

# *Giardia duodenalis* in Algeria: a review within a One Health approach

Myriam Thomas<sup>1</sup> Bruno Polack<sup>1</sup> Mohamed Mammeri<sup>1\*</sup>

## Keywords

*Giardia duodenalis*, zoonoses, disease transmission, One Health approach, molecular epidemiology, Algeria

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## Summary

*Giardia duodenalis* is a protozoan parasite that primarily infects the small intestine of various mammals, including humans. It is a complex of species composed of multiple genotypes known as assemblages A to H. Assemblages A and B, which are considered the most zoonotic, pose a significant risk to human health. Assemblages C to H are generally found in companion animals, livestock, rodents and marine vertebrates. Giardiasis, the infection caused by *G. duodenalis*, is the most common intestinal parasitic infection worldwide. In Algeria, the lack of data on the occurrence and genetic characteristics of *G. duodenalis* limits our understanding of its epidemiology, impact and zoonotic potential. This review focuses on research conducted in Algeria, covering humans, animals and the environment, with an emphasis on the “One Health” approach. PubMed and ResearchGate databases were used to access relevant publications on the presence of *G. duodenalis* in humans, animals and the environment from January 2000 to April 2023. Of the seventeen publications identified, only four articles used molecular tools to identify *G. duodenalis*. The results revealed the presence of *G. duodenalis* in humans, livestock (cattle, sheep and camels), and the environment (water and soil samples). The prevalence and genetic diversity of *G. duodenalis* isolates varied across regions and age groups in both humans and animals. Assemblage A was commonly found in humans and animals, indicating potential zoonotic transmission. Further studies are necessary to fully grasp the transmission dynamics, zoonotic potential and public health and animal welfare implications of *G. duodenalis* in Algeria. Veterinarians, biologists, ecologists and health professionals should work together to tackle *G. duodenalis* as part of the “One Health” approach. Implementing prevention and control strategies tailored to specific regions and improving hygiene and animal husbandry practices are vital to reduce the burden of giardiasis in both humans and animals.

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## ■ INTRODUCTION

*Giardia duodenalis* (also known as *G. intestinalis* or *G. lamblia*) is a protozoan parasite that causes giardiasis. It generally infects the small intestine of mammals, including humans (Cacciò and Sprong, 2010). Previous studies on the parasite’s genetic makeup have revealed that

it is a species complex composed of genetically distinct groups or assemblages. Assemblages A and B are considered the most zoonotic and, thus, pose a significant risk to human health. In comparison, host-adapted assemblages C and D are generally found in canines, assemblage F in felines, assemblage E in livestock, assemblage G in rodents and assemblage H in marine vertebrates (Ryan and Zahedi, 2019). Therefore, assemblages C to H are thought to represent a lower risk to humans.

Giardiasis is the most common intestinal parasitic infection in humans worldwide. Comprehensive genetic analysis is required to decipher the infection’s complex epidemiology. Despite high estimates

1. Anses, INRAE, Ecole Nationale Vétérinaire d’Alfort, UMR BIPAR, Laboratoire de Santé Animale, 94700, Maisons-Alfort, France

\* Corresponding author

Phone: +33 1 43 96 70 62; E-mail: mohamed.mammeri@vet-alfort.fr

suggesting that approximately 33% of the population is infected in developing countries (Cardoen et al., 2009; Dunn and Juergens, 2023), few genetic surveys have been conducted on the parasite in developing countries. Instead, most available genetic data originates from research in developed countries. Therefore, conducting research in regions where the pathogen is endemic is essential to improve our understanding of its genetic diversity. Further studies would also enhance our knowledge of the epidemiology of human giardiasis, as well as improve the effective management of infections in vulnerable populations. Although giardiasis is common in North Africa, little is known about its epidemiology in the region. *G. duodenalis* infections in humans and animals have been reported in many parts of Algeria. However, most published studies have used easily-accessible microscopy techniques to identify *G. duodenalis* assemblages, which are less sensitive and specific than molecular characterisation. Research is urgently required, involving analyses of the parasite's molecular variations and its geographic spread, as well as studies on the environmental and climatic factors, which may impact its prevalence or explain its spread and circulation dynamics among both humans and animals (Squire and Ryan, 2017).

The lack of available information on the occurrence and genetic characteristics of *G. duodenalis* in Algeria limits our understanding of the parasite's epidemiology, impact and zoonotic potential in the region. This review provides a concise overview of the existing research, which has been conducted in Algeria, covering humans, animals and the environment with a focus on the "One Health" approach.

## MATERIAL AND METHODS

We conducted a systematic review of the literature available in the PubMed and ResearchGate databases to identify the articles or studies focusing on the presence of *G. duodenalis* in humans and animals, published between 1<sup>st</sup> January 2000 and 14<sup>th</sup> April 2023. Using the keywords "Giardia", "giardiasis" and "Algeria", we identified 13 potentially relevant publications (original articles). Then, using the open-source reference manager software Zotero, we screened the titles and abstracts in more detail. This allowed us to identify four more relevant articles, which were cited in the publications selected in the first round of screening. A total of 17 publications were identified, providing the basis for our comprehensive review. Of the articles reporting the presence of *G. duodenalis* in humans (n = 6), in animals (n = 6) or in the environment (n = 1), only four used molecular tools (PCR) to identify *G. duodenalis* in both human and animal hosts. Our review involved the phylogenetic analysis of sequences of *G. duodenalis* genes triosephosphate isomerase (*tpi*) and glutamate dehydrogenase (*gdh*), isolated from the Algerian samples, using the phylogeny.fr website (Castresana, 2000; Guindon and Gascuel, 2003; Edgar, 2004; Nisimova and Gascuel, 2006; Dereeper et al., 2008, 2010).

