Epidemiological Insights into Toxoplasmosis in Egypt: A Review of Transmission, Risk Factors, Diagnostics, and Molecular Diversity of *Toxoplasma gondii* in Humans and Livestock Animals

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ABSTRACT

Toxoplasma gondii is a globally distributed zoonotic parasite affecting both humans and animals, with significant implications for public health and livestock production. Egypt represents a critical epidemiological setting owing to its agricultural economy, widespread animal husbandry, and high human-animal interaction. This review summarizes the existing situation supported by recent literature on the epidemiology of *T. gondii* infection in humans, camels, sheep, goats, and cattle across various Egyptian locations. The prevalence of infection demonstrates wide variation across host species and geographic localities, with consistently higher infection rates in camels and small ruminants compared to cattle. In humans, particularly among pregnant women, infection has been frequently associated with cat exposure, undercooked meat consumption, and poor hygiene. Among animals, species susceptibility, age, sex, and environmental conditions contribute to varying infection dynamics. In the following, we will highlight the endemic nature of toxoplasmosis in Egypt and underscore the necessity for integrated public health and veterinary measures, taking the recent approaches to mitigate this serious disease into consideration.

Keywords: *Toxoplasma gondii*; Egypt; Humans; Camels; Small ruminants; Cattle; Risk factors.

INTRODUCTION

Toxoplasma gondii is an obligate intracellular protozoan parasite capable of infecting nearly all warm-blooded vertebrates, including humans and a wide range of domestic animals. It is the causative agent of toxoplasmosis, a globally prevalent zoonotic disease that poses considerable public health and veterinary concerns due to its potential for congenital transmission and adverse impacts on animal productivity (Tenter et al., 2000). The parasite's life cycle includes felids as definitive hosts, which excrete unsporulated oocysts into the environment, and numerous intermediate hosts such as humans, sheep, goats, cattle, buffaloes, poultry, and camels that become infected primarily through ingestion of food or water contaminated with sporulated oocysts, or by consuming undercooked meat harboring tissue cysts (Montoya & Rosso, 2005). Once infected, animals can harbor latent tissue cysts for life, contributing to the chronicity and transmission of the infection.

In Egypt, *T. gondii* is considered endemic, with a range of ecological, agricultural, and socio-economic factors favoring its widespread transmission. The presence of abundant stray and domestic cats facilitates continuous environmental contamination with oocysts, especially in densely populated and agriculturally intensive regions. Traditional husbandry systems and frequent human-animal interactions in rural communities further amplify transmission risk (Ibrahim et al., 2017; Ghoneim et al., 2009; Fereig et al., 2022). Among animal hosts, small ruminants especially sheep and goats are highly susceptible and serve as major reservoirs of infection. In these species, toxoplasmosis is a well-documented cause of reproductive disorders, including abortion, stillbirth, and neonatal mortality, leading to significant economic losses (Saad et al., 2018; Khattab et al., 2021; Barghash & Sadek, 2025). Cattle and buffaloes, though historically considered more resistant, have also shown

measurable seroprevalence rates in recent studies, raising questions about their epidemiological role and contribution to transmission dynamics (Zeedan et al., 2022; Barghash et al., 2024; Elsharkawy et al., 2024).

Camels (*Camelus dromedarius*) integral to Egypt's livestock economy and dietary culture have received increasing attention in recent toxoplasmosis research due to their potential role as intermediate hosts. Multiple studies have reported *T. gondii* antibodies and DNA in camel blood and tissues, indicating natural exposure and possible involvement in the parasite's life cycle. When camel meat and milk are widely consumed, often raw or undercooked in some regions, the species represents a potential but under recognized source of human infection. Risk factors in camels, including sex, age, and origin, appear to affect prevalence rates, and their contribution to environmental contamination and foodborne transmission warrants further surveillance (Shaapan & Khalil, 2008; Barghash et al., 2017; El Sayed et al., 2017; Khattab et al., 2022; Toaleb & Shaapan, 2024).

Over the past two decades, numerous studies across Egypt have explored the seroprevalence, risk factors, and diagnostic approaches for *T. gondii* in both humans and animals. However, findings remain dispersed, with notable regional and methodological variation. This review synthesizes current epidemiological data on *T. gondii* infection in Egypt spanning humans, camels, small ruminants, cattle, and buffaloes to highlight infection trends, assess diagnostic and molecular approaches, and identify key risk factors. Emphasizing the camel's role within this zoonotic framework, the review supports a One Health perspective for future surveillance, risk mitigation, and public awareness efforts (Fereig et al., 2022; Khattab et al., 2019; Toaleb & Shaapan, 2024).

