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Authors: Ali Rostami, Seyed Mohammad Riahi, Yadollah Fakhri, Vafa Saber, Hooman Hanifehpour, Soghra Valizadeh, Majid Gholizadeh, Rokhsane Hosseini Pouya, H.Ray Gamble



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The global seroprevalence of *Toxoplasma gondii* among wild boars: a systematic review and meta-analysis

Ali Rostami ^{a,b}, Seyed Mohammad Riahi ^{c,d}, Yadollah Fakhri ^e, Vafa Saber ^a, Hooman Hanifehpour ^f, Soghra Valizadeh ^h, Majid Gholizadeh ⁱ, Rokhsane Hosseini Pouya ^j, H. Ray Gamble ^k

^a Infectious Diseases and Tropical Medicine Research Center, Babol University of Medical Sciences, Babol, Iran

^b Department of Parasitology and Mycology, School of Medicine, Shahid Beheshti University of Medical Sciences, Tehran, Iran

^c Faculty of Health, Birjand University of Medical Sciences, Birjand, Iran

^d Department of Epidemiology, School of Public health, Shahid Beheshti University of Medical

Sciences, Tehran, Iran

^e Student Research Committee, Department of Environmental Health Engineering, School of Public Health, Shahid Beheshti University of Medical Sciences, Tehran, Iran

^f Department of Biological Control and Vaccine, FDA (Food and Drug Administration) , Tehran, Iran

^h Department of Food Hygiene and Quality Control, Faculty of Veterinary Medicine, Urmia University, Urmia, Iran.

ⁱ Department of Microbiology, Khazar University, Mahmood Abad, Iran

^j Food Health Research Center, Hormozgan University of Medical Sciences, Bandar Abbas, Iran.

^k National Academy of Sciences, 500 5th Street N.W., Washington, D.C., 20001, USA

Corresponding Authors:

* Ali Rostami, Department of Parasitology and Mycology, School of Medicine, Shahid Beheshti University of Medical Sciences, Tehran, Iran. Tel: +982122439962, E-mail: Alirostami1984@gmail.com, Alirostami@sbmu.ac.ir

* Seyed Mohammad Riahi, Department of Epidemiology, School of Public health, Shahid Beheshti University of Medical Sciences, Tehran, Iran. Tel: +982122439962, E-mail: riahim61@gmail.com

Highlights

- We evaluate the worldwide seroprevalence of *T. gondii* infection among wild boar.
- A total of 43 articles that included 16788 wild boar from 23 countries were assessed
- The global seroprevalence of toxoplasmosis in wild boars was 23% (95% CI: 19%–27%)
- The highest prevalence was observed in North America (32%) and Europe (26%)
- An increased seropositivity was observed with elevation in geographical latitude
- The pooled seroprevalence was higher in females (19%) compared to males (17%)
- The seroprevalence was higher in wild boar older than 12 months (28%) v.s. <12 months (20%)

Abstract

This systematic review and meta-analysis study was performed to evaluate the worldwide seroprevalence of *Toxoplasma gondii* among wild boar. We searched PubMed, Science Direct, Web of Science, Cochrane, Scopus, EBSCOhost and Google Scholar databases for studies reporting *T. gondii* seroprevalence in wild boars between January 1995 and March 2017. Inclusion and exclusion criteria were applied. We estimated the pooled seroprevalence of *T. gondii* in wild boars using a random-effects model, and evaluated overall seroprevalence in different geographical areas. A total of 43 articles that included 16788 wild boar from 23 countries fulfilled our eligibility criteria. Of these, 4759 wild boar had been defined *T. gondii* seropositive and we estimated the pooled worldwide seroprevalence of toxoplasmosis in wild boars to be 23% (95% CI: 19%–27%). The pooled seroprevalence in North America (32%, 20%–45%; odds ratio [OR] 2.09) and Europe (26%, 21%–30%; OR 1.72), was higher than Asia (13%, 5%–23%). The lowest seroprevalence was estimated in South America (5%, 3%–8%). An increased seropositivity was observed with elevation in geographical latitude. In subgroup analyses, the pooled seroprevalence of *T. gondii* was higher in wild boar older than 12 months of age (28%, 22%–35%; OR 1.57) compared to

those up to 12 months of age (20%, 16%–25%). Our findings suggest that wild boar have an important role in human infection and the epidemiological cycle of *T. gondii* infection.

Keywords: *Toxoplasma gondii*, wild boar, global, seroprevalence, meta-analysis

1. Introduction

Toxoplasmosis is important zoonotic disease with a worldwide distribution that is caused by the protozoan apicomplexan parasite *Toxoplasma gondii* (Hill and Dubey, 2015). This infection is the fourth most common cause of hospitalization and the second leading cause of death due to food-borne infections in the United States (Scallan et al., 2011). Toxoplasmosis may have serious consequences in certain groups, causing preeclampsia, psychiatric disorders, abortion and fetal abnormality in pregnant women (Montaya and liesenfeld, 2004; Shiadeh et al., 2016a; Shiadeh et al., 2017); encephalitis, brain abscesses and death in immunocompromised patients (Pereira-Chiocola et al., 2009; Rostami et al., 2014) and also behavioral changes, neuropsychiatric disorders and infertility in otherwise healthy humans and animals (Fallahi et al., 2017; Rostami et al., 2016; Shiadeh et al., 2016b; Sutherland et al., 2015). Ingestion of raw or undercooked meat from infected animals (notably, lamb, goat meat, and pork among meat of food animals) is considered the most important source of human infection (Hill and Dubey, 2015).

