

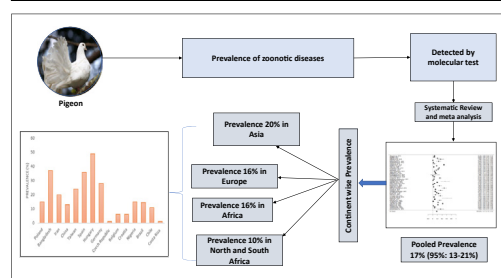


## Research article

## Global prevalence of zoonotic pathogens from pigeon birds: A systematic review and meta-analysis

Md. Mukhtar Mia<sup>a,b</sup>, Mahamudul Hasan<sup>b,\*</sup>, M. Rashed Hasnath<sup>a</sup><sup>a</sup> Department of Poultry Science, Faculty of Veterinary, Animal and Biomedical Sciences, Sylhet Agricultural University, Sylhet 3100, Bangladesh<sup>b</sup> Faculty of Veterinary, Animal and Biomedical Sciences, Sylhet Agricultural University, Sylhet 3100, Bangladesh

## GRAPHICAL ABSTRACT



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## ABSTRACT

Pigeons have been considered the most preferred companion for human civilizations since prehistoric times. Despite the fact that pigeons offer the most palatable and nutritious food and provide pleasure to humans, they can pose a health risk because of carrying infectious and zoonotic organisms. Moreover, the scanty of systematic reports on the occurrence of zoonotic pathogens in pigeon makes the situations worst. Hence, the current study conducted a systematic review and meta-analysis to evaluate the global prevalence of zoonotic pathogens among the pigeon population from existing segregated literatures. Four internationally recognized databases including Google Scholar, Scopus, PubMed, and Science Direct were used to search the published studies from January 2000 to October 2021. Analyzing the total 18,589 samples, mean prevalence estimates of pigeon pathogens worldwide were found to be 17% (95% CI:13–21) whereas serological and molecular prevalence were reported as 18% (95% CI:12–23) and 17% (95% CI:10–23). Meanwhile, virus, bacteria, and protozoal pathogens were found to be 21% (10–32%), 17% (12–23%), and 14% (10–19%), respectively. Moreover, continent wise analysis of all zoonotic pigeon pathogens has revealed the highest prevalence rate in Asia 20% (95% CI: 14–26%), followed by Europe 16% (95% CI: 08–24%), Africa 16% (95% CI: 07–24%), and America (North and South) 10% (95% CI: 03–17%). Furthermore, the highest number of studies were reported from Iran showed the prevalence rate of 20%, China 13%, Bangladesh 37%, and Poland 15%. Therefore, this prevalence of data would be helpful to the policymakers to develop appropriate intervention strategies to prevent and control diseases in their respective locations.

\* Corresponding author.

E-mail address: [mhasan.student@sau.ac.bd](mailto:mhasan.student@sau.ac.bd) (M. Hasan).

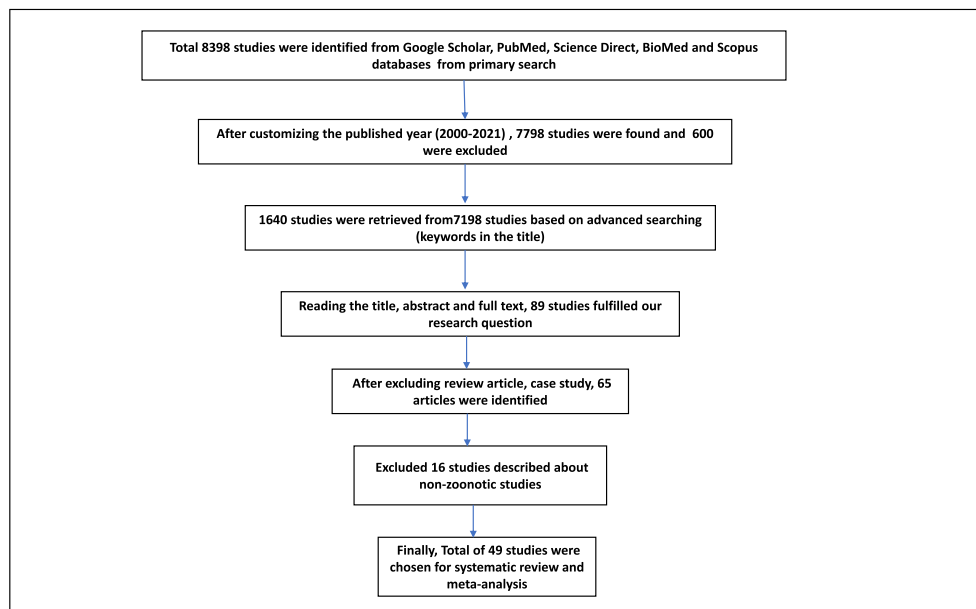


Figure 1. Flow chart describing the procedures of choosing eligible studies.

## 1. Introduction

Pigeon farming is one of the most profitable and enjoyable businesses in the world; people have kept pigeons in their homes for personal consumption since ancient times. Pigeons are frequently used as a symbol of peace, and different countries employ them to establish diplomatic connections. However, because of their near proximity to humans and vast range of flying ability, they may be responsible for the spread of a wide range of zoonotic infections (Perez-Sancho et al., 2020; Rose et al., 2006). Moreover, the ability to adapt with various urban habitats and indoor nesting behavior favor their potential role as a source of infection for other animals and humans.

More than 110 of zoonotic diseases including deadly pathogens *Campylobacter* species, *Coxiella burnetii*, *Toxoplasma* species, *Escherichia coli* O157 and *Cryptococcus* species can be transferred to human through inhalation of dust and consumption of inadequately refrigerated or undercooked meat of pigeon (Haag-Wackernagel and Bircher, 2010; Dudzic et al., 2016; Sürsal et al., 2017). Furthermore, pigeon acts as the carriers of antibiotic-resistant *Salmonella* species, which may pose a health risk to other birds and humans (Bupasha et al., 2020). Likely, *Chlamydia psittaci* is the most prevalent zoonotic causal agent causes psittacosis originated from pigeons along with parrots, doves, and mynah birds.