Historical Background and Taxonomy of *Toxoplasma gondii*

The protozoan parasite *T. gondii* was first discovered in 1908 by Nicolle and Manceaux at the Pasteur Institute in Tunis during investigations of a North African rodent known as the gundi (*Ctenodactylus gundi*). Initially classified as a species of *Leishmania* and named *Leishmania gondii*, the organism was later correctly recognized as a new genus and reclassified as *T. gondii*, a name reflecting both its crescent-like morphology (from the Greek *toxon* meaning bow, and *plasma* meaning form) and its original host (Dubey, 2009). In the same year, Splendore independently reported a similar protozoan in a rabbit in Brazil, providing early evidence of its global distribution (Dubey, 2009).

Although *T. gondii* was known to science for decades, its clinical relevance in humans became evident only in 1939, when it was identified in the tissues of a congenitally infected infant showing classical signs such as hydrocephalus, retinochoroiditis, and intracranial calcifications (Dubey, 2008). A major breakthrough came with the development of the Sabin–Feldman dye test in 1948, which facilitated serological diagnosis and led to the recognition of the parasite's wide distribution in warm-blooded animals (Sabin & Feldman, 1948). The parasite's veterinary significance emerged in 1957 following reports of abortion storms in sheep herds, underscoring its economic and reproductive impacts in livestock (Dubey, 2008). Further advancements in the 1960s through electron microscopy revealed the ultrastructural similarity between *T. gondii* and other coccidian parasites such as *Eimeria*, placing it within the phylum *Apicomplexa* (Tenter, 2009). The role of the immune system in controlling infection became particularly apparent in the 1980s, when toxoplasmosis emerged as a major opportunistic infection among AIDS patients (Innes, 2010). Moreover, the detection of *T. gondii* in marine mammals such as sea otters highlighted its capacity to contaminate aquatic ecosystems, likely via land-based oocyst runoff (Dubey, 2008).

Taxonomically, *T. gondii* is a eukaryotic, unicellular protozoan that belongs to the domain Eukaryota. It is classified within the kingdom Alveolata, which comprises protists with common structural features believed to have evolved from a shared ancestor. Within this kingdom, *T. gondii* belongs to the phylum *Apicomplexa*, a group of intracellular parasites characterized by an apical complex structure used for host invasion. The parasite is further grouped in the class *Coccidia*, order *Eucoccidiorida*, and family *Sarcocystidae* (Delgado et al, 2022). Members of this family typically require two hosts to complete their life cycle, often involving predator–prey interactions. *T. gondii* is the only known species within its genus *Toxoplasma* and requires felids as definitive hosts for sexual reproduction, with a wide range of intermediate hosts including humans and livestock (Zaki et al., 2024).

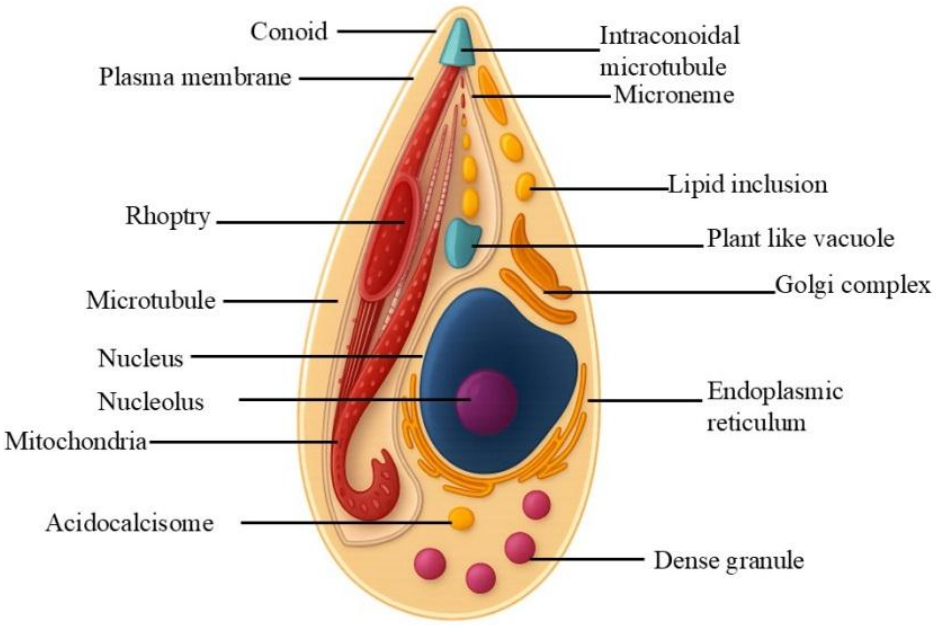

Fig.(**1).** Diagrammatic longitudinal section of the tachyzoite form of *Toxoplasma gondii* indicating the main structures and organelles (Attias et al**.,** 2020).

