Case report

The emergence of amoebic dysentery mimicking COVID-19: A human case report from Iran

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Abstract

Identical symptoms of coronavirus disease-19 (COVID-19) with infectious and non-infectious disease have become challenging issue for health professions. In the present study, we describe a human case of amoebic dysentery mimicking severe acute respiratory syndrome coronavirus 2 (SARS–CoV-2) infection in Iran with an emphasis on morphological and molecular diagnostic aspects of *Entamoeba histolytica* parasite. A 32-year-old woman with a history of abdominal pain, diarrhea, and mild fever of 38°C was diagnosed as COVID-19 with no prescription of real-time RT-PCR. The patient was prescribed having azithromycin 500 mg/day for 5 days. Her later aggravated conditions such as fulminant dysentery has led to the diagnosis of *E. histolytica* with parasitological and molecular methods. SARS-CoV-2 infection was ruled out in the second visit using real-time RT-PCR and ELISA. Treatment was completed with antiparasitic drugs including oral metronidazole 500 mg, 3 times/day for ten days, and oral iodoquinol 650 mg 3 times/day for twenty days. In general, health professions must be vigilant in all aspects of diagnosis, treatment, and management of patients to prevent any medical errors and misdiagnosis.

Keywords: Entamoeba histolytica, Amoebiasis, Dysentery, SARS-CoV-2, COVID-19

1. Introduction

Since December 2019, the coronavirus disease-19 (COVID-19) crisis, an unprecedented outbreak, was emerged in Wuhan, Hubei Province, China [1]. Despite global efforts and quarantine attempts, the incidence continued to increase, spread to many other countries, and resulted in huge numbers of cases and deaths through a worldwide pandemic [2]. Apart from respiratory complications, different extrapulmonary manifestations, such as abdominal pain and diarrhea have been reported in the majority of symptomatic

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Received: November, 23, 2022 Accepted: February, 09, 2023 patients identical to those usually reported in the intestinal protozoan infections that could confuse clinicians in diagnosis, treatment, and management of patients [3, 4]. On the other hand, the occurrence of fever in any other febrile diseases might mislead the health professions in diagnosis and management of the patients. The resemblance of the mentioned symptoms with other parasitic, bacterial and viral infectious diseases as well as the possibility of coinfection of severe acute respiratory syndrome coronavirus 2 (SARS–CoV-2) with other infectious





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agents in the recent year may mislead the physicians in diagnosis and treatment of the patient's complications [5]. In the present study, we describe a human case of amoebic dysentery mimicking SARS–CoV-2 infection in Iran with an emphasis on morphological and molecular diagnostic aspects of *Entamoeba histolytica* parasite.

2. Case presentation

A 32 years old woman with 5 days history of abdominal pain, diarrhea, and mild fever of 38°C was referred to a general physician (GP) in July 2022 in Tehran, Iran. As SARS-CoV-2 infection might accompany the similar mentioned symptoms of the patient, and the onset of complications occurred concurrently with the Covid-19 pandemic, the GP diagnosed her complications as initial symptoms of SARS-CoV-2 infection with no prescription of realtime RT-PCR as standard confirmatory laboratory tests. The patient was prescribed having azithromycin 500 mg/day for 5 days and guarantined herself for 2 weeks. However, her gastrointestinal symptoms were aggravated with the onset of fulminant dysentery. SARS-CoV-2 infection was ruled out in the second visit using real-time RT-PCR. Furthermore, the anti-SARS-CoV-2 antibodies were investigate using ELISA (Pishtaz Teb; PT-Q SARS-COV IgG-96, Iran) which the results showed no history of SARS-CoV-2 infection. The patient was referred to hospital, and in laboratory diagnosis, numerous ameboid trophozoites of Entamoeba histolytica, as well as red blood cells (RBCs), were observed microscopically. The patient complete blood count (CBC) represented abnormal findings is embedded in Table 1.

Blood index	Result	Normal range
WBC	$15.2 \times 10^{3}/\mu L$	4-11×10 ³ /µL
RBC	3.8×10 ⁶ /µL	4.5-5.1×10 ⁶ /µL
Hemoglobin	10.1 g/dL	12.3-15.3 g/dL
Hematocrit	31.2%	35.9-44.6%
MCV	75.9 fL	80-101 fL

Table 1. Complete blood count test results of the patient.

Abbreviations: CBC: complete blood count, WBC: white blood cell, RBC: red blood cell, MCV: mean concentration volume, MCH: mean concentration of hemoglobin.

29-39 pg

23.2 pg

MCH

For complementary confirmation of the diagnosis, the patient's fresh stool specimen (Figure 1A) was transferred quickly to the Department of Medical Parasitology at Tehran University of Medical Sciences. The macroscopic examination of the specimen indicates fulminant dysentery. Not only were hematophagous trophozoites of E. histolytica observed in the trichrome-stained slides using a light microscope (Zeiss, Germany) (1000×) (Figure 1B), but also PCR and subsequent sequencing confirmed the diagnosis. For molecular diagnosis, total DNA was extracted using a stool DNA extraction kit (Yekta Tajhiz Azma, Iran) and followed by a nested-PCR assay for detection of Entamoeba genus with speciesspecific primers [6]. Based on the species-specific product size of the 900-bp and 439-bp products in the first and second stages of 18S rRNA-nested PCR, respectively the sample was positive for *E. histolytica*. Moreover, the PCR product of the 18S rRNA gene related to the current sample was purified and sequenced using the Sanger sequencing method on an ABI PrismTM 3730 Genetic Analyzer by the Macrogen Company (Macrogen® Corp., Seoul, South Korea). The sequence chromatogram was observed using Chromas Version 1.0, and nucleotide sequences were edited using BioEdit, version 7.0.5, and examined using the phylogenetic program MEGA X. To different phylogenetic analysis for the Entamoeba complex (E. histolytica. Entamoeba moshkovskii, and Entamoeba dispar) we selected the Neighbor-Joining method (NJ) using Kimura 2-parameter models in MEGA X.