Since pigeon have the ability to act as vector carrying zoonotic agent with high probability of pathogens transmission between humans and pigeons (Perez-Sancho et al., 2020), it is become an urgent issue to know the systematic reports regarding global magnitude of pigeon borne infections. In this regard, meta-analysis is an extremely useful statistical tool and the goal of the tools is to synthesize, integrate, and compare the findings of a huge number of primary research that look into the same issues. Moreover, the meta-analysis calculated a more precise estimate of the effect size of a specific event with better statistical power than a single research (Borenstein et al., 2021). Therefore, present research focuses on evaluating the global prevalence of the infectious zoonotic pathogens spread by the pigeons, taking into account geographical diversity. The thorough data gathered in this study will aid policymakers in developing prevention as well as control measures.

## 2. Methodology

The current study quantitatively summarized and compared the prevalence of zoonotic pathogens from pigeon globally. At first

systematic review was performed followed by data extraction and conducted meta-analysis, which compiled last 21 years' time series data for analyzing the pooled prevalence with risk factors.

### 2.1. The study protocol and literature search strategy

The current systematic study focuses on calculating the prevalence of zoonotic pathogens from pigeon birds using the PRISMA standards for systematic review and meta-analysis (<http://www.prisma-statement.org>). Thus, a systematic literature search between the years 2000–2021 was conducted using a combination of keywords such as 'pigeon', 'zoonotic pathogens' and 'prevalence' in globally recognized four electronic databases such as Google Scholar, PubMed, Science Direct and Scopus; meanwhile, for obtaining the various country's studies, the database was scrutinized randomly. Besides, additional studies were gathered by manually searching the cross references or bibliographies section of eligible studies and finally, the eligible studies were extracted by two reviewers (MMM and MH) for eliminating the bias. In the case of disagreement, a third reviewer (MRH) assessed the article in question to determine its relevance. The agreement was reached by group discussion with a third reviewer.

### 2.2. Inclusion criteria

The current meta-analysis covered all original descriptive studies published in the English language that explored the prevalence of zoonotic pathogens aroused from pigeon birds. The studies those were confirmed by (polymerase chain reaction) PCR, (enzyme-linked immunosorbent assay) ELISA, (hemagglutination inhibition) HI, and (hemagglutination assay) HA, latex agglutination, modified agglutination tests were included for current meta-analysis. The studies which were synthesized from 2000 to 2021 and only from domestic pigeons were included.

### 2.3. Exclusion criteria

Review articles, duplicates, qualitative studies, case reports, case series, and studies published in non-peer reviewed journals were excluded. Moreover, the studies those were not confirmed by PCR, ELISA, HI, and HA tests were excluded for current meta-analysis. Identified the zoonotic pathogens from wild pigeons were excluded.

**Table 1.** Characteristics of the included studies.

Authors name and year	Representativeness of the sample	Diagnostic method
(Stenzel et al., 2014)	Cloacal and pharyngeal swabs	TaqMan Real-Time PCR Screening
(Al-abodi, 2017)	Blood samples	Conventional PCR
(Altamimi, 2020)	Faecal samples	Nested PCR
(Saifullah et al., 2016)	Cloacal swabs, pharyngeal swabs	PCR
(Dolz et al., 2013)	Fecal sample	Nested PCR
(Mahzounieh et al., 2020)	Cloacal swab samples,	PCR
(Geigenfeind et al., 2012)	Pharyngeal and cloacal samples	Nested PCR
(Dickx et al., 2010)	Pharyngeal swabs	Nested PCR
(Gargiulo et al., 2014)	Cloacal swab	PCR
(Ibrahim et al., 2018)	Blood and tissue samples	ELISA
(Tsai et al., 2006)	Blood serum samples	Latex agglutination test (LAT)
(Parmentier et al., 2019)	Muscle biopsies	DNA by semi-nested PCR
(Doosti et al., 2014)	Blood samples	PCR
(Akbarmehr, 2010)	Intestine, spleen and liver	PCR
(Cano-Terriza et al., 2015)	Blood samples	Blocking ELISA
(Zhang et al., 2019)	Blood samples	Indirect hemagglutination assay
(Pekmezci et al., 2021)	Droppings	Nested PCR
(Koompapong et al., 2014)	Feces	PCR
(Ghorbanpoor et al., 2015)	Pharyngeal swabs	PCR
(Perez-Sancho et al., 2020)	Samples from intestine	PCR
(Cong et al., 2013)	Blood samples	Indirect Haemagglutination assay
(Kaczorek-Lukowska et al., 2021)	Cloaca, crop and faeces of birds	PCR
(Radimersky et al., 2010)	Cloacal swabs	PCR
(Golestani et al., 2020)	Pharyngeal swab	Nested PCR
(Mattmann et al., 2019)	Choanal-cloacal swabs, liver samples	Real-time PCR
(Helen Owoya et al., 2020)	Blood sample	Haemagglutination inhibition test
(Esameili et al., 2015)	Cloacal sample	Multiplex PCR
(Bupasha et al., 2020)	Cloacal swab	PCR
(Salant et al., 2009)	Blood sample	Modified Agglutination Test
(Ballmann and Harrach, 2016)	Dead or alive, healthy pigeons	Nested PCR
(Cong et al., 2012)	Blood sample	Modified agglutination test
(Elina et al., 2017)	Blood sample	Hemagglutination Inhibition
(González-Acuña et al., 2007)	Blood, organs and intestine contents	Commercial Elisa kit
(De Lima et al., 2011)	Cloacal and tracheal swabs	Hemi-nested PCR
(Ebani et al., 2016)	Spleen samples	PCR
(Silva et al., 2009)	Fresh feces samples	Multiplex PCR
(Dudzić et al., 2016b)	Cloacal swabs	PCR
(Jahantigh and Nili, 2010)	Pigeon eggs	PCR
(Karim et al., 2020)	Oral and cloacal; swabs	PCR
(Yan et al., 2011)	Blood samples	Modified agglutination test
(Bahrami et al., 2016)	Blood samples	Neospora Agglutination test (NAT) and PCR
(Jonassen et al., 2005)	Cloacal swab samples	RT-PCR
(Tanaka et al., 2005)	Faecal samples	PCR
(Tsai and Lee, 2006)	Blood samples	Haemagglutination inhibition test