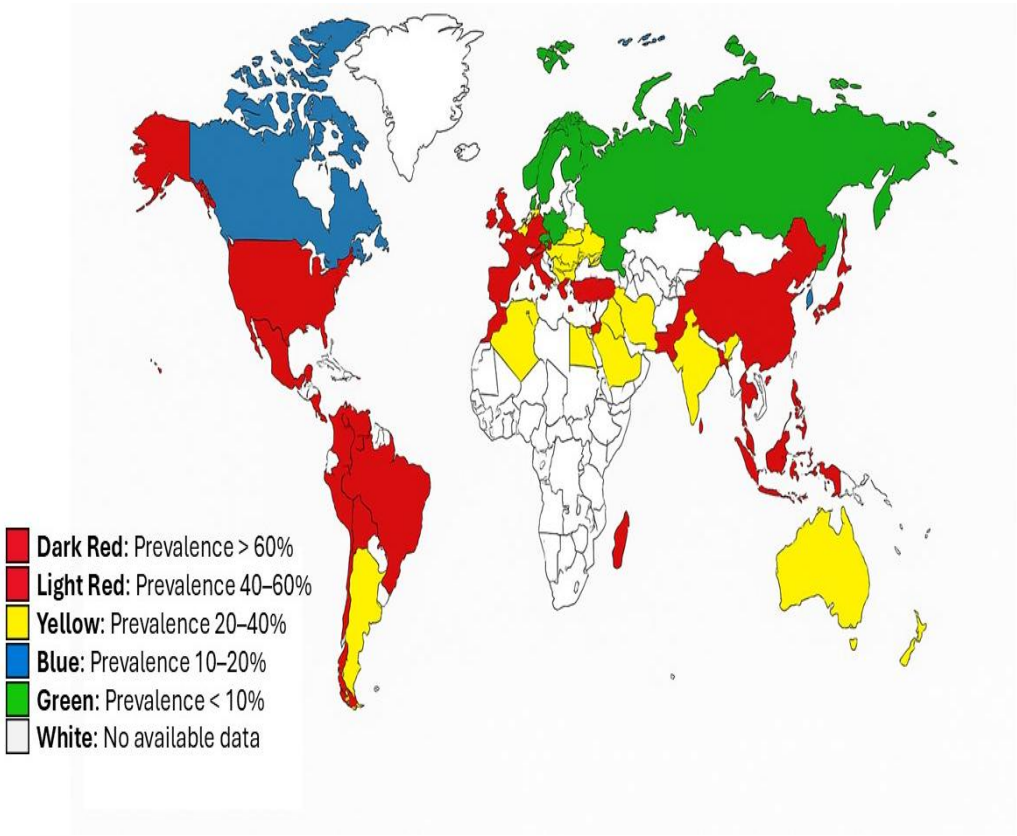

Fig.(2). Map of toxoplasmosis prevalence in the world (Attias et al., 2020).

Life Cycle and Transmission

T. gondii possesses a highly intricate life cycle involving a broad range of hosts and multiple modes of transmission. The parasite undergoes both sexual and asexual reproduction: the sexual phase is restricted to the intestinal epithelium of domestic and wild felines, while the asexual stages occur in the tissues of virtually all warm-blooded intermediate hosts (Gebremedhin et al., 2013; Attias et al., 2020; Tong et al., 2021). The life cycle includes three distinct infective forms: tachyzoites, which multiply rapidly during acute infection; bradyzoites, which reside in tissue cysts during the chronic phase; and sporozoites, contained within environmentally resistant oocysts (Sibley et al., 2009; Tenter, 2009).

Cats become infected primarily through the ingestion of bradyzoite-laden tissue cysts from prey such as rodents or birds, or via oocysts. Following ingestion, bradyzoites are liberated in the feline gastrointestinal tract and initiate multiple rounds of development before gametogenesis. Oocyst shedding begins approximately two days post-infection and can last for 2–3 weeks (Dubey, 2010; Montoya & Rosso, 2005). Sporulated oocysts can persist for extended periods—often months or years—in soil or water, contributing to widespread environmental contamination (Dubey, 1998, 2004). In contrast, tissue cysts, while more sensitive to environmental conditions, remain viable across a range of temperatures, including mild freezing (Gajadhar et al., 2006).

