of hydatid cysts in Iran, but sheep is the most common and important intermediate host found throughout the country (7).

Ten distinct genotypes of E. granulosus (G1–G10) were identified worldwide based on either morphological or molecular data (8-13). Several molecular studies on human isolates of E. granulosus have identified the genotypes G1, G3, and G6 in different regions of Iran (14, 15). Sheep, buffalo, and camels assume as main reservoirs of genotypes G1, G3, and G6 that are among common livestock in Iran. Numerous reports on the incidence of E. granulosus have indicated that G1 (common sheep strain) is the most common genotype in Iran (16, 17) and also most parts of the world (18-20). In many countries including Iran, camels have an important role in transmission cycle of G6 (common camel strain) of E. granulosus and have been reported principally from human (21, 24). Moreover, buffalo is the main intermediate host of genotype G3 in Iran (14, 18). The first molecular report in Iran for E. granulosus genotypes was done in 1998 by Zhang L et al (15). In this study a total of 16 isolates were collected from human and domestic animals and partial sequence variation of the mitochondrial cytochrome c oxidase I (cox1) and NADH dehydrogenase subunit I (nad1) genes were investigated. Accordingly, sheep and camel strains were presented as sole characterized genotypes (15). The G3 genotype was later described by other molecular studies in Iran among both human and animal samples (6, 7, 13, 16). Analysis of evolutionary sequence variations could improve our knowledge about phylogenetic relationship of these strains in compare to other ones in different countries.

The present study was aimed to characterize genotype diversity and sequence variations of E. granulosus isolates from human hydatid cyst in different tissues based on PCR sequencing of two housekeeping genes cox1 and nad1.

Materials and Methods

Suspected patients to hydatidosis from different geographic regions were referred to two hospitals, Children’s Medical Center Hospital and Masih Daneshvari Hospital in Tehran, Iran. Totally, 47 samples of human hydatid cysts were collected via surgery during 2010-2012. Thirty three cases (70.2%) were isolated from males and 14 cases (29.8%) from females. Immediately after surgery, the cyst samples were collected and were rinsed in normal saline and transported to the Molecular Laboratory of Children’s Medical Center Hospital for further analysis. The microscopic examination was performed on the cyst fluids to determine the fertility of protoscoleces. The protoscoleces were removed from each cyst, and rinsed three times with phosphate buffered saline (PBS). DNA of each sample was extracted by High Pure PCR Template preparation kit (Roche, Mannheim, Germany) according to the manufacturer’s instructions. To ensure the accuracy of DNA extraction, concentration of the extracted DNA samples were analyzed by NanoDrop. The extracted DNAs were stored at -20°C until required for PCR.

Presence and sequence diversity of two mitochondrial genes cox1 and nad1 were investigated by PCR, separately. PCR was performed in a 25 µl final volume containing 1 X PCR...
buffer, 2.5 mM MgCl₂, 0.2 mM of each deoxy-
nucleotide triphosphate (dNTP), 0.2 µM of each primer and 1.5 µM Ampli-Taq Polymer-
ase. Two primers, JB3 (forward), 5′-TTT TTT
GGG CAT CCT GAG GTT TAT -3′ and
JB4.5 (reverse), 5′-TAA AGA AAG AAC
ATA ATG AAA ATG -3′ (10), were used to
amplify a 450 bp fragment of cox1 gene under
the following conditions: initial denaturation
94°C for 5 min, followed by 35 cycles of dena-
turation at 94°C for 45s, annealing at 50°C
for 45s and elongation for 45s at 72°C. Final ex-
tension was performed at 72°C for 7 min.
Forward primer MS1: 5′-CGTAGGTATGTT
GGTGTGTTGGGT-3′ and reverse primer
MS2: 5′-CCATAATCAATGGCCGTACGAT
-3′ were used to amplify a 400 bp fragment of
the second locus, nad1 gene (25). The amplifi-
cation was carried out with 5 min initial dena-
turation at 94°C, and 30 cycles of 30s dena-
turation at 94°C, 45s annealing at 50°C and 30 s
elongation at 72°C. Final extension was pe-
formed at 72°C for 5 min. In the next step,
PCR products of nad1 and cox1 genes were
purified using a commercial purification kit
(Bioneer, South Korea) and sent to Tak-
pouzist Company (Tehran, Iran) for sequen-
cing. Consensus characteristic nucleotide se-
dquences of each genotype from relevant mtDNA
in GenBank database (Accession numbers
DQ062857 and AJ237632 for G1, M84663 and AJ237634 for G3, and M84666
and AJ237637 for G6 for cox1 and nad1, re-
spectively) were used for genotype characteri-
ization. Multiple alignments of concatameric
sequences of cox1 and nad1 genes were created
in compare to their related reference sequenc-
es. Identity and similarity of the sequences
were determined using the BioEdit software
version 7.2.