Wild boars (*Sus scrofa*) are omnivorous animals that consume a large variety of herbal material as well as live and dead animals. They are among the most widely distributed large mammals in the world and their population has increased dramatically in recent decades (Massei et al., 2015). The native range of *Sus scrofa* extends from Western Europe and the

Mediterranean basin to eastern Russia, northern Africa, Japan, and southeast Asia; some parts of North, Central and South America, Africa and the Australian continents are considered to be an introduced range. The species is absent in Antarctica, and many oceanic islands (Barrios-Garcia and Ballari, 2012). During the 20th century, the density of wild boar has grown remarkably in many part of Europe (Apollonio et al., 2010). Wild boar recently recolonized Sweden, Finland, Belgium and Estonia and their numbers are increasing in urban and suburban areas of European cities, as they have been observed in Barcelona, Berlin, Vilnius, Budapest and Rome (Apollonio et al., 2010; Massei et al., 2015). Considered an invasive species in the U.S. wild boar number nearly six million in 35 states and their range is spreading north by as much as 12.6 km per year (Snow et al., 2017).

Wild boar meat may harbor many pathogens transmissible to humans, and an increased risk in acquisition of infections from wild boar meat has been observed in recent years as a result of an increase in recreational hunting of wild boars and a growing popularity of wild boar meat in different parts of the world (Meng et al., 2009). Like trichinellosis, hunters, their families and friends may be at greatest risk of acquiring toxoplasmosis from consumption of undercooked wild boar meat (Rostami et al., 2017). Due to a reported high prevalence of infection, wild boars could be a suitable biological model for analyzing *T. gondii* dynamics in the environment (Beral et al., 2012).

In recent years, a growing number of investigations have been conducted on prevalence of *T. gondii* infection among wild boar, although there is a big gap in knowledge in many countries. Considering the public health importance of meat and meat products obtained from wild boar, a more comprehensive understanding of the occurrence of *T. gondii* infection in this animal is essential. In this report, we describe the first systematic review and meta-analysis to evaluate the global seroprevalence of *T. gondii* in wild boar.

2. Methods:

This systematic review and meta-analysis followed the Preferred Reporting Items for Systematic Reviews and Meta-Analyses Protocols (PRISMA) and MOOSE guidelines as described previously (Shamseer et al., 2015; Stroup et al., 2000).

2.1. Search Strategy and Study Selection

To identify studies eligible for meta-analysis, we searched PubMed, Science Direct, Web of Science, Cochrane, Scopus, EBSCOhost and Google Scholar electronic databases from January 1995 to March 2017. We conducted a comprehensive search using combinations of the following keywords: “*Toxoplasma gondii*”, “toxoplasmosis”, “*Toxoplasma* infection”, “seroepidemiology”, “seroprevalence”, “prevalence”, “wild boar”, “wild pig”, “*Sus scrofa*”. Search strategies in different databases are presented in supplementary Figure 1. Reference lists of retrieved citations and published reviews were searched for additional studies. We had no geographic limitations, although only studies reported in the English language were included. After removing duplicate records, the titles and abstracts of each article were assessed by two independent reviewers (A.R. and Y.F.). Inclusion criteria were primary research studies with original data either published or in press, studies with a cross-sectional design, and studies including detection of *T. gondii* infection based on serological methods using serum or meat juice. We excluded studies containing confusing text or incomprehensible analyses or studies of animals which had been experimentally infected, non-serological investigations, papers published before 1995, reviews, letters or editorial articles without original data and if a study was performed in an area where the definitive host (cat) was absent.

2.2. Data extraction and study quality assessment

Articles were assessed independently by 2 authors (Y.F. and V.S.), with a third author (A.R.) consulted when necessary. All data were recorded using Microsoft Excel software. The following information was collected for each study: the first author's last name, publication year, country, start and end dates of the study, location (latitude) of study areas, gender and age of the study population, type of serological method, sample size, number of positives and negatives, seroprevalence and associated 95% confidence interval. For studies with point seroprevalence estimates, a 95% confidence interval was calculated from the data. A quality assessment of included studies was performed using the JBI (Joanna Briggs Institute) Prevalence Critical Appraisal Tool (Munn et al., 2014).

2.3. Data Synthesis and Statistical Analysis

In this study, we used random effect models for meta-analysis to generate pooled seroprevalence estimates with 95% confidence intervals. For this purpose, we used a *metaprop* command in Stata software. Pooling seroprevalence from raw cell counts was done using a Freeman-Tukey double arcsine transformation and score confidence intervals for the individual studies were calculated (Freeman and Tukey, 1950; Harris et al., 2008; Nyaga et al., 2014). Heterogeneity between studies was examined by Cochran's Q, the I^2 statistics test and Galbraith diagram. I^2 ranges between 0 and 100%, and values of 50% or more was considered heterogeneous. A forest plot in the random effects model was used to calculate of pooled seroprevalence and OR. To determine the source of heterogeneity, meta-regression analyses and subgroup analyses were performed. Meta-regression was used for examining the effect of geographical location/latitude on seroprevalence of *T. gondii*. In a subgroup analysis, we estimated the seroprevalence of *T. gondii* in males and females, animals aged 12 months or less and those more than 12 months of age, continent of origin, type of diagnostic method and different geographic location.