The parasite can also be acquired by intermediate hosts, including humans, through ingestion of undercooked meat containing bradyzoites or food and water contaminated with sporulated oocysts. Following entry into the intestinal tract, sporozoites or bradyzoites penetrate epithelial cells, transform into tachyzoites, and disseminate through the bloodstream and lymphatic system. Eventually, tachyzoites encyst and transform into bradyzoites as the host's immune response becomes active, resulting in long-term persistence of infection (Dubey& Frenkel, 1973; Montoya & Rosso, 2005).
Humans are typically infected either by consuming contaminated food (particularly undercooked meat or unwashed produce), drinking unfiltered water, or through exposure to oocyst-contaminated environments such as soil and cat litter. Vertical transmission can occur when tachyzoites cross the placenta during maternal infection, with risk and severity influenced by factors such as the parasite strain, timing of infection during gestation, and the mother's immune status (Dubey, 2010; Jones et al., 2009).

Less common routes of horizontal transmission include organ transplantation, blood transfusion, and laboratory accidents (Tenter et al., 2000; Montoya & Rosso, 2005). Consumption of raw goat or sheep milk has also been implicated, with tachyzoites potentially shed during peripartum periods (Abdel-Rahman et al., 2012). Mechanical vectors such as flies, beetles, and cockroaches can inadvertently spread oocysts to human food or animal feed (Hill et al., 2005). Additionally, a study by Karthikeyan et al. (2021) detected *T. gondii* DNA in commercial insect-based food products, underscoring the need for proper handling and hygiene in insect farming and processing.

Interestingly, the parasite may manipulate host behavior to enhance its transmission particularly by reducing intermediate hosts' natural aversion to feline predators (Tong et al., 2021). *T. gondii* infection has also been linked to ocular and neurological diseases, with congenital toxoplasmosis associated with host genetic polymorphisms in loci such as ABCA4 and COL2A1, potentially influencing disease manifestation through epigenetic mechanisms (Jamieson et al., 2009).

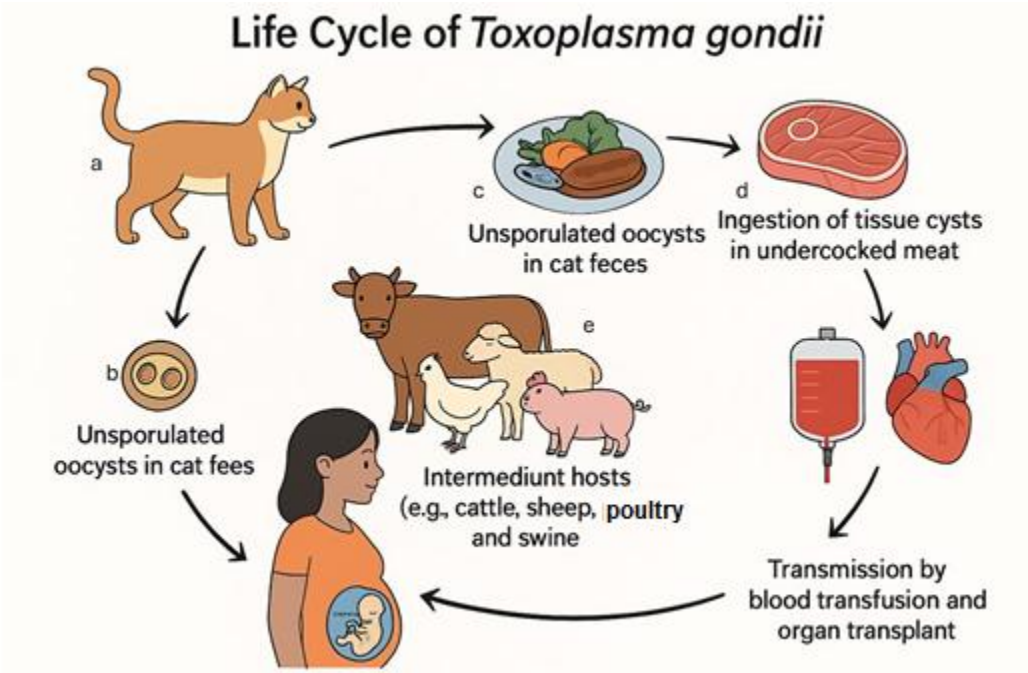

Fig. (3). *Toxoplasma gondii* pathways of transmission **(**Attias et al**.,** 2020**): a** feline definitive host (cat). **b**. Unsporulated oocysts in cat feces. **c**. Food contaminated with sporulated oocysts. **d**. Ingestion of tissue cysts in uncooked meat. **e**. Intermediate hosts (e.g., cattle, sheep, poultry, and swine). Tachyzoites are transmitted through the placenta to the fetus, transmission by blood transfusion and organ transplant.

Diagnosis of *Toxoplasma gondii*

The clinical manifestations of toxoplasmosis are generally vague and often mimic those of other infections, making clinical diagnosis unreliable without laboratory confirmation. Historically, the detection of *T. gondii* in humans and animals was limited by the lack of accurate diagnostic tools. Today, diagnosis relies on a combination of biological, histological, serological, and molecular techniques (Hill & Dubey, 2002).