**Table 1 (continued)**

Authors name and year	Representativeness of the sample	Diagnostic method
(Ibrahim et al., 2021)	Blood samples	Haemagglutination inhibition test
(Zhuang et al., 2020)	Swab and feces sample	Conserved RT-PCR assay
(Vućemilo et al., 2003)	Cloacal swabs	Haemagglutination inhibition
(Gronesová et al., 2009)	Oropharynx and cloaca	Nested RT-PCR
(Mohammadi et al., 2010)	Blood sample	Haemagglutination inhibition

**Table 2.** Continent wise zoonotic diseases' prevalence from pigeon bird.

Region/Continent with total prevalence	Country	Infection/Disease(s)
Asia (20%) (95% CI: 14–26) % No. of Studies: (25)	Iraq, Bangladesh, Iran, Taiwan, China, Thailand, Israel, Japan, Taiwan	<i>Cryptosporidium meleagridis</i> , <i>Salmonella</i> species, <i>Chlamydia psittaci</i> , <i>Toxoplasma gondii</i> , <i>Haemoproteus columbae</i> , <i>Toxoplasma gondii</i> , <i>Escherichia coli</i> O, <i>Newcastle Disease Virus</i> , <i>Neospora caninum</i> , <i>Chlamydia pecorum</i> , <i>Newcastle disease</i> , <i>Coronaviruses (CoVs)</i> , <i>Avian influenza</i> .
Europe (16%) (95% CI: 08–24) No. of Studies: (16)	Poland, Switzerland, Belgium, Italy, Germany, Spain, Czech Republic, Hungary, Norway, Croatia, Slovak Republic	<i>Chlamydia psittaci</i> , <i>Campylobacter jejuni</i> , <i>Sarcocystis calchasi</i> , <i>flaviviruses of the Japanese Encephalitis antigenic complex (JEV)</i> , <i>Salmonella</i> species, <i>Escherichia coli</i> , <i>Adenovirus</i> , <i>Anaplasma phagocytophilum</i> , <i>Bartonella</i> species, <i>Coxiella burnetii</i> , <i>Rickettsia</i> species, <i>Chlamydia</i> species), <i>Coronaviruses</i> , <i>Avian influenza A</i>
Africa (16%) (95% CI: 07–24) No. of Studies: (3)	Egypt, Nigeria	<i>Toxoplasma gondii</i> , <i>Newcastle disease virus (NDV)</i>
North and South America (10%) (95% CI: 03–17) No. of Studies: (4)	Costa Rica, Chile, Brazil	<i>Chlamydia psittaci</i> , <i>Chlamydia psittaci</i> , <i>Escherichia coli</i> ,

#### 2.4. Quality assessment

A predefined rating system was used to measure the quality of various studies to accurately judging study type and minimizing the bias of selected studies (Kuralayanapalya et al., 2019; Patil et al., 2021). The rating was on a scale of 0–5, with each part receiving the maximum of two stars. For calculating the score, the author's name with the study year, utilized representative sample, comparability, exposure ascertain, and result were taken in the consideration. Thus, the total quality rating score was confined between 3 and 4 (Supplementary Table 1).

#### 2.5. Screening and data extraction

The information was gathered from qualified studies that included the name of first author, published year, location of study, total sample size, detection or diagnostic test, and kind of pathogens like bacterial, viral or protozoal. In this study, individual zoonotic pathogens obtained from pigeon around the world were used to categorize as a parameter; besides, continent-by-continent and country-by-country stratification of studies was undertaken. Then, each selected study was double-checked to rule out any possible consensus, and all the relevant data were

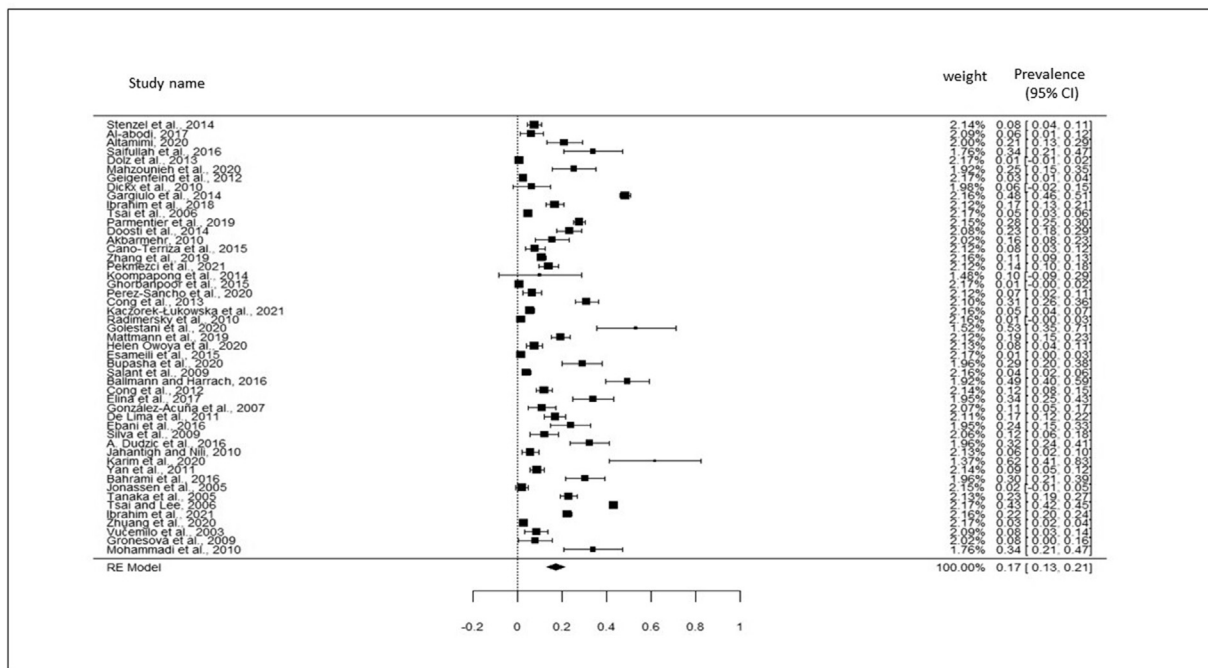


Figure 2. Visualizing forest plot described pooled prevalence of zoonotic diseases from pigeon.