Publication bias was evaluated graphically and statistically by applying the Egger's and Begg's publication bias method (Begg and Mazumdar, 1994; Egger et al., 1997). In all statistical analyses, the significance level was considered as P value < 0.05 and Meta-analysis was done by using STATA version 13 (STATA Corp., College Station, Texas).

3. Results

3.1. Study characteristics

A flow diagram depicting of the study selection process is presented in Figure 1. Based on the literature search strategies, a total of 630 records were identified. After removal of duplicates and initial screening using title and abstract, we reviewed 54 studies in total. After exclusion of additional ineligible reports, our final sample included 43 studies ($n=16788$ animals), including 29 studies (13959 animals) in Europe, 8 studies (1752 animals) in Asia, 4 studies (737 animals) in North America and 2 studies (340 animals) in South America. Of the 43 studies, 14 and 16 included data for gender and age, respectively. In total, data from 23 countries were evaluated. No data was available for Africa or Australia. MAT was the most commonly used diagnostic method (15 studies), followed by ELISA (14 studies), IFAT (5 studies), DAT (4 studies), LAT (4 studies) and the dye test (one study). Main characteristics of the included studies are presented in Table 1.

3.2. Results of meta-analysis

As shown in Table 1 and Figure 2, the estimates of seroprevalence of *T. gondii* among wild boar ranged from 1.1% to 56.7% and heterogeneity was substantial ($I^2=96.9\%$, $P<0.001$; Figure 2). The global pooled seroprevalence of *T. gondii* among wild boar from 1995 to 2017 was 23% (95% CI: 19%–27%, 4759/16788). Significant geographic differences in pooled *T. gondii* seropositivity rates among wild boars were estimated. The seroprevalence

was higher in North America and Europe, where the *T. gondii* seropositivity rate were 32% (95%CI: 20%–45%) and 26% (95%CI: 21%–30%), respectively. The pooled seroprevalence in Asia was 13% (95%CI: 5%–23%). The lowest seroprevalence was estimated in South America with the rate of 5% (95% CI: 3%–8%). A GIS map summarizing the seroprevalence of *T. gondii* among wild boar in different countries is shown in Figure 3). No data were available for Africa or Australia.

The pooled seroprevalence of *T. gondii* in male and female wild boar were 17% (95% CI: 10%–25%) and 19% (95% CI: 13%–27%), respectively (Supplementary Figure 2, A and B). The pooled seroprevalence of *T. gondii* among wild boar up to 12 months of age was 20% (95% CI: 16%–25%) and 28% (95% CI: 22%–35%) in wild boar more than 12 months of age (Supplementary Figure 3, A and B).

In a subgroup analysis based on diagnostic methods, the highest *T. gondii* seroprevalence was detected by enzyme-linked immunosorbent assay (ELISA) 30% (95% CI: 23%–37%), followed by modified or direct agglutination test (MAT or DAT) 25% (95% CI: 20%–31%), indirect fluorescent antibody test (IFAT) 15% (95% CI: 8%–23%), Dye Test 15% (95% CI: 10%–23%) and latex agglutination test (LAT) 5% (95% CI: 3%–8%) (Supplementary Figure 4).

An interesting result was an increase in seroprevalence of *T. gondii* among wild boar at higher latitudes. The pooled seroprevalence in latitudes of 0-30, 31-40, 41-50 and 51-64°N, were 9% (95% CI: 3%–16%), 21% (95% CI: 15%–27%), 24% (95% CI: 18%–31%) and 32% (95% CI: 23%–41%), respectively (Figure 4 and Supplementary Figure 5).

We further compared seroprevalence based on geographical regions, gender and age using univariate analysis. The pooled seroprevalence of toxoplasmosis in wild boar in North America (OR, 2.09; 95% CI, 1.71–2.54) and Europe (OR, 1.72; 95% CI, 1.52–1.96) was

significantly higher than in Asia and South America (Table 2). To calculate odds ratio (OR) for different continents, Asia was considered as the reference category. The difference between male and female was not statistically significant (OR, 1.16; 95% CI, 0.92–1.44) (Figure 5. A). The pooled OR of toxoplasmosis in adult wild boar (≥ 12 months) was significantly higher than young wild boar (< 12 months) (OR, 1.58; 95% CI, 1.16–2.16) (Figure 5. B).

Heterogeneity between studies can be shown using Galbraith diagram (Figure 6, A). To identify the possibility of publication bias, we used of Begg's and Egger's test and graph based on the symmetry assumption. Begg's test ($P=0.35$) and Egger's ($P=0.36$) test did not detect a significant publication bias (Figure 6, B).

4. Discussion

Results of this study demonstrated that, worldwide, approximately one third of wild boar were *T. gondii* seropositive. In recent years, wild game meat has increased in popularity as a food source for humans in many countries (Amici et al., 2015), and hunting of wild boar is a popular recreational sport as well as a population control method supported by wildlife agencies. These factors could contribute to an increased rate of consumption of wild boar meat. Therefore, a high prevalence of *T. gondii* infection in wild boar, as suggested by seroprevalence data, poses an important public health concern in countries where wild boar meat is consumed.

To our knowledge, this is the first systematic review and meta-analysis of the global seroprevalence of *T. gondii* in wild boar. Our findings demonstrated a 32% seroprevalence of *T. gondii* in the North America, 26% in Europe; 13% in Asia and 5% in South America, although it should be considered that the number of studies for North and South America and

Asia were relatively low (14 studies in total), and also only two studies (340 animals) were included from South America.