Microscopic detection

Microscopy can aid in identifying *T. gondii* oocysts in environmental samples (such as feces or water) through filtration or centrifugation. Staining tissue cysts with hematoxylin and eosin (H&E) or Giemsa remains cost-effective and widely accessible, yet light microscopy is inherently limited in sensitivity and specificity. It can misidentify closely related species like *Hammondia hammondi*, especially when oocyst concentrations fall below 1,000 per gram of sample (Elmore et al., 2010). Though electron microscopy offers high-resolution imaging for parasite stages in tissues, its labor-intensive nature makes it unsuitable for routine diagnostics (Sims et al., 1989).

Recent innovations include a transfer learning–based image recognition method using a fuzzy cycle generative adversarial network (FCGAN), which leverages the crescent-shaped morphology of *T. gondii* to achieve high diagnostic accuracy (Li et al., 2020).

Serological techniques

Serological testing is the most commonly used approach for detecting *T. gondii* exposure in both humans and animals, particularly through the detection of specific antibody classes. Traditional tests include the Sabin–Feldman dye test, indirect fluorescent antibody test (IFAT), complement fixation (CF), indirect hemagglutination (IHA), agglutination tests, and enzyme-linked immunosorbent assays (ELISA) (Proctor& Banerjee 1994; Hashemi-Fesharki, 1996).

Antibody profiles are critical to interpreting infection status:

- **IgM** appears within a week and persists for months or longer but may not confirm acute infection on its own.
- **IgA** typically emerges earlier and may offer better temporal specificity.

- **IgG** indicates exposure but not timing.
- IgE, with its shorter half-life, may help pinpoint recent infection (Bessieres et al., 1992).

ELISA remains the most widely adopted method due to its high sensitivity, cost-effectiveness, and scalability. Both direct and indirect formats are used, with the latter employing secondary enzyme-linked antibodies to amplify the signal. While commercial kits are typically based on tachyzoite lysate antigens (TLA), recent developments include recombinant antigens (e.g., GRA1–8, ROP1–2, MIC2–5, SAG1–2), which have demonstrated improved specificity and sensitivity (Kotresha & Noordin, 2010; Shaapan et al., 2008).

In Egypt, seroprevalence in camels for *T. gondii* and *Neospora caninum* ranged from 3.3% to 96.4%, underscoring the diagnostic variability and importance of robust tools (Fereig et al., 2022). ELISA detected *T. gondii* in the samples under investigation (38.92%), with a greater incidence in camels (64.51%) and sheep (43.75%) than in goats (27.93%) and cattle (13.46%) in North-West Egypt (Khattab et al., 2022).

ELISA offers quantitative interpretation through optical density measurements, enabling automation and high-throughput testing. It is particularly effective in detecting both IgG and IgM antibodies and is more suitable for large epidemiological surveillance studies than methods like MAT, IHA, or IFAT, which are less sensitive or prone to false negatives and cross-reactions (Chao et al., 1990; Obwaller et al., 1995; Macri et al., 2009; Eissa et al., 2012). A promising antigen, *T. gondii* surface antigen 2 (TgSAG2), has shown potential when expressed in bacterial or insect systems, offering high sensitivity and specificity in ELISA formats (Huang et al., 2010; Rostami et al., 2018).

Molecular diagnostics

Nucleic acid-based diagnostics, particularly polymerase chain reaction (PCR), offer high specificity and sensitivity for detecting *T. gondii*, even from minimal biological material such as a single tachyzoite (Su et al., 2010). These techniques are divided into two broad categories: (1) detection of *T. gondii* DNA in biological samples through conventional PCR (cPCR), nested PCR (nPCR), and quantitative PCR (qPCR); and (2) genotyping methods using multilocus PCR-RFLP, microsatellites, and multilocus sequence typing (MLST) for strain differentiation.

PCR amplification targeting multicopy genomic sequences such as the B1 gene, 529-bp repeat element, and ITS-1 rDNA has become standard in routine and research diagnostics. For instance, B1-based PCR remains widely used for congenital toxoplasmosis and immunocompromised patients, whereas 529-bp repeat-based PCR offers even greater sensitivity (Homan et al., 2000). Nested PCRs enhance detection capabilities, especially when tissue samples may contain low parasite burdens or when DNA is extracted from minute amounts (Hurtado et al., 2001; Jones et al., 2003).