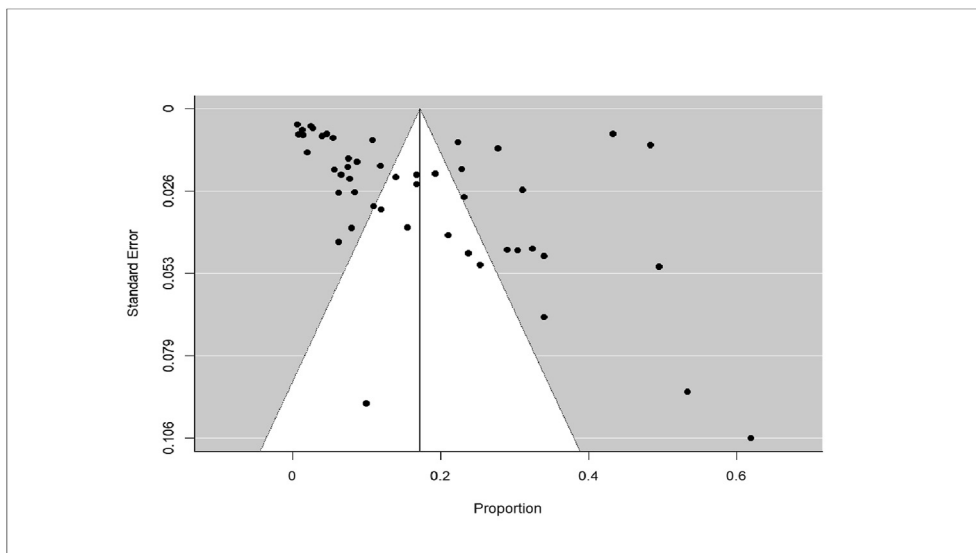


Figure 3. Graphically representation of funnel plot described studies heterogeneity.

extracted from the eligible studies; the study selection steps were visualized in Figure 1.

2.6. Assessment of bias, data preparation, and analysis

The Jamovi software (version 1.2.27, <https://www.jamovi.org>) was used to conduct the meta-analysis. This study enables the generation of a weighted average percentage of prevalence from numerous studies, paving the path for optimal planning. The statistical analysis was carried out using meta-analysis (Major) packages. The percentage of variation owing to heterogeneity among the numerous reports included in this study was calculated using the tau<sup>2</sup>, I<sup>2</sup> (Higgin's I<sup>2</sup>), and p value. Moreover, the pooled prevalence of individual pathogens was calculated using the fixed and random effect model because of expecting significant variability. Furthermore, displaying the Standard Error (SE) of each

study, the funnel plot was created with the y-axis and the x-axis was used to show the effect of each study. Consequently, representing the publication bias by presenting the non-symmetrical shape of a funnel with dropping the points exterior to the funnel. Whenever the publication bias is practically negligible, studies with high precision concentrate along with the typical line, and those with low accuracy disperse consistently on both side of the median line, resulting in a funnel-shaped scatter (Egger et al., 1997). Forest Plot was used to visualize the data graphically. For calculating the result, the limited maximum-likelihood estimation has been used to establish the relationship between prevalence estimates and variance of study, which were presented as a percentage with a 95% confidence interval (CI). Finally, subgroup analysis was carried out based on the species affected, the type of pathogens, the method of diagnostic test, continents of the world, and the countries to evaluate the heterogeneity in each group and their comparison.

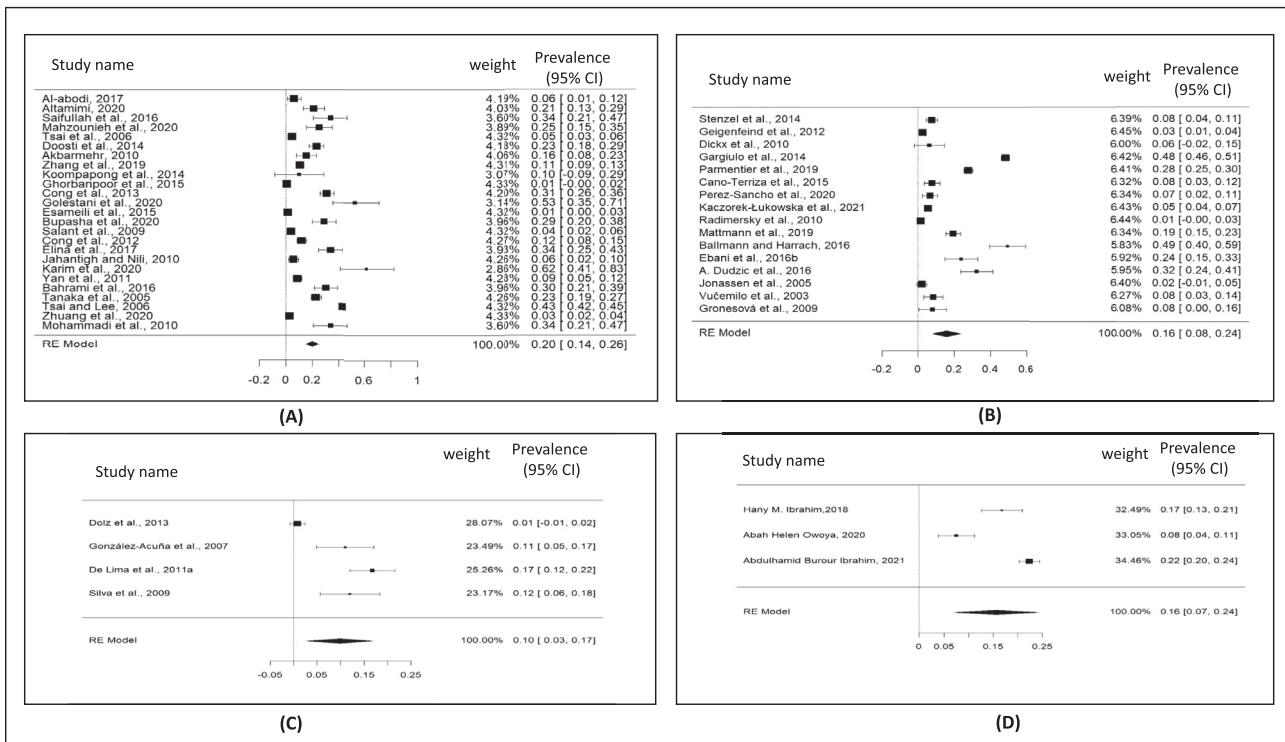


Figure 4. Forest plot for representation of continent wise prevalence; A) Asia; B) Europe; C) North and South America; and D) Africa