## RESULTS

These studies determined the presence of *G. duodenalis* in humans, animals and the environment in 14 of the 58 Algerian departments (called "Wilaya", Figure 1).

### *G. duodenalis* in humans

Six microscopy-based studies conducted in different regions of Algeria set out to assess the prevalence of intestinal parasitic infections, including *G. duodenalis*, and to identify the associated risk factors for humans (Table I). The studies considered individuals spanning different age groups, both in outpatient and hospitalised settings. A range of clinical manifestations was observed for both asymptomatic

and symptomatic patients. Symptoms included abdominal pain and cramps, diarrhoea, steatorrhea, vomiting, nausea, anorexia, weight loss and fever. The prevalence of *G. duodenalis* infection varied from 0.3% to 67.2%, with a higher prevalence in children. Inadequate hygiene and poor living conditions were found to contribute to the high prevalence of the infection (Hamaidi et al., 2013; Sebaa et al., 2021; Belkessa et al., 2021). Contact with animals also emerged as a major risk factor (Sebaa et al., 2021).

Despite its prevalence worldwide – particularly in developing countries – there is limited molecular epidemiological data for *G. duodenalis* infection in humans from Algeria. In fact, only three studies focused on the molecular epidemiology and genetic characterisation of *G. duodenalis* infections in the country. These studies revealed a high prevalence of *G. duodenalis* infection, with significant genetic polymorphism observed among isolates of both assemblages A (AI, mostly AII and novels), and B (BIII, BIV, BS1, BS6, and novels). Furthermore, the studies highlighted that assemblage B isolates exhibited allelic sequence heterozygosity or mixed infection, unlike assemblage A isolates (Lalle et al., 2009; Benhassine et al., 2020; Rebih et al., 2020).

### *G. duodenalis* in animals

The prevalence and molecular detection of *G. duodenalis* in animals were only reported in livestock (n = 6). No studies on companion animals or wildlife were found (Table II). *G. duodenalis* was mainly reported in dairy cattle (Ouchene et al., 2012; Baroudi et al., 2017), sheep (Baroudi et al., 2015; Sahraoui et al., 2019; Benhassine et al., 2020), and to a lesser extent in dromedary camels (Maxamhud et al., 2023).

### *G. duodenalis* in cattle

The prevalence and genotypic distribution of *G. duodenalis* infections vary according to the region and the animals' age. The first report of *G. duodenalis* infection in dairy cattle occurred in 2012 in the Sétif Province (Ouchene et al., 2012). In this study, *G. duodenalis* was detected in calves from 8 days of age until adulthood. The highest infection rates were reported in calves aged 4 to 12 months. The first study to use molecular techniques was performed in dairy calves (< 3 months). *G. duodenalis* was more prevalent in older calves (2 months, 42.9%; and 3 months, 28.9%), than in younger calves (< 1 month, 6.9%). Genotypes included the predominant zoonotic assemblage A and the host-specific assemblage E (Baroudi et al., 2017). Findings showed that diarrhoeic calves only shed assemblage A or a mixed infection of assemblages A+E.

### *G. duodenalis* in sheep

The first investigation to determine the presence and molecular characterisation of *G. duodenalis* in lambs (< 3 months old) was performed in the Djelfa department. Only the zoonotic assemblage A was isolated from animals with diarrhoea and weight loss (Baroudi et al., 2015). A complementary study was conducted in younger lambs (< 40 days old) across a large area comprising four provinces. Authors reported the presence of the ruminant-specific assemblage E, assemblage D (the canine assemblage), and A+E mixed assemblages. This study was the first to identify assemblage D in sheep (Sahraoui et al., 2019). Another recent study was also conducted in the Djelfa department. It included lambs aged up to 6 months from a large number of farms (n = 28). In contrast to the observations in calves, the authors reported higher infection rates (9.1%) among lambs under 3 months compared to older lambs (4.0%). Infection rates were higher among lambs with diarrhoea (15.9%) than lambs without (5.6%). Authors reported the presence of assemblages A and E, and A+E mixed assemblages. Assemblage A was exclusively found in pre-weaned lambs with diarrhoea, while assemblage E

was predominantly present in post-weaned lambs without diarrhoea (Benhassine et al., 2020).

### G. duodenalis in dromedary camels

*Giardia duodenalis* was identified for the first time in camels (*Camelus dromedarius*) of the Sahraoui breed from the El-Oued region. Ten stool samples from 63 dromedary camels yielded positive results (15.9% prevalence), which were not genotyped. The infected animals were not diarrhoeic at the time of sample collection. Of the ten infected camels (five males, two females and three unknown), seven were under five years old (Maxamhud et al., 2023).