An important application includes real-time PCR (qPCR), which has been shown to reliably detect *T. gondii* DNA in feral cats and meat samples (Opsteegh et al., 2010; Adriaanse et al., 2020). Furthermore, molecular methods remain essential for confirming ELISA results and identifying acute infections in immunocompromised patients (Khattab et al., 2022). Advanced typing methods based on sequencing allow for the detection of single nucleotide polymorphisms (SNPs), although these require sophisticated platforms and higher costs (Sibley et al., 2009).

In the Egyptian context, studies such as those by Khattab et al. (2022) demonstrated that PCR targeting P30 provided better sequencing results compared to B1, despite the latter's superior amplification efficiency. This highlights the practical considerations when selecting gene targets based on study goals (e.g., surveillance vs. phylogenetic analysis).

Molecular Characterization and Genotyping of *Toxoplasma gondii*:

Molecular studies on *T. gondii* revealed a significant global diversity in population structure, affecting transmission dynamics, host susceptibility, and virulence. In North America and Europe, three dominant clonal lineages—Types I, II, and III—are most frequently encountered, with Type II predominating in domestic animals and humans (Sibley et al., 2009; Dubey et al., 2011). Virulence studies in murine models suggest that Type I strains are the most pathogenic, often causing death after inoculation with very few tachyzoites. In contrast, Types II and III establish chronic, often asymptomatic infections, making them more common in both animal reservoirs and human populations (Howe & Sibley, 1995; Dardé & Peyron 2014). Notably, the genetic variation among *T. gondii* strains affects their ability to cross the placental barrier and cause severe congenital or ocular

manifestations, especially in immunocompromised individuals or during early pregnancy (Saeij et al., 2007).

In Egypt, a fourth lineage, Type 12, has been recently identified in camels from Matrouh Governorate (Khattab et al., 2022). The genetic distances between submitted strains from camels and small ruminants had gene sub-structuring, which appears to be a clonal population structure within and between local strains of the several geographical regions selected in Matrouh and Alexandria Governorates. In particular, there is a genetic variability between two isolates from different geographic locations belonging to the same host species (goat). Otherwise, the goat isolation from Maryout in the province of Alexandria was the same as the sheep isolation of *T. gondii* from Matrouh, which was 240 kilometers apart. The camel strain of *T. gondii* from Matrouh was 100% identical to the two most dangerous strains of *T. gondii*—RH from France and Malaysia. Whereas, African genotyping has revealed both clonal and non-clonal strains, including Africa 1 and Africa 3 genotypes (Dardé & Peyron 2014).

Epidemiology of Toxoplasmosis in Egypt

Toxoplasmosis in humans

Several epidemiological studies have assessed the seroprevalence and risk factors of *T. gondii* infection in humans across various Egyptian regions. Ghoneim et al. (2009) conducted a study in El-Fayoum and found high seroprevalence among both pregnant (IgG 45.8%, IgM 30.5%, PCR 21.5%) and non-pregnant women (IgG 41.4%, IgM 24.2%, PCR 9.0%) using combined serology and PCR diagnostics, emphasizing the role of undercooked meat, raw milk, and cat exposure as key risk factors. Ibrahim et al. (2009) in Dakahlia, found a seroprevalence of 51.5% among pregnant women, highlighting zoonotic risk from infected cattle and rabbits. Ibrahim et al. (2017) reported ELISA and PCR positivity of 33.8% and 11.8%, respectively, in pregnant women from Menofiya and Gharbiya, with significant associations with cat contact, soil exposure, and consumption of undercooked mutton. Abdelbaset et al. (2020) observed a 22.9% overall seroprevalence among pregnant women in El-Minya, with higher infection rates during the second and third trimesters and among those exposed to cats and undercooked meat. The comprehensive multi-host meta-analysis by Abbas et al. (2020) also confirmed a wide prevalence range (2.5–97.4%) in humans across Egypt, further associating it with rural living, poor hygiene, and contact with cats.

Toxoplasmosis in camels

Recent studies have highlighted camels as notable intermediate hosts for *T. gondii* in Egypt. Saad et al. (2018) reported a 3.33% seroprevalence in camels using ELISA and qPCR in Upper Egypt, with raw milk consumption and environmental contamination as likely risk factors. Khattab et al. (2022) recorded a strikingly high prevalence of 64.51% among camels in Alexandria and Matrouh, using ELISA and nested PCR targeting the B1 and P30 genes, with risk factors linked to age, sex, species, and geographic location. Another significant study by Selim et al. (2023) reported a 46.9% seroprevalence in dromedary camels from Kafr El-Sheikh, Qalyubia, and Marsa Matrouh using an ELISA based on the P30 antigen. Key risk factors included advanced age (>8 years), female sex, contact with ruminants, abortion history, and high parity levels. Elmahallawy et al. (2025) found an overall MAT-based seroprevalence of 13.84% in Cairo and Aswan, with higher rates in Lower Egypt (19.92%) and among older animals. Fereig et al. (2022) observed a milk-based ELISA prevalence of 29.26% and PCR detection rate of 4.8% in camels across multiple governorates, including Alexandria and Sharqia. Lastly, imported camels in Shalateen and Abu Simbel showed a prevalence of 25.7%, with significantly higher rates in Shalateen (31.5%) compared to Abu Simbel (2.2%), reflecting regional exposure differences.