Our results showed an increase in seroprevalence of *T. gondii* infection with increased geographical latitude. Although it should be noted that these data are shown only for the regions for which seroprevalence data is reported, as information in many tropical and subtropical areas were rare. Seroprevalence of *T. gondii* in different hosts varies in different geographical latitude, mainly with respect to climatic conditions that are required for sporulation and survival of oocysts. In fact, the prevalence of toxoplasmosis is higher in areas with higher humidity and warmer climate (Dubey, 2010). In our analysis, the majority of studies were from European countries and areas located at latitudes from 20° to 60°, therefore our results should be interpreted only in these geographical latitudes. These areas have suitable conditions for oocyst survival and also have higher densities of domestic cats which serve as the definitive host. Whereas, the seroprevalence of *T. gondii* decreases in subarctic and arctic areas (higher altitude than 65°), where environment temperature is low and domestic cats are rare, and, when present are mostly kept indoors. In support of this statement, a geographical north-south gradient in seroprevalence of *T. gondii* was estimated in domestic moose, sheep, farmed wild boars, and lynx in Finland (Jokelainen et al., 2010; 2012; 2013). Moreover, Flegr et al. (2014) showed that prevalence of human toxoplasmosis decreases with an increase in geographical latitude. In their study, a higher prevalence of human toxoplasmosis was estimated at latitudes between 10° and 50°, whereas it decreased significantly at latitudes higher than 60°.

Our findings demonstrated an association between *T. gondii* seropositivity and the age of wild boar. This finding is in agreement with other studies in various hosts. Jittapalapong et al. (2005) reported that older goats were more likely to be seropositive than those under 1-year old; Gorman et al. (1999) found significantly higher seroprevalence in adult sheep than in

young ones. This could be explained in several ways. With respect to feeding habits, weaning occurs gradually, and therefore young wild boar have a lower risk for exposure to environmental oocysts. Adult wild boars are exposed to *Toxoplasma* oocysts when foraging on contaminated soil and vegetables or by ingestion of carcasses of *Toxoplasma*-infected wild or domestic animals harboring tissue cysts (bradyzoites and tachyzoites). Young wild boar may be protected against infection while nursing by maternal antibodies. It is generally believed that IgG antibodies against *T. gondii* persist lifelong in most hosts; therefore higher seropositivity in older wild boar simply reflects extended opportunity for exposure to *T. gondii* (Tenter et al., 2000). This pattern exists for majority of parasitic diseases (especially for chronic or long-lasting infections) in both animals and humans; the prevalence of parasitic diseases increases with increased life-time (Fallahi et al., 2016; Omrani et al., 2015; Yakhchali et al., 2011).

With respect to diagnostic methods, our findings suggest that the diagnostic methods may be a source of heterogeneity. Studies using ELISA and MAT/DAT reported the highest seroprevalence of *T. gondii*, while those that used LAT as the diagnostic method reported the lowest seroprevalence. Comparison of these diagnostic methods was evaluated in several studies (Gamble et al., 2005; Han et al., 2008; Mazumder et al., 1988). The majority of these studies reported good agreement between ELISA and MAT (Gamble et al., 2005; Sroka et al., 2008; Zhu et al., 2012). Moreover, it was demonstrated that IFAT and DAT had moderate agreement between these two methods and with other methods (Garcia et al., 2006; Marca et al., 1996; Seefeldt et al., 1989). In other studies, although LAT was reported to be a useful method for detection of *T. gondii* seropositivity, its sensitivity and specificity was lower when compared with other methods (Dubey et al., 1995; Mazumder et al., 1988; Sroka et al., 2008). Another aspect when comparing test methods is the cut-off selected in different studies to define a wild boar as seropositive; these differences can lead to false negative or

positive results and consequently a negative impact on sensitivity and specificity of the applied methods. Therefore, results of this study must be interpreted based on possible differing sensitivities and specificities of the methods used for testing.

Our results showed a high seroprevalence for *T. gondii* among wild boars in North America and also in Europe. Therefore, hunters and other consumers of wild boar meat in these regions are at greater risk of acquiring infection through ingestion of raw or undercooked wild boar meat. In some countries, there are markets that sell wild boar meat and also some companies that sell wild boar meat commercially and export it to other countries. This is especially the case in Europe, where many kilos of wild boar meat are consumed each year. These factors along with increasing the popularity of wild game meat consumption among consumers, emphasizes public human health significance of *T. gondii* infection in wild boar as a potential source of meat-borne toxoplasmosis in human.

The strengths of this study included the rigorous methodology, data extraction and quality assessment applied by 2 independent reviewers, the large sample size of the wild boar included in this meta-analysis and subgroup analyses considering to geographical location, gender and age. However, this systematic review and meta-analysis has several limitations. First, despite our comprehensive search using seven databases, it is possible that some data were missed as many investigators publish results in local journals with language other than English. For example, we did not find studies conducted in Africa and Australian continents and studies from North and South America were rare, emphasizing the need for more robust surveillance of *T. gondii* in wild boar in these regions. Moreover, we removed some data based on the exclusion criteria. For example, in a study by Dubey et al., (1997) we removed data related with Ossabaw Island (seroprevalence of *T. gondii* was 0.9%, 11/1264) due the absence of cats as definitive host in this Island. Second, the gold standard for detection of *T. gondii* infection is bioassay, while the prevalence studies in this study were based on

serological methods that have variable sensitivity and specificity. Therefore, our results may not be an accurate estimate of *T. gondii* prevalence among wild boar. Moreover, the results of this study must be interpreted based on substantial heterogeneity of quality and publication bias among the included studies; some of the studies recruited free-ranging wild boar, while some other (e.g. Fornazari et al., 2009) recruited farmed wild boar or those kept in fenced areas.