Figure 1. (A) Patients' dysenteric stool specimen. (B) Hematophagous trophozoite of *E. histolytica* (1000×).

The sequence was submitted to GenBank under the accession number using BankIt - NCBI - NIH (GenBank Acc. No: MW659191). The current sequence was 99-100% identical to the available GenBank sequences for *E. histolytica* isolated from Iran and other regions of the world (Figure 2). In addition, bootstrap resampling analysis (1,000 replications) was used to assess branch confidence in clades in each tree.

Finally, the patient's treatment was completed with antiparasitic drugs as follows: oral metronidazole 500 mg, 3 times/day for ten days, and oral iodoquinol 650 mg 3 times/day for twenty days. After four weeks post-treatment, no cysts and trophozoites of *E. histolytica* were detected in the patients' stool samples.

worldwide [6]. Colonization of *E. histolytica* in most of the patients is asymptomatic. However, a variety of manifestations including mild diarrhea and intestinal pain to fulminant dysentery are expectable [6]. Mortality with fulminant amoebic dysentery is higher than 40% in most cases, and risk factors such as receiving immunosuppressant drugs, pregnancy, and diabetes as well as having immunocompromising disorders like acquired immunodeficiency syndrome (AIDS) intensifies the mortality [7]. Up to now, there have been several studies on the prevalence of *E. histolytica/dispar* in Iran, and the prevalence of *E. histolytica/dispar* infection in different geographic regions of Iran varies from 0.1 to 24% [8], and the weighted overall prevalence of *E. histolytica/dispar*



Figure 2. Phylogenetic tree of 18S rRNA gene sequences of *E. histolytica* in the current study and other *Entamoeba* species obtained from GenBank. *Entamoeba bovis* served as an outgroup. The scale bar represented 0.01 changes per nucleotide.

3. Discussion

Despite health and hygiene promotion in today's societies, there is still the risk of transmission and incidence of parasitic infections. Amebiasis is the second leading cause of death from parasitic diseases with an estimation of 40000–100000 annual deaths

infection among Iranian healthy population is reported to be 1.3 % [9].

COVID-19, as the most recent emerging infectious disease globally, has led to plenty of mortalities, and this dilemma might result in misdiagnosis and negligence of numerous infectious and non-infectious

diseases [2]. The diagnosis of infectious diseases becomes challenging in tropics where the febrile diseases such as malaria, scrub typhus, leptospirosis, and typhoid fever occur significantly [10]. For example, due to the similarity of symptoms between malaria and Covid-19, especially fever and fatigue, malaria patients may be misdiagnosed as COVID-19 and in reverse [11]. Also, the coincidence and epidemic of infectious diseases such as dengue fever could complicate the situation in many developing countries [12]. What gives rise to a complicated situation is the co-infection of infectious diseases and Covid-19 when the diagnosis, treatment, and prognosis of patients suffering SARS-CoV-2 and other pathogens have become challenging for clinicians [13]. It is undeniable that co-infection usually increases the need for a higher level of care in patients. It is reported that the bacterial co-infection was associated with a 2.5-fold surge in the mortality of SARS-CoV-2 patients which bespeaks a significant interaction between the pathogens and COVID-19 [14]. Furthermore, there have been growing reports of mucormycosis coinfection in COVID-19 patients with frequent fatalities worldwide [15]. On the other hand, although little information is available regarding the interaction of parasites and COVID-19, there is evidence suggesting that helminths may have a mitigating effect upon the SARS-CoV-2 infection [16]. A recent study in Iran has reported co-morbidity of Lophomonas blattarum and COVID-19 in a pregnant woman who was treated successfully with metronidazole [17]. Therefore, the occurrence of any febrile diseases, as well as the coinfection of SARS-CoV-2 with other infectious agents during the pandemic, could confuse clinicians in the diagnosis, treatment, and management of patients.

In the present study, we described invasive intestinal amebiasis mimicking COVID-19. Pandemics like COVID-19 may cause neglect the other infectious diseases, and given that future pandemics are inevitable, clinicians must be vigilant of parasitic illnesses whose symptoms overlap with COVID-19 to prevent any medical errors and misdiagnosis. Moreover, that the possibility of co-infection of parasitic diseases with SARS–CoV-2 is lurking, health professions must be aware of the administration of appropriate diagnostic tools and treatment to overcome fatalities during this dilemma.

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Authors' contributions

All Authors contributed equally and approved the final version of manuscript.

Conflict of interests

The authors declare no competing interests.

Ethical declarations

A written consent was obtained from the patient, and confidentiality of the details of the patient was assured. A copy of the written consent is available for review by the Editor-in-Chief of this journal.

Consent for publication

Written informed consent was obtained from the patients for publication of this case report. A copy of the written consent is available for review by the Editor-in-Chief of this journal.

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