These cumulative findings underscore the epidemiological relevance of camels as a reservoir of *T. gondii*, emphasizing the need for improved surveillance, public education, and food safety measures in regions with high camel-human interaction.

Toxoplasmosis in sheep and goats

T. gondii infection in small ruminants is widespread in Egypt, with variable prevalence rates across regions and time. Ghoneim et al. (2010) reported IgG seropositivity of 98.4% in sheep and 41.7% in goats in El Fayoum, with PCR positivity of 67.7% and 25.0%, respectively. Barakat et al.

(2009) found seroprevalence rates of 44–47.5% in sheep and 55.4–59.4% in goats in Giza using IHAT and ELISA. Younis et al. (2015) documented high seroprevalence in Dakahlia: sheep (41.7–66.1%), goats (49.4–64.2%), confirmed by bioassay in cats. Fereig et al. (2016) found prevalence in sheep (38.7%) and goats (28.7%) across several governorates. Al-Kappany et al. (2018) reported goat prevalence of 62% and sheep rates ranging from 4.1% to 26%. Saad et al. (2018) recorded a higher prevalence in goats (90%) than sheep (60%) in Upper Egypt. Abd El-Razik et al. (2018) observed wide-ranging results based on multiple diagnostics, including ELISA, PCR, and viability testing, with up to 100% viability in goats. Abdelbaset et al. (2020) noted significant locality-based variations (Matay: 57.4%, Dayr Mawas: 8.8%). Fereig et al. (2022) detected *T. gondii* in sheep (66.7%) and goats (81.8%) using ELISA and PCR. Zeedan et al. (2022) found comparable prevalence using milk ELISA and PCR (sheep: 34.18%, goats: 33.7%). In 2023, Selim et al. (2023) reported lower rates (sheep: 24%, goats: 38.3%), while Aboelwafa et al. (2022) found 26.1% in sheep. The most recent study by Fereig et al. (2022) showed an overall prevalence of 46.1%, with higher infection in goats (66.9%) than sheep (35.6%).

Toxoplasmosis in cattle

Cattle in Egypt show generally lower seroprevalence rates compared to small ruminants and humans. Ibrahim et al. (2009) reported a 10.75% infection rate in cattle in Sharkia. Fereig et al. (2016) observed a rate of 23.6% in multiple governorates. Khattab et al. (2022) found a relatively low prevalence of 13.46% in cattle in Alexandria and Matrouh. Farag et al. (2023) found a higher prevalence of 59.4% among cattle using MAT in Sohag. Metwally et al. (2023) observed a prevalence of 5.3% in dairy and beef cattle in Beheira, while Fereig et al. (2024) reported a prevalence of 9.1% in serum and 9.7% in milk samples, with increased infection in cattle aged ≥3 years. Abdel-Aziz et al. (2020) also noted a 31.3% infection rate in beef, although viability was lost after freezing. Abbas et al. (2020) confirmed a prevalence range in cattle from 2.5% to 97.4% across studies. Ibrahim et al. (2021) found 3.05% IgG positivity in cattle in Menofiya, and Fereig et al. (2022) reported an extremely low rate of 2.4% in cattle based on milk samples.

Risk Factors Associated with Toxoplasmosis in Egypt

Multiple studies conducted across Egypt have consistently identified a range of epidemiological risk factors influencing the prevalence of *T. gondii* in both humans and domestic animals. In human populations, particularly among pregnant women, high-risk behaviors such as the consumption of undercooked or raw meat (especially mutton and goat), drinking unpasteurized milk, contact with cats or their litter, and exposure to contaminated soil were frequently reported as significant contributors to infection (Ghoneim et al., 2009; Ibrahim et al., 2017; Abdelbaset et al., 2020). Age and trimester of pregnancy were also important, with increased prevalence noted in later trimesters. In animals, species susceptibility was a major factor goats and sheep consistently showed higher seropositivity than cattle and buffaloes (Barakat et al., 2009; Saad et al., 2018; Fereig et al., 2022). The geographic location was also influential, with variations in infection rates observed between Upper and Lower Egypt and among rural versus urban settings (Abdelbaset et al., 2020; Al-Kappany et al., 2018). Other reported risk factors in livestock included age (older animals showing higher prevalence), sex (females often more affected), housing conditions, and the presence of cats on farms (Khattab et al., 2021; Mousa et al., 2023; Zeedan et al., 2022). Additionally, environmental contamination and poor sanitation were cited as broader contributors to the endemicity of toxoplasmosis in Egypt (Abbas et al., 2020). These findings collectively underscore the need for targeted public health interventions and integrated veterinary control strategies.