Phylogenetic analysis was performed using
Maximum Likelihood method based on the
Tamura-Nei model. Nucleotide sequence of T.
saginata (GenBank accession number NC
009938) was used as outgroup.

Results

Out of the 47 collected hydatid cysts, DNA
extracts of 30 samples were used for molecu-
lar analysis. Extracts of the remained unfertile
17 samples showed low quality for amplifica-
tion and sequencing experiments, which were
excluded from the study. The obtained sam-
ple were related to cysts of lung (53.3%), liver
(43.3%), and spleen (3.3%). All of the DNA
samples successfully present amplicons of the
cox1 and nad1 genes as was shown for the con-
trol samples (450 and 400 bp respectively).

Three genotypes G1, G3 and G6 were iden-
tified among our DNA samples based on cox1
and nad1 sequences data. Genotype 1 was the
most common available genotype in the stud-
ed population. Out of the 30 studied samples,
26 samples (86.7%) belonged to genotype G1.
These samples belonged to lung (57.7%), liver
(38.5%), and spleen (3.3%). Three isolates
belonged to the genotype G3 (10%), all related
to samples from liver (Strains HT13, HT22,
HT55), and one isolate belonged to genotype
G6, that obtained from the lung. Analysis of
the strains with genotype G1 indicated com-
mon nucleotide sequences in position 66 (C)
and 257 (T). Presence of mutation at position
56 (a definitive mutation for genotype G2)
was also detected among 10 strains with G1
genotype. Point mutations in other positions
are summarized in table 1. Among all the strains
with G3 genotype, mutation at position
40 (A to G) was observed in compare to re-
ference strain M84663. However, no sequence
diversity was observed in the identified strain
with G6 genotype compared with camel strain
M84663.

In the case of nad1 gene, the analysed se-
dquences showed common point mutations at
positions 43 (A and G) and 429 (A and G) for
all the strains with G1 and G3 genotypes, re-
spectively. Presence of point mutation in posi-
tion 282 (C to T; a definitive point mutation
for strains with G2 genotype) was observed
among all but one strain with G1 genotype.
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Based on their cox1 nucleotide sequence, the only obtained strain with G6 genotype (Strain HM42, from Isfahan Province) displayed 100% identity with nad1 gene of E. granulosus camel strain (Accession no. Aj237637). Other point mutations for nad1 gene are summarized in Table 1. Comparison of concatameric sequence data presented a total of 11 haplotypes among our isolates. Nine of these haplotypes belonged to the strains with G1 genotype (Table 1).

The phylogenetic analysis of concatenated sequences of cox1+nad1 showed three clusters A, B and C. Cluster A represents all strains related to G1 genotype, and cluster B and C characterize strains related to G3 and G6 genotypes, respectively. The largest cluster included 26 concatenated sequences that were grouped as G1 genotype (Fig. 1).

Table 1: Echinococcus granulosus haplotypes, accession numbers and nucleotide substitution detected in this study using concatenated sequence (cox1 + nad1)

<table>
<thead>
<tr>
<th>Representative genotypes &amp; haplotypes</th>
<th>Isolation source</th>
<th>ACCESSION NUMBERS (cox1)</th>
<th>ACCESSION NUMBERS (nad1)</th>
<th>Nucleotide substitution (cox1)</th>
<th>Nucleotide substitution (nad1)</th>
</tr>
</thead>
<tbody>
<tr>
<td>G1</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Haplotype 1 (n=9)</td>
<td>Lung 3, Liver 5, Spleen 1</td>
<td>KF 612381</td>
<td>KF 612357</td>
<td>ND</td>
<td>282 C→T</td>
</tr>
<tr>
<td>Haplotype 2 (n=7)</td>
<td></td>
<td></td>
<td>KF 612356</td>
<td>56 C→T</td>
<td>282 C→T</td>
</tr>
<tr>
<td>Haplotype 3 (n=5)</td>
<td></td>
<td>KF 612390</td>
<td>KF 612360</td>
<td>ND</td>
<td>342 and 345 T→C</td>
</tr>
<tr>
<td>Haplotype 4 (n=2)</td>
<td></td>
<td>KF 612380</td>
<td>KF 612358</td>
<td>ND</td>
<td>375 T→C</td>
</tr>
<tr>
<td>Haplotype 5 (n=1)</td>
<td></td>
<td>KF 612376</td>
<td>KF 612349</td>
<td>252 T→C</td>
<td>282 C→T</td>
</tr>
<tr>
<td>Haplotype 6 (n=1)</td>
<td></td>
<td>KF 612395</td>
<td>KF 612350</td>
<td>252 T→C</td>
<td>ND</td>
</tr>
<tr>
<td>Haplotype 7 (n=1)</td>
<td></td>
<td>KF 612396</td>
<td>KF 612355</td>
<td>56 C→T, 123 T→C</td>
<td>282 C→T</td>
</tr>
<tr>
<td>Haplotype 8 (n=1)</td>
<td></td>
<td>KF 612394</td>
<td>KF 612343</td>
<td>150 T→C, 282 C→T</td>
<td></td>
</tr>
<tr>
<td>Haplotype 9 (n=1)</td>
<td></td>
<td>KF 612386</td>
<td>KF 612351</td>
<td>56 C→T</td>
<td>170 G→A, 282 C→T</td>
</tr>
<tr>
<td>G3</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Haplotype 10 (n=3)</td>
<td></td>
<td>KF 612397</td>
<td>KF 612369</td>
<td>40 A→G</td>
<td>ND</td>
</tr>
<tr>
<td>G6</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Haplotype 11 (n=1)</td>
<td></td>
<td>KF 612400</td>
<td>KF 612372</td>
<td>ND</td>
<td>ND</td>
</tr>
</tbody>
</table>