### G. duodenalis in the environment

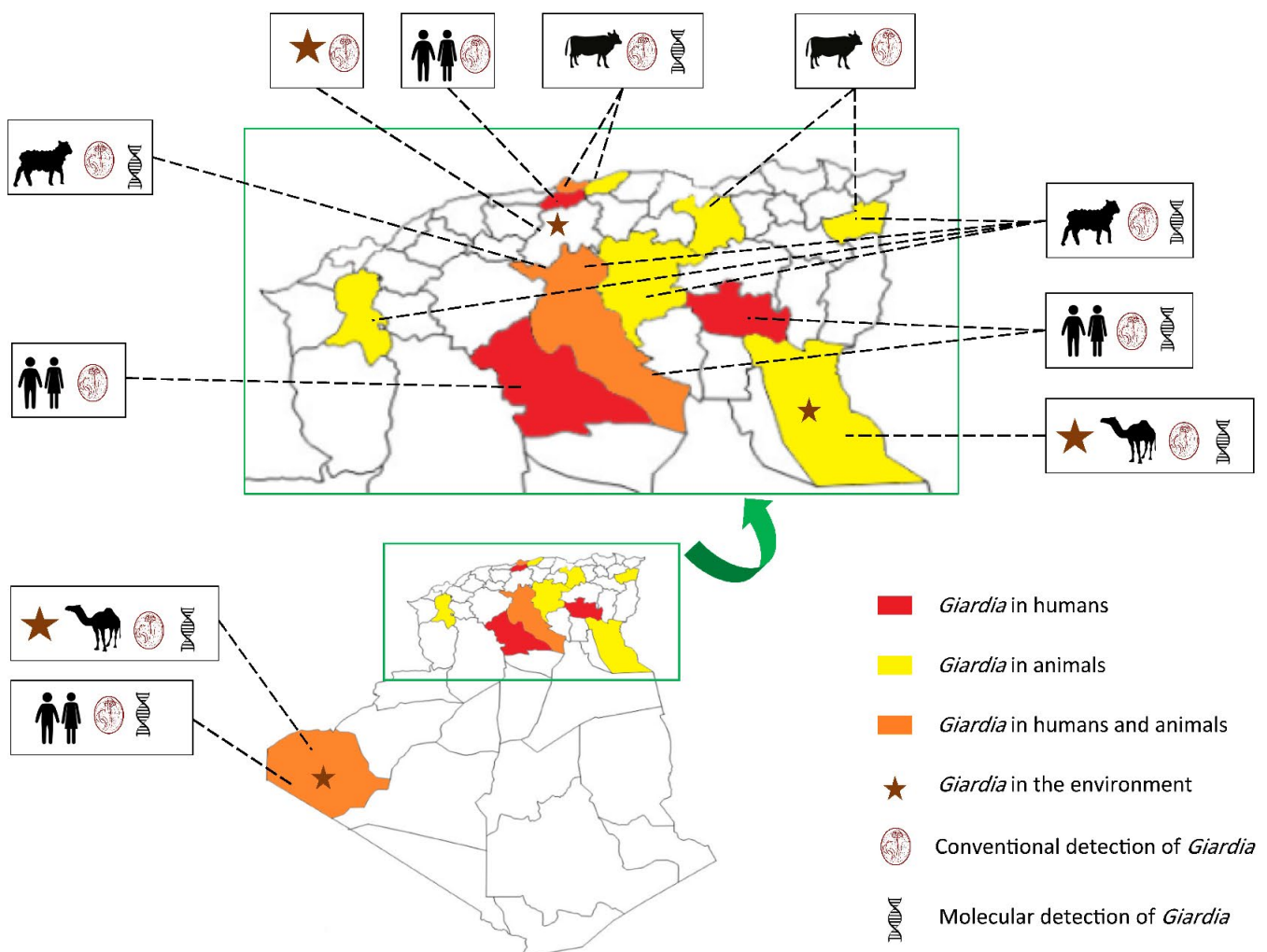
Only two studies investigated the presence of *G. duodenalis* in water and soil samples (Hamaidi-Chergui et al., 2019; Maxamhud et al., 2023). The first study aimed to detect parasites in wastewater, which represents a risk of exposure to both humans and animals. *G. duodenalis* cysts were found in raw wastewater samples (26 cysts/L), while none were detected in the treated wastewater from the Médéa sewage treatment plant (Hamaidi-Chergui et al., 2019). In a subsequent investigation, *G. duodenalis* was also detected in stool

samples from camels and five environmental samples. Specifically, *G. duodenalis* was identified in drinking water from one tap water sample drawn from a groundwater source near the farms. *G. duodenalis* was also found in one soil sample (sand). The isolate belonged to assemblage E (Maxamhud et al., 2023).

### Phylogenetic analysis and molecular epidemiology of G. duodenalis

Drawing on the limited available data on the NCBI nucleotide database, we assessed the genetic characterisation of *G. duodenalis* in humans and animals in Algeria to improve our understanding of the parasite's complex epidemiology. Only three articles (Lalle et al., 2009; Benhassine et al., 2020; Belkessa et al., 2021), which used molecular tools to characterise *G. duodenalis*, were in the NCBI database. They concerned sequences generated from triosephosphate isomerase (*tpi*) and glutamate dehydrogenase (*gdh*) genes with accession numbers (Table III).