CONCLUSION

This comprehensive epidemiological investigation of *T. gondii* in Egypt reveals a complex interplay between zoonotic transmission dynamics, diagnostic capabilities, and strain diversity, reflecting the pathogen's pervasive presence in both animal reservoirs and human populations. The wide-ranging seroprevalence in camels, sheep, goats, and other domestic animals ranging from 3.3% to over 90%—indicates a substantial and under recognized public health burden, especially in rural and pastoral regions where close human-animal contact and consumption of undercooked meat are common.

Our analysis confirms that both horizontal and vertical transmission pathways are active in Egypt. Routes such as ingestion of contaminated meat or water, handling of infected animal products, and transplacental passage contribute significantly to human infection rates. The detection of viable *T. gondii* DNA in camel meat and milk, along with reports of anti-*Toxoplasma* antibodies in livestock, reinforces the zoonotic potential and underscores the need for improved veterinary hygiene and public health education. Advances in serological and molecular diagnostics, particularly ELISA and PCR targeting high-copy sequences like the B1 gene and 529-bp element have significantly enhanced our ability to detect and monitor infection. However, these methods must be standardized and combined to overcome limitations such as cross-reactivity and sampling errors. Molecular data further highlight the circulation of multiple clonal lineages (notably Type II and recombinant strains) within Egyptian livestock, aligning with global patterns while suggesting unique regional genotypic signatures, including similarities with highly virulent RH strains. Congenital toxoplasmosis remains a critical concern, especially in areas with poor prenatal screening. The lack of reliable and early diagnostic protocols for pregnant women limits intervention opportunities, despite the known risks of fetal neurological and ocular complications.

In summary, *T. gondii* poses a persistent and multifaceted epidemiological threat in Egypt. Addressing this requires a national strategy integrating routine molecular diagnostics, enhanced veterinary surveillance, targeted health education, and comprehensive genotyping studies to inform risk assessment and control policies. Future research should emphasize the mapping of infection hotspots, identification of atypical genotypes and the Desand evaluation of the socioeconomic factors influencing transmission risk in Egypt's diverse ecological settings. As the Desert is willing to carrying out different research activities under the most desert areas and marginal environmental conditions, this topic will be an important subject to take into consideration, particularly when we throw some lights on the sustainable development program under such conditions.

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الملخص العربي

رؤى وبائية حول داء المقوسات في مصر: مراجعة لانتقال داء التوكسوبلازما، وعوامل الخطر، والتشخيص، والتنوع الجزيئي لداء التوكسوبلازما الغوندية لدى البشر والحيوانات

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التوكسوبلازما غوندي طفيلي حيواني المنشأ منتشر عالميًا، يصيب كلًا من البشر والحيوانات، وله آثار كبيرة على الصحة العامة وإنتاج الثروة الحيوانية. تُمثل مصر بيئة وبائية حرجة نظرًا لاقتصادها الزراعي، وتربية الحيوانات على نطاق واسع، والتفاعل الكبير بين الإنسان والحيوان. تُلخص هذه المراجعة الوضع الراهن، مدعومة بالدراسات الحديثة حول وبائيات عدوى *التوكسوبلازما غوندي* لدى البشر والإبل والأغنام والماعز والأبقار في مختلف المواقع المصرية. يُظهر انتشار العدوى تباينًا كبيرًا بين الأنواع المضيفة والمناطق الجغرافية، مع ارتفاع معدلات الإصابة باستمرار لدى الإبل والمجترات الصغيرة مقارنةً بالأبقار. لدى البشر، وخاصةً بين النساء الحوامل، ارتبطت العدوى في كثير من الأحيان بالتعرض للقطط، واستهلاك اللحوم غير المطهوة جيدًا، وسوء النظافة. أما بين الحيوانات، فتساهم قابلية الأنواع للإصابة، والعمر، والجنس، والظروف البيئية في تباين ديناميكيات العدوى. وفيما يلي، سوف نسلط الضوء على الطبيعة المتوطنة لداء المقوسات في مصر ونؤكد على ضرورة اتخاذ تدابير متكاملة في مجال الصحة العامة والطب البيطري، مع الأخذ في الاعتبار الأساليب الحديثة للتخفيف من حدة هذا المرض الخطير.

الكلمات الدالة: *التوكسوبلازما غوندي*، داء المقوسات، طفيل، مصر