In conclusion, despite the aforementioned limitations, the analysis and interpretation presented here furthers our understanding of the global seroprevalence of *T. gondii* among wild boar and suggests a need for additional studies to further clarify the seroprevalence of *T. gondii* in wild animals that are consumed by humans to guide the development of appropriate public health interventions.

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Specific author contributions: A.R., S.M.R., Y.F., V.S., H.H, S.V., M.G., and R.H.P. conceived the study; A.R., V.S., H.H, S.V., M.G., and R.H.P initially searched the literature; A.R. Y.F, S.V., M.G., and R.H.P. collected all data; A.R. Y.F, and V.S., assessed the included articles; A.R., S.M.R. and Y.F analyzed and interpreted the data; A.R. and H.R.G. drafted the manuscript; and all authors commented on the drafts of the manuscript and approved the final draft of the paper.

Conflict interest: The authors declare that there is no conflict of interests regarding the publication of this paper.

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Figure captions:

Figure 1. Flow chart of the study selection process showing inclusion and exclusion of studies identified.

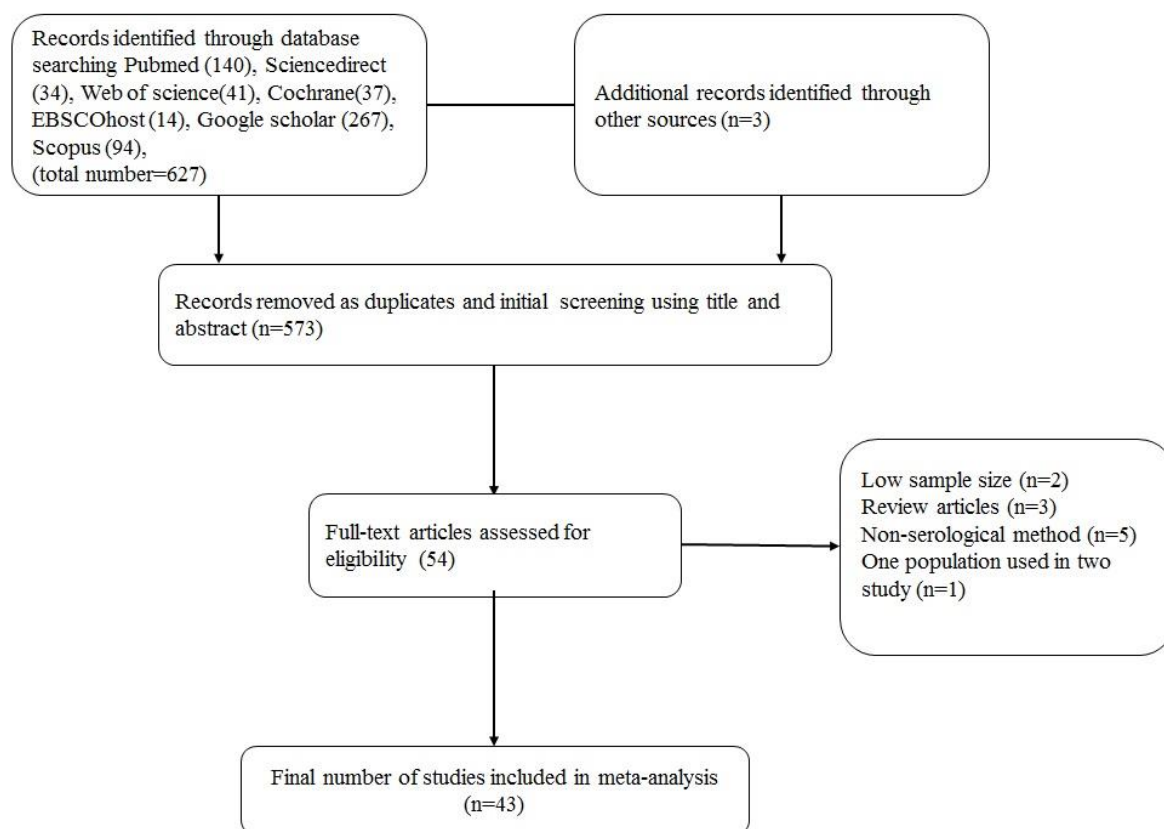


Figure 2. Forest plots for random-effects meta-analysis of *Toxoplasma gondii* infection in wild boar.