Analysis of *tpi* gene locus sequences revealed the presence of human-adapted assemblages A and B in humans, and assemblage E in sheep. Interestingly, sequence analysis of the *gdh* gene locus revealed the



**Figure 1:** Map of Algeria highlighting the main regions where the presence of *Giardia* was investigated. We designed the map by drawing on the published studies included in this review // Carte de l'Algérie mettant en évidence les principales régions où la présence de *Giardia* a été étudiée. Nous avons conçu cette carte en nous appuyant sur les études publiées incluses dans cette revue

Sources: Lalle et al., 2009; Ouchene et al., 2012; Hamaidi et al., 2013; Baroudi et al., 2017; Sahraoui et al., 2019; Belkessa et al., 2020, 2021; Benhassine et al., 2020; Rebih et al., 2020; Sebaa et al., 2021; Maxamhud et al., 2023.

**Table 1:** *Giardia duodenalis* prevalence and assemblages reported in humans // Prévalence de *Giardia duodenalis* et assemblages signalés chez l'homme

| Department       | Faecal samples | Study period                | Diagnosis method  | Study population  | Giardia prevalence (%)  | Age of study population (years)         | Association with age/symptoms  | No. of samples typed/ No. samples tested             | Targeted gene / Assemblage   | Reference               |
|------------------|----------------|-----------------------------|---|---|---|---|--|--|--|-------------------------|
| Tindouf          | 120            | 2003-2005                   | Immunofluorescence microscopy + PCR ( <i>tpi</i> + <i>gdh</i> ) + RFLP + sequencing     | Sahrawi children from both settled and nomadic communities (42% males, 58% females) | 34.16 (41/120)  | 8-13                                    | NR   | 32/41 ( <i>tpi</i> gene)<br>28/41 ( <i>gdh</i> gene) | <i>tpi</i> :<br>Ass. A (12/32; 37.5%);<br>1 A1, 6 AII, 5 novels<br>Ass. B (18/32; 56.2%):<br>1 BIII, 1 BSI, 1 BIV, 1 BS6,<br>5 novels<br>Mixed A+B (2/32; 6.2%)<br><i>gdh</i><br>Ass. A (16/28; 57.1%);<br>2 AII, 14 novels<br>Ass. B (12/28; 42.8%);<br>1 novel, 11 mixed | (Lalle et al., 2009)    |
| Blida            | 542            | March-October 2011          | Lugol's Iodine staining microscopy  | Patients with digestive disorders   | 41.67 (25/542)  | 0-75                                    | NR   | NP   | NP   | (Hamaidi et al., 2013)  |
| Algiers + Biskra | 119            | 2013-2018                   | Real-time PCR + Assemblage specific nested PCR + Nested PCR <i>tpi</i> + Sequencing     | 55 children (< 15 y), 37 adults, 27 undetermined age                                | 67.2 (80/119)   | 2-74                                    | Higher in children (81.9%)<br>In children: 40% assemblage A and 60% assemblage B.<br>In adults: 85.7% assemblage A and 14.3% assemblage B.                       | 48/80  | <i>tpi</i><br>Ass. AII (22/48; 45.8%)<br>Ass. B (26/48 ;54.2%)   | (Belkessa et al., 2020) |
| Djelfa           | 355            | 2018-2019                   | Lugol's Iodine staining microscopy + PCR ( <i>beta-giardin</i> gene) + RFLP+ sequencing | School children, symptomatic and asymptomatic                                       | 8.4 (30/355)  | 6 - 11                                  | Symptomatic children 13/30 (43.3%)<br>Assemblage A more prevalent than assemblage B in symptomatic cases   | 28/30  | <i>Beta-giardin</i><br>Ass. A 14/28 (50%)<br>Ass. B 6/28 (21.42%)  | (Rebih et al., 2020)    |
| Algiers          | 2054           | September 2012-October 2013 | Direct microscopy and Formalin-ether sedimentation                                      | Outpatients and hospitalised patients   | 4.7 (97/2054)   | 1-90 (smaller children aged 1-10 years) | Higher prevalence in smaller children (63.9%).<br>Giardiasis was not linked to gender nor to intestinal symptoms   | NP   | NP   | (Belkessa et al., 2021) |
| Laghouat         | 2277           | March 2015-July 2018        | Direct microscopy, Formalin-ether sedimentation and flotation                           | Symptomatic (623) and asymptomatic (1654) population from urban and rural areas     | 14.6 (91/623) in symptomatic population and 0.3 (5/1654) in asymptomatic population | 1-89                                    | Higher prevalence in symptomatic population (14.6%) in female subjects (21.2%) who had contact with animals Vs. male subjects (13.8%), and in spring and summer. | NP   | NP   | (Sebaa et al., 2021)    |