*Haplotypes 1-11 defined based on concatenated nucleotide sequences of cox1 + nad1.

ND: No sequence diversity was detected in compare to definitive reference mutations presented by Bowel et al. for cox1 and nad1 (10).
Fig. 1: Phylogenetic tree of Iranian *E. granulosus* isolates from human hydatidosis using the Maximum Likelihood method based on the Tamura-Nei model. The scale bar indicates the number of substitutions per site for each isolate. Partial DNA sequences of concatenated mitochondrial *cox1*+*nad1* genes were used as input data. Isolate HM42 represent genotype G6, isolates HT13, HT22, HT55 represent G3 genotype, and the other ones represent G1 genotype. Accession numbers of M84666-AJ237637, M84663-AJ23763, and DQ062857-AJ237632 represent reference sequences of *Echinococcus granulosus* genotypes G6, G3, and G1, respectively. *Taenia saginata* NC 009938 was used as out group sequence data.

**Discussion**

*E. granulosus* is known to be widespread in whole country, with “sheep–dog” and “camel–dog” strains described in the literature as infecting humans (21-24). There are many reports on the molecular identification of *E. granulosus* genotypes in domestic animals (6-8, 13-17). Three *E. granulosus* genotypes, including genotype G1 in human, sheep, cattle, cam-
el and goat, genotype G3 in buffalo, sheep, cattle and human and genotype G6 in sheep, camel and human, were reported from different studies (6-8, 13-17, 21-26). Various mitochondrial and nuclear genes have previously been applied effectively in differentiation of these genotypes. Rostami Nejad et al. investigated genotype diversity of three mitochondrial genes cox1, nad1 and atp6 and also partial sequences of the 12S rRNA gene in their isolates and confirmed the presence of G1 and G6 genotypes in different intermediate hosts, including cattle, camels, sheep, buffalo and goats in different geographic areas in Iran (17). Fasihi Harandi et al. (16) and Ahmadi & Dalimi (5) genotyped their isolated using PCR-RFLP of the internal transcribed spacer (ITS1) region. They demonstrated that sheep and camel strains are similarly detected in cattle and also humans as well. According to the results of our study, G1 genotype was the predominant genotype of *E. granulosus* in infected patients that is in accordance with other reports from Iran and other countries. In the preliminary study in 1998 by Zhang et al., the G1 genotype was found in all four human isolates examined (15). In a study in Golestan province in Iran, PCR products and RFLP patterns of ITS1 gene of *E. granulosus* showed presence of G1 genotype in all 30 human samples (27). Our findings also confirmed by two studies of Dousti et al. in Ilam province and Khademvatan et al. in Khuzestan provinces, which all of their human isolates belonged to G1 genotype (28, 29). On the other hand, there are few reports for existence of human infection with strains belonged to G3 genotype. In a study in Ardabil province, two human isolates of G3 genotype were described for the first time in Iran (26). The presence of *E. granulosus* genotype G6 (camel genotype) has been reported previously in domestic animals and humans in different countries (21, 30, 31). In Shahnazi et al. study using RFLP patterns of ITS1 gene, 6 out of 31 human samples (19.3%) were infected with the camel genotype (24). Diversity of these results could be explained by type of the studied samples, difference in geographic area, and exploited method for genotyping. Results of our study showed presence of various point mutations in both cox1 and nad1 genes that are region specific in compare to other strains in the world. Many of the studied strains didn’t show described mutations by Bowel et al. for differentiation of strains with genotypes G1-G3 at positions 56 (for cox1 gene) and 282 (for nad1 gene).

**Conclusion**

The results of this study showed presence of the three common genotypes G1, G3, and G6 among our isolates. Higher frequency of strains with G3 genotype compared with other reports in Iran is of great concern that suggest human as new appropriate host for G3 genotype. The described sequence variations in cox1 and nad1 genes among the human isolates proposed incompatibility of point mutations 56 (C to T) and 282 (C to T) in differentiation of G1-G3 genotypes in Iran. Further studies with more sample size from different geographic areas of Iran are needed to evaluate these results for genetic mapping of *E. granulosus*.

**Acknowledgements**

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