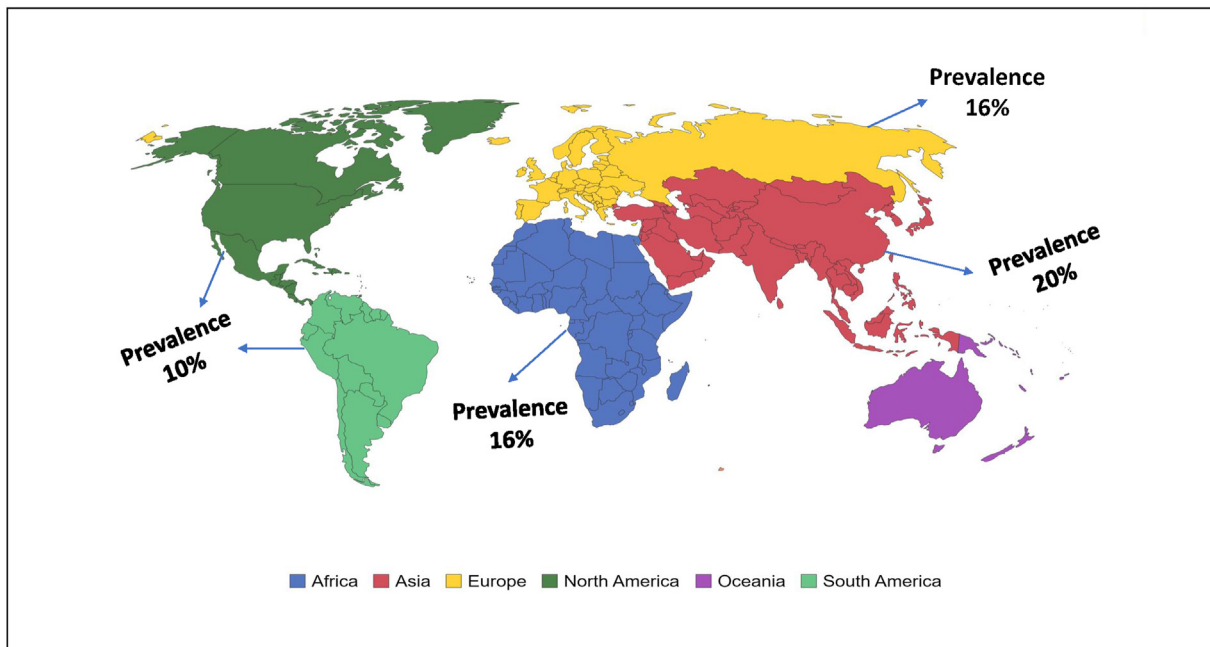


Figure 5. Graphical representation of continent wise prevalence in world map.

### 3. Results

In the present study, a systematic review of scientific publications on the prevalence of zoonotic pigeon pathogens was conducted for 21 years (2000–2021). Studies regarding the prevalence of zoonotic pathogen from pigeon were rigorously screened, and irrelevant studies were removed. A number of 49 studies came from Europe, Asia, Africa, South America, and North America were chosen for systematic review and meta-analysis in this study (Table 1).

#### 3.1. Estimated pooled prevalence of pathogens

Total selected 49 studies were obtained from Asia (8 countries), Europe (11 countries), North America and South America (3 countries), Africa (2 countries), and Eurasia (Turkey) regions (Table 2). The current meta-analysis analyzed a total of 18,589 samples from the years January 2000 to October 2021, and revealed that the global prevalence of pigeon-borne zoonotic pathogens was 17% (95% CI: 13–21%) (Figure 2); besides funnel plot of all the studies was showed in Figure 3. Subsequent that,