NR: not reported; NP: not performed // NR : non rapporté ; NP : non réalisé

**Table II:** *Giardia duodenalis* prevalence and assemblages reported in livestock. /// Prévalence et assemblages de *Giardia duodenalis* signalés dans le bétail

| Animal                      | Department   | Study period                  | No. animal;<br>No. farm   | Age group   | Diagnosis method   | Apparent prevalence;<br>farm prevalence | Association with diarrhoea   | Association with age  | No. of samples typed/ No. samples tested         | Assemblage/subtype |    |               | References                   |
|-----------------------------|--|-------------------------------|---|---|--|---|--|---|--|--------------------|----|---------------|------------------------------|
|                             |  |                               |   |   |  |   |  |   |  | A                  | E  | Other         |                              |
| Dairy cattle                | Sétif  | July 2006-<br>April 2007      | 634<br>(302 calves and<br>332 cows);<br>13 farms                          | Calves<br>(1 day – 12 months)<br>and cows<br>(> 12 months)              | Formalin-ether<br>sedimentation technique<br>+ microscopy  | 13.8% (88/634);<br>53.8% (7/13)         | 34.8% of diarrhoeic<br>calves excreting <i>Giardia</i><br>(17/49); not significant<br>association  | Present in calves from<br>8 days of age and<br>adults<br>Higher prevalence in<br>calves aged from 4 to<br>12 months   | NP   | -                  | -  | -             | (Ouchene<br>et al., 2012)    |
| Sheep<br>(lamb)             | Djelfa   | 2015                          | 47 lambs;<br>7 farms  | < 3 months  | Diethyl ether formalin<br>sedimentation +<br>microscopy + nested<br>PCR ( <i>tpi</i> ) & sequencing                              | 21.27% (10/47);<br>NR                   | Association with<br>diarrhoea and<br>weight loss (specially<br>assemblage A)   | Present in lambs<br>(<3 months)   | 7 A: A1<br>(n=3),<br>A2<br>(n=2),<br>A6<br>(n=2) | -                  | -  | -             | (Baroudi<br>et al., 2015)    |
| Dairy<br>cattle<br>(calves) | Algiers,<br>Boumerdes                              | January 2013-<br>January 2014 | 102 pre-<br>weaned<br>dairy calves;<br>19 farms                           | Pre-weaned dairy<br>calves (< 3 months)                                 | PCR ( <i>tpi</i> ) & sequencing  | 27.5% (28/102);<br>NR                   | Higher prevalence in<br>non-diarrhoeic calves<br>(82.14%).<br>Diarrhoea was<br>associated with<br>assemblage A or with<br>mixed infection (A<br>and E)   | Higher prevalence<br>in older calves aged<br>between 2 and<br>3 months (42.9% and<br>28.9%, respectively)<br>compared to 1-month-<br>old calves (6.9%).   | 28/28  | 14 A2              | 6  | 8 A+E         | (Baroudi<br>et al., 2017)    |
| Sheep<br>(lamb)             | Djelfa<br>Msila<br>Sidi Bel<br>Abbès<br>Souk Ahras | November 2015-<br>March 2017  | 83 lambs;<br>14 farms   | < 40 days old   | Formalin-ether<br>sedimentation technique<br>+ microscopy (IF) +<br>nested PCR ( <i>tpi</i> + <i>gdh</i> ) +<br>RFLP+ sequencing | 27.7% (23/83);<br>71.4% (10/14)         | Higher prevalence in<br>asymptomatic lambs<br>(56.5%).   | Higher prevalence in<br>older lambs<br>(> 21 days).   | 16/23  | -                  | 10 | 4 D, 2<br>A+E | (Sahraoui<br>et al., 2019)   |
| Sheep                       | Djelfa   | May 2014-<br>June 2016        | 346 lambs<br>(197 pre-<br>weaned and<br>149 post-<br>weaned);<br>28 farms | Pre-weaned lambs<br>(< 3 months)<br>Post-weaned lambs<br>(3 - 6 months) | Zinc sulfate flotation +<br>microscopy + IF + PCR<br>( <i>tpi</i> + <i>gdh</i> ) + sequencing                                    | 6.9% (24/346);<br>32.1% (9/28)          | Higher prevalence in<br>lambs with diarrhoea<br>(15.9%:7/44) than in<br>non-diarrhoeic lambs<br>(5.6%:17/302).<br>The assemblage A was<br>only found in diarrhoeic<br>lambs and the<br>assemblage E mostly in<br>non-diarrhoeic lambs. | Higher prevalence in<br>lambs under 3 months<br>of age (9.1%) than in<br>older animals (4.0%).<br>The assemblage A was<br>seen in pre-weaning<br>animals (≤6 weeks)<br>and the assemblage<br>E mostly in post-<br>weaned lambs. | 15/24  | 6                  | 7  | 2 A+E         | (Benhassine<br>et al., 2020) |
| Camels                      | El-Oued<br>Tindouf                                 | April 2017-<br>September 2021 | 63 animals;<br>NR   | < 3-5 years   | qPCR (SSU gene)  | 15.9% (10/63)                           | Any signs of diarrhoea at<br>the time of collection.   | Only in young animals<br>(< 5 years old)  | 0/10   | -                  | -  | -             | (Maxamhud<br>et al., 2023)   |

NR: not reported; NP: not performed; qPCR: quantitative real-time PCR /// NR : non rapporté ; NP : non réalisé ; qPCR : PCR quantitative en temps réel