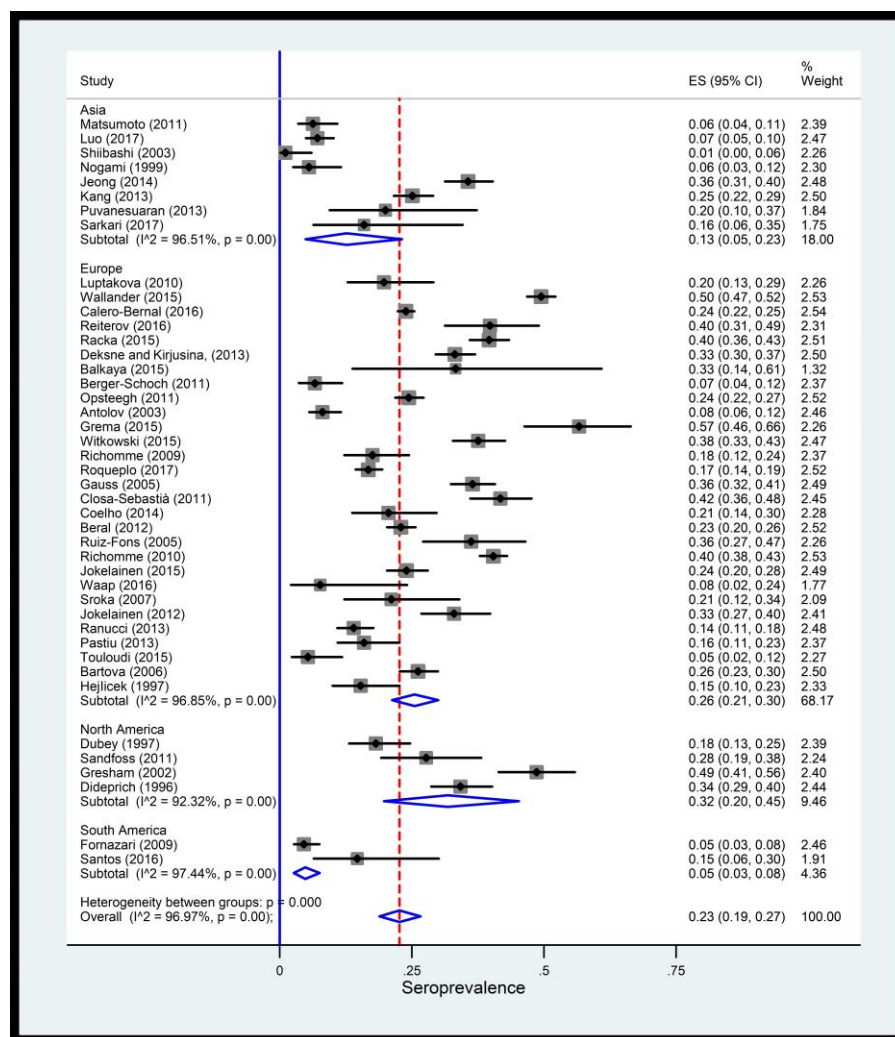


Figure 3. Distribution of *Toxoplasma gondii* infection in wild boar in different countries using geographic information system (GIS).

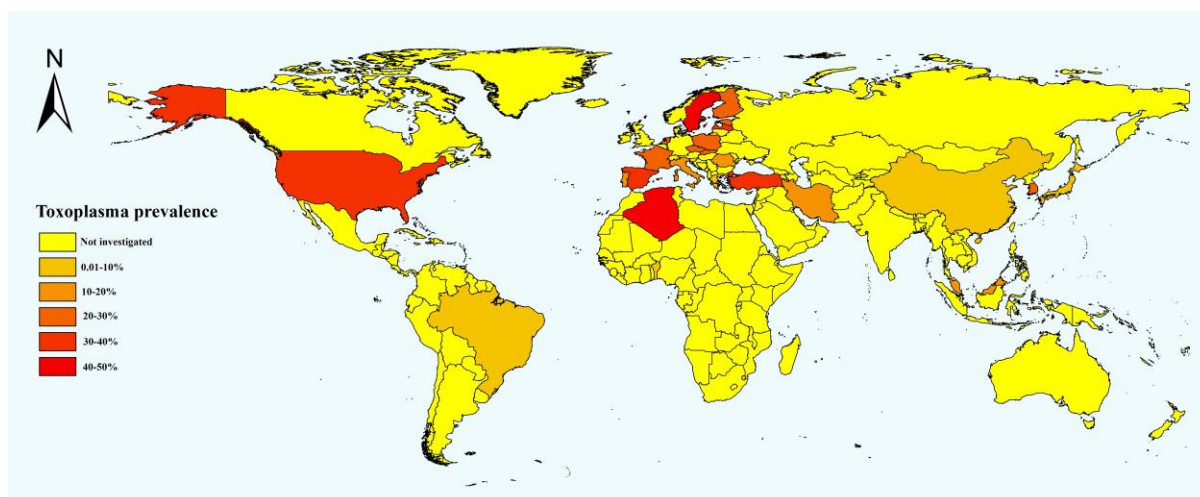


Figure 4. Meta-regression regarding the effects of geographical location (latitude) on the prevalence of *Toxoplasma gondii* infection in wild boar.