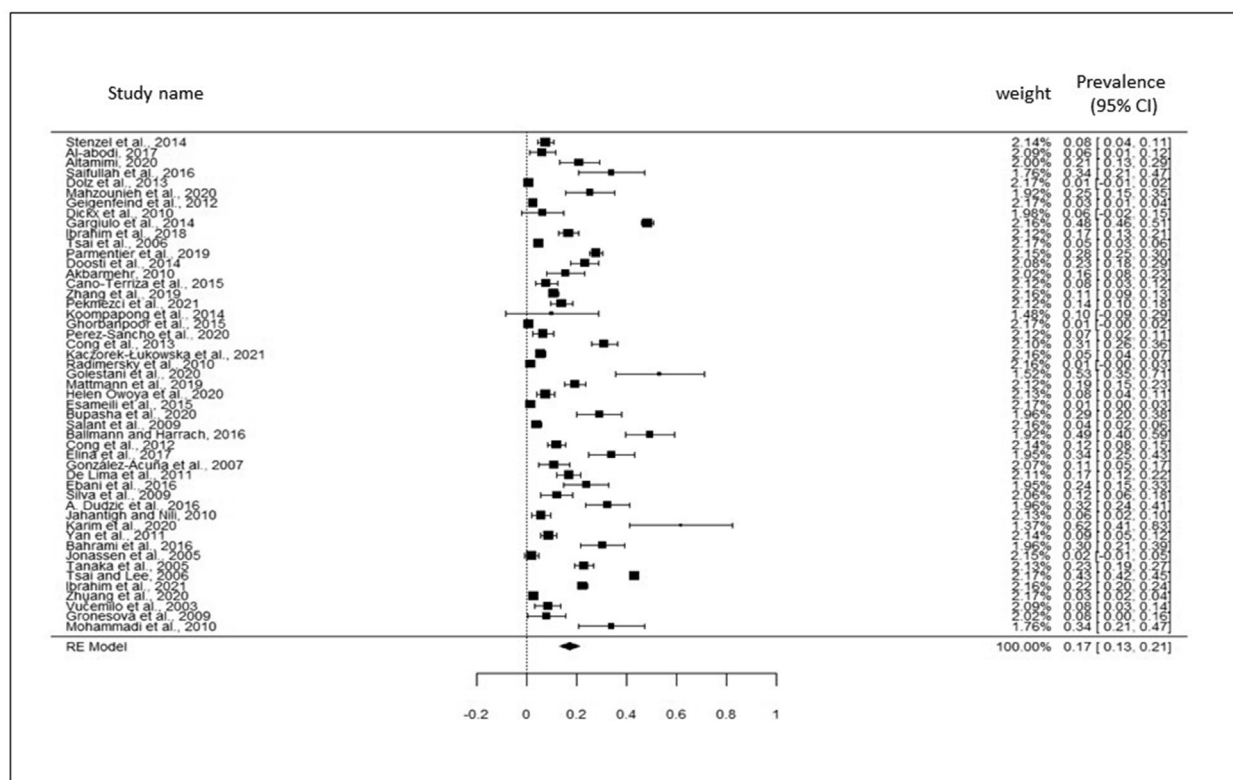


Figure 6. PCR based pooled prevalence.

Table 3. Prevalence of zoonotic diseases from pigeon based on different diagnostic tests.

Diagnostic test	Random effect model					Fixed model
	No. of Studies	Prevalence (%) (95% CI)	I <sup>2</sup> (%)	H <sup>2</sup>	Tau <sup>2</sup>	Prevalence (%) (95% CI)
PCR (Molecular)	34	18 (12–23)	99.18	122.4	0.022	06 (06–07)
ELISA/Agglutination test/Haemagglutination assay/Haemagglutination inhibition (Serological)	15	17 (10–23)	98.66	74.6	0.014	17 (16–17)

analyzing the continent-wise result of all zoonotic pathogens from pigeon (Figure 4), the highest prevalence rate was found in Asia 20% (95% CI: 14–26%), followed by Europe 16% (95% CI: 08–24%), Africa 16% (95% CI: 07–24%), and America (North and South) 10% (95% CI: 03–17%) (Figure 5) (Table 2). Finally analyzing the result based on test procedure, PCR (molecular method) showed 18% (95% CI: 12–23%) prevalence rate (Figure 6) (Table 3).

### 3.2. Country wise prevalence

In case of country wise prevalence among the European countries from multiple studies, the prevalence rate 15% (95% CI: -02–31%) was found in Poland; whereas, 36%, 11%, and 7.5% prevalence rate were found in Spain, Italy, and Switzerland, respectively. Similarly, single study from Hungary, Germany, Croatia, Belgium, and Czech Republic reported 49%, 28%, 8%, 6%, and 1% prevalence rate, respectively. In contrast, among the Asian countries, the pooled prevalence was found to be 37% (95% CI: 26–48%) in Bangladesh (Figure 7), 20% (95% CI: 09–30%) in Iran, and 13% (95% CI: 04–22%) in China. Likely, two studies individually from Taiwan, and Iraq reported 24% and 13.5% prevalence rate, correspondingly. Besides, single study from Japan, Thailand and Israel reported 23%, 10%, and 4% prevalence rate. However, the maximum prevalence was reported as 17% in Egypt; meanwhile, 15% prevalence was found in Nigeria among the African

countries. Among the American countries (North and south), 14.5% prevalence rate was reported from Brazil; whereas, Chile and Costa Rica reported 11% and 1% prevalence rate (Table 4).

### 3.3. Bacterial, viral and protozoal pathogens' prevalence

Among the bacterial pathogens, *Campylobacter* species showed comparatively higher prevalence in pigeon 24% (95%CI: 04–44%), whereas *Escherichia coli* showed prevalence rate of 18% (95%CI: -09–44%). Similarly, *Chlamydia psittaci* revealed the prevalence rate of 17% (95%CI: 09–26%) and *Salmonella* species reported 17% (95% CI: 06–28%) (Figure 8). In conjunction, prevalence of *Chlamydophila psittaci* and tick-borne bacteria (*Anaplasma phagocytophilum*, *Bartonella* species, *Coxiella burnetii*, *Rickettsia* species, *Chlamydophila* species) was found to be 6% and 24%, respectively. However, a total of 26 studies on bacterial zoonotic pathogens from pigeon reported a prevalence of 17% (95% CI: 12–23%) with heterogeneity I<sup>2</sup> = 99.2%, Tau<sup>2</sup> value was 0.022, p < 0.001 (Figure 9) (Table 5).

Moreover, Pigeon birds are the potential stake holders for the spreading of viral zoonoses by variety of medium. The prevalence of overall viral zoonotic pathogens from pigeon was 21% (95% CI: 10–32%), I<sup>2</sup>: 99.35%, Tau<sup>2</sup> value: 0.030, p < 0.001, which is highest among the zoonotic agents; meanwhile, studies on Newcastle disease virus infection revealed a prevalence of 27% (95% CI: 11–42) globally