**Table III:** Sequences of *Giardia* genes triosephosphate isomerase (*tpi*) and glutamate dehydrogenase (*gdh*) identified in Algeria // Séquences des gènes triosephosphate isomérase (*tpi*) et glutamate déshydrogénase (*gdh*) de *Giardia* identifiées en Algérie

| Host  | <i>tpi</i> gene             | <i>gdh</i> gene                       | References                |
|-------|-----------------------------|---------------------------------------|---------------------------|
| Human | EU41735-EU41761 (n=9)       | EU278608- EU278609 (n=2)              | (Lalle et al., 2009)      |
|       | MW 251133- MW 251180 (n=48) | –                                     | (Belkessa et al., 2021)   |
| Sheep | MT321650 & MT321652 (n=2)   | MT321644-MT MT321649 & MT321651 (n=7) | (Benhassine et al., 2020) |

presence of assemblages A and B in humans, as well as assemblage E in sheep. Furthermore, sheep also excreted the human-adapted assemblage A (MT321652), which clustered with two other sequences of assemblage A in humans (EU041754 and EU041756).

### ■ DISCUSSION AND PERSPECTIVES

Intestinal parasitic infections are of major importance worldwide. They have been recognised as a foremost contributor to illness and death, particularly in marginalised populations. *G. duodenalis* – a parasitic organism affecting both animals and humans – is ubiquitous in a wide range of environments. However, the potential economic impact and welfare implications of *G. duodenalis* infection in North Africa remain largely unexplored. As yet, no comprehensive analysis has compared the situation in North Africa with the global situation. This review reveals that *G. duodenalis* is increasingly being recognised as a significant infectious pathogen in Algeria.

Data drawn from PubMed reveal the widespread prevalence of *G. duodenalis* in both humans and various animal species in North Africa, suggesting the presence of both anthroponotic and zoonotic transmission cycles. These results provide valuable insights into the dynamics of *G. duodenalis* transmission in different regions of Algeria. Genotyping *G. duodenalis* is crucial for exploring isolate variability, particularly when it comes to understanding potential transmission cycles. Despite these significant findings, the epidemiology of *G. duodenalis* assemblages in Algeria remains largely unexplored. To date, investigations have only focused on a few areas of the country and limited hosts. Thus, further studies are essential to bridge the knowledge gap and identify the full molecular diversity of *G. duodenalis* in humans, as well as wild and domestic carnivorous or ruminant animal populations. Conducting research in regions where data is scarce or lacking is particularly important.

Our review presents valuable findings, but it has several limitations. First, given the scarcity of reports on *G. duodenalis* infection in animals and humans, our understanding of *G. duodenalis* infection in Algeria remains limited. Second, our review did not encompass all available data sources, such as theses, conference abstracts and reports, which could have provided additional information. Furthermore, only four studies used molecular tools to characterise *G. duodenalis*, which did not allow for a more detailed genetic analysis. To establish accurate estimates of the regional burden of *G. duodenalis* in Algeria, continuous monitoring is essential. This would also help develop effective intervention and control strategies. In general, several risk factors contribute to the occurrence of human giardiasis in Algeria, including geographical location (temperature and humidity) and lifestyle factors, including poor hygiene linked to poverty and overcrowding, which may contribute to the incidence of diarrhoea in households, contaminated drinking water and close contact with animal waste. Indeed, the epidemiology of *G. duodenalis* is closely linked to poor hygiene, which means that developing countries are particularly affected.

The prevalence of protozoa co-infection in humans, due to poor hygiene in the affected regions, can be attributed to the fact that several parasites share a common mode of transmission. We found that there was a significant association between combined protozoan infection and asymptomatic populations living in rural areas. In contrast, the symptomatic population exhibited a higher protozoan infection rate during the hot season (Sebaa et al., 2021). Given the highly unfavourable climatic conditions, it is reasonable to suggest that transmission is likely to occur indoors, where higher moisture levels and lower temperatures are conducive to transmission. For instance, the assemblages A and B were initially identified in children. This reveals a distinct rural cycle in situations where animals, especially sick animals, are kept near human dwellings and cared for by women and children. This cycle may also affect passing tourists (Lalle et al., 2009). Recently, close contact with domestic animals (cat, poultry) have been specifically linked to the detection of assemblage A in humans (Rebih et al., 2020). On the other hand, both assemblages A and B were frequently observed and showed no specific associations with sociodemographic data (Belkessa et al., 2020). More comprehensive molecular typing studies are recommended (Thompson and Ash, 2016) to enhance our understanding of giardiasis epidemiology—including transmission dynamics and variations in clinical presentation. Further studies would also allow us to develop more effective intervention strategies to deal with this urgent health issue.