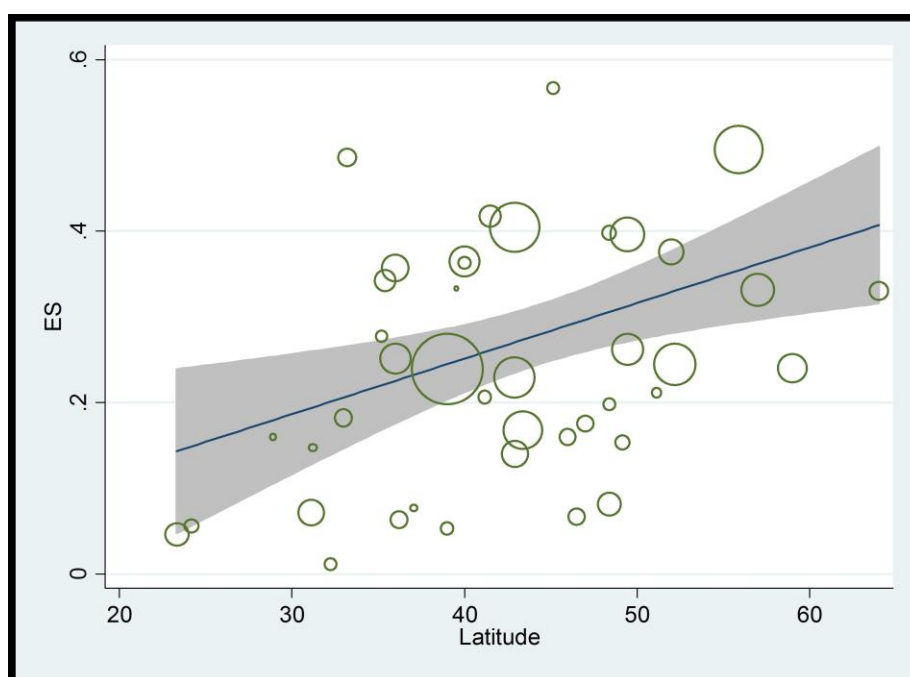


Figure 5. Forest plots for pooled odds ratio (OR) of *Toxoplasma gondii* infection with respect to gender (A) and age (B). Male gender and age under 12 months are considered as reference categories to estimate OR.

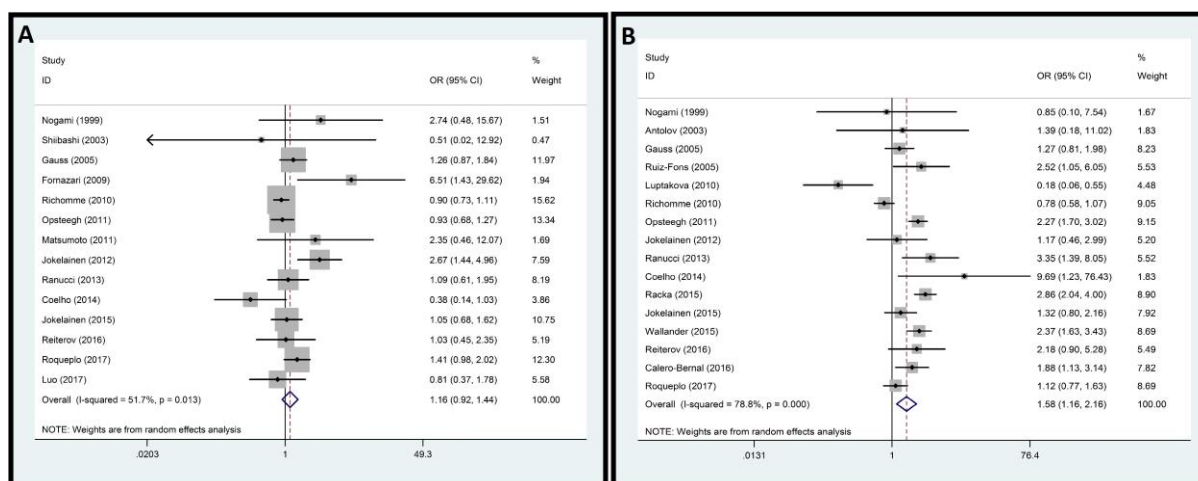


Figure 6. Heterogeneity and publication bias. (A), heterogeneity using a Galbraith diagram; (B), Publication bias using Begg's and Egger's plot.

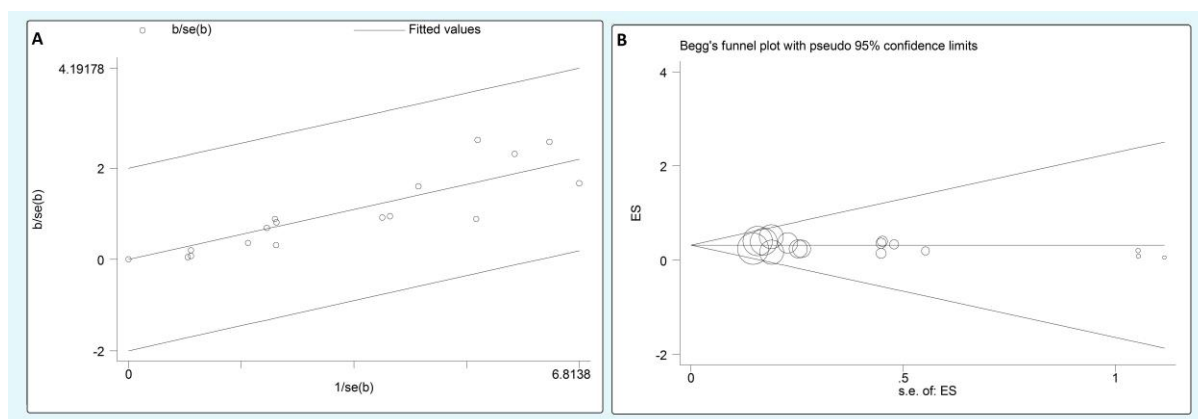


Table 1: Main characteristics of selected studies reporting seroprevalence of *T. gondii* in wild boar.