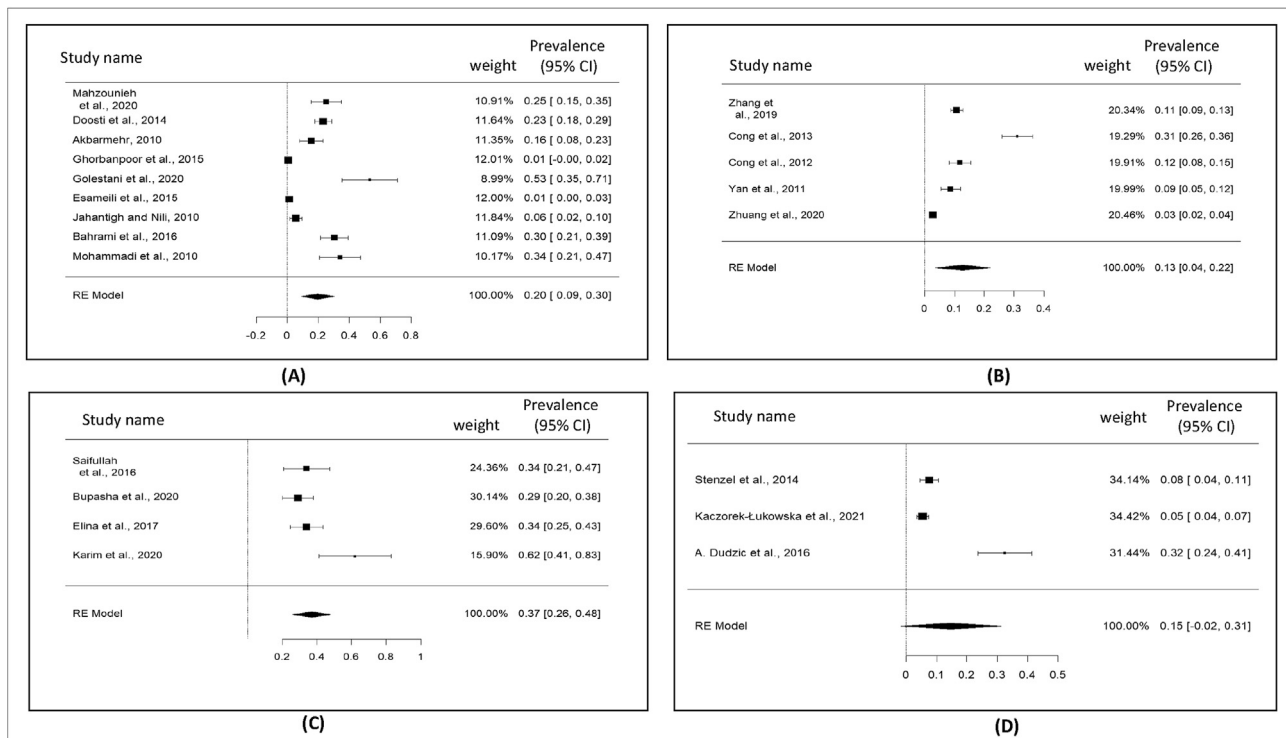


Figure 7. Forest plot for representation of country wise prevalence; A) Iran; B) China; C) Bangladesh; and D) Poland.

Table 4. Country wise disease prevalence with causal agent.

Country	Type of causal agent	Random effect model				
		No. of Studies	Prevalence (%) (95% CI)	I <sup>2</sup> (%)	H <sup>2</sup>	Tau <sup>2</sup>
Iran	<i>Chlamydia psittaci</i>	09	20 (09–30)	99.11	111.9	0.024
	<i>Haemoproteus columbae</i>					
	<i>Salmonella</i> species					
	<i>Chlamydotheca psittaci</i>					
	<i>Chlamydia psittaci</i>					
	<i>Escherichia coli</i>					
	<i>Neospora caninum</i>					
<i>Avian influenza</i>						
China	<i>Toxoplasma gondii</i>	05	13 (04–22)	98.56	69.2	0.010
	<i>Chlamydia psittaci</i>					
	Coronaviruses (CoVs)					
Bangladesh	<i>Salmonella</i> species	04	37 (26–48)	69.81	3.3	0.008
	Newcastle Disease Virus					
	<i>Escherichia coli</i>					
Poland	<i>Chlamydia psittaci</i>	03	15 (-02–31)	98.54	68.2	0.020
	<i>Salmonella</i> species					
	<i>Campylobacter</i> species					

(Figure 10). Similarly, Coronaviruses (CoVs) and avian influenza were found to be 25% and 21%, respectively. A single study on Japanese encephalitis from India showed 8% (95%CI: 03–12%) prevalence rate.

Furthermore, thirteen studies on zoonotic protozoal pathogen of pigeon were selected in this study. The overall prevalence was reported 14% (95% CI: 10–19%), I<sup>2</sup>: 96.50%, Tau<sup>2</sup> value: 0.030, <0.001; whereas, *Toxoplasma gondii* was found to be 7% (95% CI: 06–12%) (Figure 8) (Table 6). Likely, the reported prevalence of the single study on three protozoa was 14% (95% CI: 10–18%) for *Enterocytozoon bienewi*, 23% (95% CI: 18–29%) for *Haemoproteus columbae*, and 30% (21–39%) for *Neospora caninum*. During the last decades, pigeon populations have increased exponentially in different countries, reaching densities higher than 2000 birds/km<sup>2</sup> in many European cities and may cause a serious threat because of carrying zoonotic infectious pathogen (Cano-Terriza et al., 2015; Patil et al., 2021).

#### 4. Discussion

Pigeons, as a sociable bird, remain closer to humans, perhaps posing health risks due to the presence of infectious and zoonotic pathogens. A systematic comprehensive data about the occurrence of zoonotic diseases in pigeon is important to take the proper interventional measures. Analyzing the results, mean prevalence of zoonotic pathogens was found 17%; meanwhile, Asian region reported 24% prevalence rate followed by Africa and Europe 16% and North with South American continent 10%. Frequent contact with pigeons, popularity of pigeon games in Middle East countries (PCRC, 2021), poor hygiene practices in developing countries specially in Asia could be the possible reason for comparatively higher prevalence in Asian region. More specifically, analyzing multiple studies among Asian countries, Bangladesh possesses comparatively higher prevalence rate than others; meanwhile, the prevalence rate in China and