*G. duodenalis* exhibits considerable variation in terms of its prevalence across the different studies that focus on various ages and groups of dairy cattle, sheep and camels in Algeria. Among the *G. duodenalis* assemblages, A and B are known to have a broad host distribution and strains belonging to these assemblages have zoonotic potential. Assemblage A isolates are commonly found in humans and livestock, whereas assemblage B isolates are frequently found in humans. In fact, the subtyping of *G. duodenalis* in animals from Algeria revealed the presence of zoonotic assemblage A, underscoring the importance of the role of cattle and sheep in the epidemiology of human giardiasis. Across the four genotyping studies, four *G. duodenalis* assemblages (A, B, E and D) were identified. Three of the studies reported mixed infections with A and E, indicating that sheep may be a significant potential reservoir for this protist (Baroudi et al., 2015, 2017; Sahaoui et al., 2019; Benhassine et al., 2020). These results highlight the need for more comprehensive research to improve our understanding of the dynamics of *G. duodenalis* transmission among animals in Algeria and its implications for human health. Indeed, it is widely recognised that livestock (cattle, sheep, goats and pigs) primarily harbour *G. duodenalis* assemblage E, which has recently been reported to have zoonotic potential. Assemblage A is the next most prevalent in these animals (Ryan and Zahedi, 2019). Interestingly, assemblage A was exclusively detected in pre-weaned lambs with diarrhoea, while assemblage E was primarily observed in post-weaned lambs without diarrhoea (Benhassine et al., 2020). These findings raise the question: is assemblage A more pathogenic than assemblage E? Interestingly, current evidence suggests that there is no association between specific symptoms and particular assemblages in either humans or animals (Cardona et al., 2011; Puebla et al., 2014; Scorza et al., 2021;

Zajackowski et al., 2021). Further broad and long-term studies could provide some answers, for example, by investigating the host immune system and/or the role of gut microbiota.

The available data from Algeria is too limited to provide an in-depth understanding of *G. duodenalis* transmission dynamics. Subtyping studies in both animals and humans are lacking, in particular for assemblages less adapted to domestic animals. Determining the genetic basis of *G. duodenalis* is crucial for understanding infection routes and for the development of national preventive measures. While some molecular investigations have provided insights into genetic diversity, more research is required. For example, broader sampling and extensive long-term systematic molecular epidemiological studies across different regions could provide essential data on the epidemiology of giardiasis in humans and animals, including prevalence, host-adapted species/genotypes and public health significance. More extensive sampling with a higher number of herders and families would generate more statistically significant results. In addition, more environmental samples are necessary to clarify the role of livestock, companion animals and wild animals, as sources or reservoirs of intestinal parasites. Notably, the whole genome sequence availability of *G. duodenalis* isolates has facilitated studies focused on population genetics. Multi-locus sequence typing (MLST) tools are now increasingly used for characterising the infective potential of *G. duodenalis* in humans and animals (Ryan and Zahedi, 2019). A thorough and systematic study using MLST analysis could provide an in-depth assessment of the burden of giardiasis, originating from both humans and animals.

Wastewater constitutes a significant reservoir of highly resistant *G. duodenalis* cysts in the environment. Indeed, wastewater discharge is a potential source of contamination, which poses a risk for drinking water and water for recreational use (Hamaidi-Chergui et al., 2019). It also constitutes an environmental risk (for surface water and soil samples), in areas where camels and ruminants coexist (Maxamhud et al., 2023). The discharge of wastewater of animal and human origin presents a well-known risk, by potentially introducing resistant *G. duodenalis* cysts into surface water (used for drinking and recreational purposes). Further investigations on the prevalence and genetic diversity of *G. duodenalis* in drinking water supplies and food sources, in conjunction with case-control studies, are essential to understand the complete epidemiological picture. To reduce *G. duodenalis* infection, we need to improve water, sanitation and hygiene strategies, for example, by installing effective drinking water purification and water monitoring systems.

Global warming and population growth exacerbate malnutrition and increase the prevalence of giardiasis. This is particularly the case in impoverished regions, where livestock provide a primary source of income and are often in close contact with children (Squire and Ryan, 2017). To mitigate environmental contamination and safeguard both human and animal health, it is crucial to implement disease prevention and control strategies in livestock, for example, improving hygiene and animal husbandry practices, and fencing livestock away from water sources to minimise direct contamination. In addition, providing health education and adequate sanitation could effectively reduce the burden of intestinal parasitic infections (Jidda et al., 2023).

To limit the circulation of these zoonotic agents and prevent giardiasis, "veterinarians, biologists, ecologists, and medical doctors" must work together in the framework of the unifying "One Health" approach.

## ■ CONCLUSION

This article reviews data on the occurrence and genetic characterisation of *G. duodenalis* in Algeria. Further studies are necessary

in various regions of Algeria to provide a more accurate depiction of the epidemiological situation across the entire country. Research should include factors linked to lifestyle, particularly for populations in rural areas, where close contact with animal waste is more frequent. Prevention and control programmes should be tailored to specific regions to effectively reduce the transmission of *G. duodenalis*. In many areas, the prevalence of *G. duodenalis* in both animals and humans has yet to be reported. Therefore, epidemiological surveillance is essential to assess the disease burden and develop effective management strategies for giardiasis in the "One Health" framework.

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## Conflicts of interest

The authors declare that there is no conflict of interest.

## Author contributions statement

All authors (MT, BP, MM) participated in the conception and design of the review; MT and MM analysed data and drafted the first version of the article; all authors (MT, BP, MM) critically reviewed the manuscript.