Continent/ References	Country	Implementation year	Diagnostic Method	Sample size	Infected (%)	Quality score
Asia						
Nogami et al., 1999	Japan	NA	LAT	108	6 (5.6)	6
Shiibashi et al., 2003	Japan	2000-1	LAT	90	1 (1.1)	6
Matsumoto et al., 2011	Japan	2004-7	LAT	175	11 (6.3)	6
Kang et al., 2013	South Korea	2009-11	ELISA	521	131 (25.1)	6
Puvanesuaran et al., 2013	Malaysia	2011-2	MAT	30	6 (20)	8
Jeong et al., 2014	South Korea	2008-12	ELISA	426	152 (36)	5
Sarkari et al., 2017	Iran	2013	MAT	25	4 (16)	7
Lou et al., 2017	China	2010-6	LAT	377	27 (7.2)	9
Europe						
Hejlícek et al., 1997	Czech Republic	1981-90	DT	124	19 (15)	7
Gauss et al., 2005	Spain	1993-2004	MAT	507	185 (38.4)	8
Ruiz-Fons et al., 2005	Spain	2000-3	MAT	91	33 (36.3)	7
Bartova et al., 2006	Czech Republic	1999-2005	IFAT	565	148 (26.2)	9
Sroka et al., 2007	Poland	NA	DAT	52	11 (21.1)	7

Antolová et al., 2007	Slovak Republic	2003	ELISA	320	26 (8.1)	6
Richomme et al., 2009	France	2002-8	MAT	148	26 (17.6)	8
Richomme et al., 2010	France (Corsica)	2006-8	MAT	1399	566 (40.4)	7
Luptakova et al., 2010	Slovak republic	NA	ELISA	91	18 (19.8)	7
Closa-Sebastià et al., 2011	Spain	2004-7	MAT	273	114 (43.5)	7
Opsteegh et al., 2011	Netherlands	2002-7	ELISA	973	238 (24.4)	9
Berger-Schoch et al., 2011	Switzerland	2006-8	ELISA	150	10 (6.7)	8
Beral et al., 2012	France	2003-4	MAT	938	215 (23)	6
Jokelainen et al., 2012	Finland	2007-8	DAT	197	65 (33)	7
Paștiu et al., 2013	Romania	2008-10	IFAT	150	24 (16)	7
Deksne and Kirjusina, 2013	Latvia	2010-11	ELISA	606	201 (33.2)	7
Ranucci et al., 2013	Italy	2009–11	IFAT	400	56 (14)	7
Coelho et al., 2014	Portugal	2011-2	MAT	97	20 (20.6)	5
Račka et al., 2015	Czech Republic	2008-10	ELISA	656	260 (40)	9
Jokelainen et al., 2015	Estonia	2012-3	DAT	471	113 (23.9)	8
Balkaya et al., 2015	Turkey	2011	ELISA	12	4 (33.3)	4
Wallander et al., 2015	Sweden	2005-9	ELISA	1327	657 (50)	8
Touloudi et al., 2015	Greece	2006-10	IFAT	95	5 (5.2)	8
Grema et al., 2015	Romania	2013-4	ELISA	90	51 (56.7)	6

Witkowski et al., 2015	Poland	2009-11	ELISA	367	138 (36.7)	6
Waap et al., 2016	Portugal	2010-3	DAT	26	2 (7.7)	9
Calero-Bernal et al., 2016	Spain	2003-11	ELISA	2881	688 (23.8)	6
Reiterová et al., 2016	Slovak republic	2010-1	ELISA	113	45 (39.7)	7
Roqueplo et al., 2017	France	2011-2	MAT	841	141 (16.8)	5
North America						
Dideprich et al., 1996	USA	1990-3	MAT	257	88 (34.2)	7
Dubey et al., 1997	USA	1992-4		170	31 (18.2)	8
Gresham et al., 2002	USA	1999	MAT	227	181 (49)	5
Sandfoss et al., 2011	USA	2007-9	MAT	83	23 (27.7)	8
South America						
Fornazari et al., 2009	Brazil	NA	MAT	306	14	4.5
Santos et al., 2016	Brazil	2013-4	IFAT	34	5	14.2

Studies are listed in order of year published. NA=not available (parameter not provided). IFAT=indirect fluorescent antibody test. DT=dye test. LAT=latex agglutination test. MAT= modified agglutination test. DAT= direct agglutination test. ELISA=enzyme-linked immunosorbent assay.

Table 2: Pooled seroprevalence of *T. gondii* in wild boar.

	Number of studies	Sample size	infected	Prevalence of <i>T. gondii</i> (95% CI)	Heterogeneity				Univariate-analysis
					χ^2	df	<i>P</i> value	I ² (%) (95% CI)	Odds ratio (95% CI)
Region									
Asia	8	1752	338	13% (5%-23%)	200.67	7	<0.001	96.5 (95-98)	Reference
Europe	29	13959	4079	26% (21%-30%)	889.96	28	<0.001	96.8 (96-97)	1.72 (1.52-1.96)
North America	4	737	323	32% (20%-45%)	39.04	3	<0.001	92.3 (84-96)	2.09 (1.71-2.54)
South America	2	340	19	5% (3%-8%)	39.04	1	<0.001	97.4 (88-98)	0.24 (0.15-0.39)
Gender									
Male	14	2993	714	17% (10%–25%)	366.95	13	<0.001	96.46 (95-97)	Reference
Female	14	2767	723	19% (13%–27%)	267.52	13	<0.001	95.14 (93-96)	1.16 (0.92–1.44)
Age									
<12 months	16	2324	538	20% (16%–25%)	98.77	15	<0.001	84.81 (77-90)	Reference
≥12 months	16	4965	1409	28% (22%–35%)	383.32	15	<0.001	96.09 (95-97)	1.58 (1.16–2.16)