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## Résumé

**Thomas M., Polack B., Mammeri M.** *Giardia duodenalis* en Algérie : une revue dans le cadre de l'approche Une seule santé

*Giardia duodenalis* est un parasite protozoaire qui infecte principalement l'intestin grêle de divers mammifères, y compris les humains. Il s'agit d'un complexe d'espèces composé de plusieurs génotypes connus sous le nom d'assemblages A à H. Les assemblages A et B sont considérés comme les plus zoonotiques, présentant ainsi un risque significatif pour la santé humaine, tandis que les assemblages C à H se trouvent chez les animaux de compagnie, le bétail, les rongeurs et les vertébrés marins. La giardiose, due à *G. duodenalis*, est l'infection parasitaire intestinale la plus courante dans le monde. En Algérie, il existe des données limitées sur l'occurrence et les caractéristiques génétiques de *G. duodenalis*, entravant la compréhension de son épidémiologie, de son impact et de son potentiel zoonotique. Cette revue se concentre sur la recherche menée en Algérie, couvrant les humains, les animaux et l'environnement, en mettant l'accent sur l'approche «Une seule santé». Les bases de données PubMed et ResearchGate ont été utilisées pour accéder aux publications pertinentes sur la présence de *G. duodenalis* chez les humains, les animaux ou dans l'environnement de janvier 2000 à avril 2023. Dix-sept publications ont été identifiées, parmi lesquelles seuls quatre articles utilisaient des outils moléculaires pour identifier *G. duodenalis*. Les résultats ont révélé la présence de *G. duodenalis* chez les humains, les animaux d'élevage (bovins, ovins et chameaux) et dans l'environnement (échantillons d'eau et de sol). La prévalence et la diversité génétique des isolats de *G. duodenalis* variaient selon les régions et les groupes d'âge, aussi bien chez les humains que chez les animaux. L'assemblage A était couramment trouvé chez les humains et les animaux, indiquant une transmission zoonotique potentielle. Des études supplémentaires sont nécessaires pour comprendre de manière approfondie la dynamique de transmission de *G. duodenalis*, son potentiel zoonotique et les implications pour la santé publique et le bien-être animal en Algérie. Aborder *G. duodenalis* nécessite des efforts collaboratifs dans le cadre du concept «Une seule santé», impliquant des vétérinaires, des biologistes, des écologistes et des professionnels de la santé. La mise en œuvre de stratégies de prévention et de contrôle adaptées à des régions spécifiques et l'amélioration des pratiques d'hygiène et d'élevage sont essentielles pour réduire la charge de la giardiose tant chez les humains que chez les animaux.

**Mots-clés :** *Giardia duodenalis*, zoonose, transmission des maladies, approche Une seule santé, épidémiologie moléculaire, Algérie

## Resumen

**Thomas M., Polack B., Mammeri M.** *Giardia duodenalis* en Argelia: una revisión en el contexto del enfoque Una salud

La *Giardia duodenalis* es un parásito protozoario que infecta principalmente el intestino delgado de varios mamíferos, incluidos los humanos. Se trata de un complejo de especies compuesto por varios genotipos conocidos bajo el nombre de ensamblajes A a H. Los ensamblajes A y B se consideran los más zoonóticos, por lo que presentan un riesgo significativo para la salud humana, mientras que los ensamblajes C a H se encuentran en los animales de compañía, el ganado, los roedores y los vertebrados marinos. La giardiosis, causada por la *G. duodenalis*, es la infección parasitaria intestinal más corriente en el mundo. En Argelia existen datos limitados sobre la incidencia y las características genéticas de la *G. duodenalis*, lo que dificulta la comprensión de su epidemiología, su impacto y su potencial zoonótico. Esta revisión se centra en las investigaciones llevadas a cabo en Argelia en humanos, animales y medio ambiente, aplicando el enfoque «Una salud». Las bases de datos PubMed y ResearchGate se utilizaron para acceder a las publicaciones pertinentes sobre la presencia de *G. duodenalis* en humanos, animales y medio ambiente de enero de 2000 a abril de 2023. Se identificaron diecisiete publicaciones, entre las cuales solo cuatro artículos utilizaban herramientas moleculares para identificar a la *G. duodenalis*. Los resultados revelaron la presencia de *G. duodenalis* en humanos, en ganado (bovinos, ovinos y camellos) y en el medio ambiente (muestras de agua y de suelo). La prevalencia y la diversidad genética de las cepas aisladas de *G. duodenalis* variaban según las regiones y los grupos de edad, tanto en humanos como en animales. El ensamblaje A se encontraba a menudo en los humanos y los animales, indicando una transmisión zoonótica potencial. Son necesarios estudios suplementarios para comprender en profundidad la dinámica de transmisión de la *G. duodenalis*, su potencial zoonótico y las implicaciones para la salud pública y el bienestar animal en Argelia. Abordar la *G. duodenalis* requiere esfuerzos colaborativos en el planteamiento del concepto «Una sola salud», que impliquen a veterinarios, biólogos, ecologistas y profesionales de la salud. La aplicación de estrategias de prevención y de control adaptadas a regiones específicas y la mejora de las prácticas de higiene y de cría de ganado son esenciales para reducir la carga de la giardiosis tanto en los humanos como en los animales.

**Palabras clave:** *Giardia duodenalis*, zoonosis, transmisión de enfermedades, enfoque Una salud, epidemiología molecular, Argelia