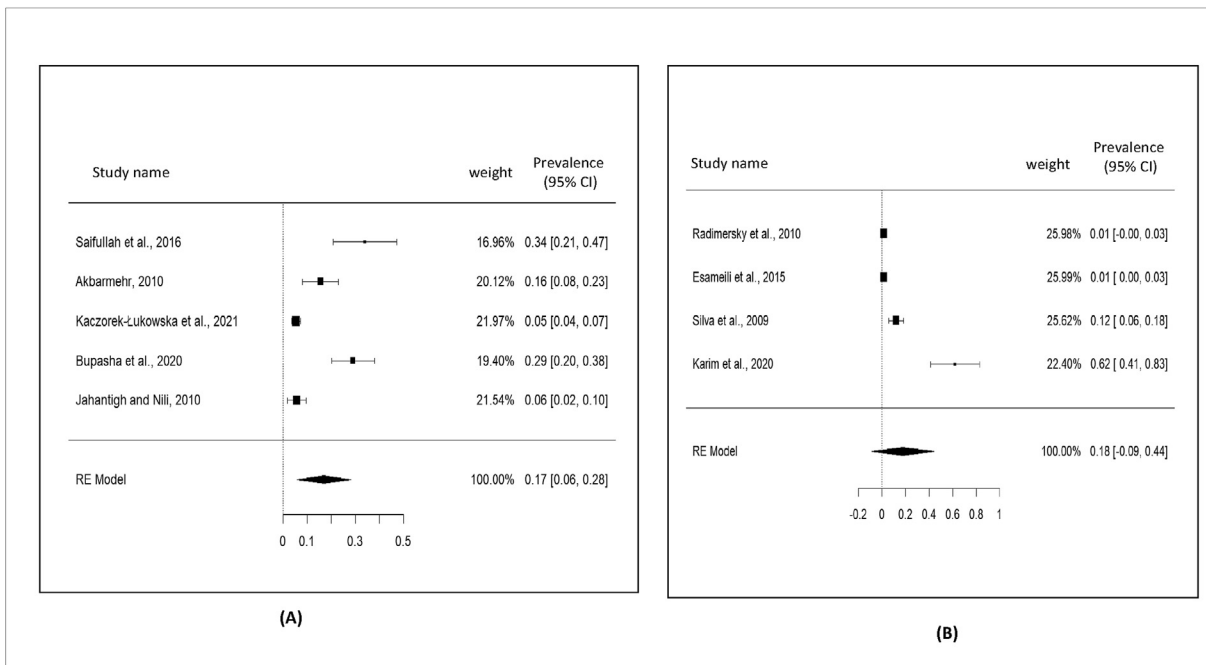


Figure 8. Forest plot showing the pooled prevalence rate based on causal agent; A) *Salmonella spp.*; B) *Escherichia coli*.

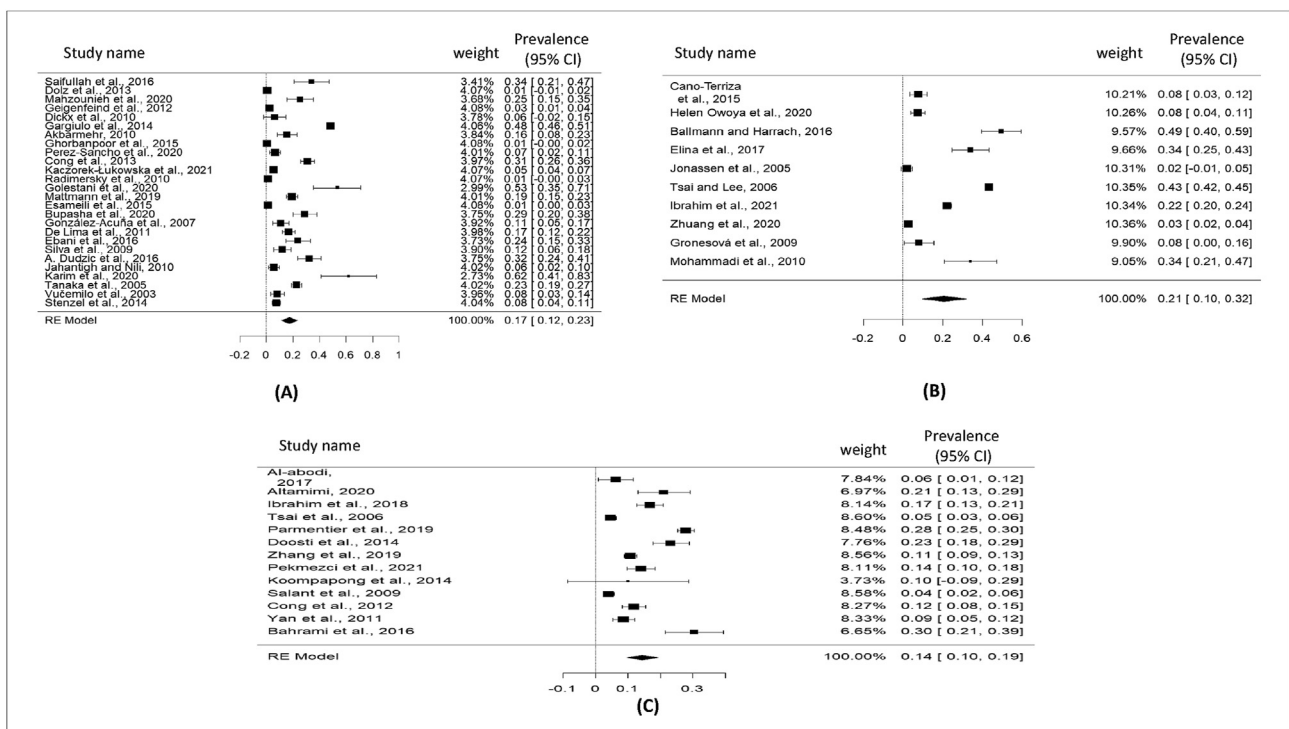


Figure 9. Forest plot showing the pooled prevalence of diseases; A) Bacterial; B) Viral; and C) Protozoal.

Iran was in moderate level. Pigeons are sold in the small and large live bird markets associated with chicken and ducks in Bangladesh, which create huge public gatherings at live bird markets with unhygienic environments may favor the maximum transmission of infectious agent from bird to bird and bird to human (Dey et al., 2013). In contrast, result from the multiple studies of each country within the European region, Spain and Poland reported higher susceptibility to zoonotic pigeon born pathogen. Likely, from African and American region, maximum prevalence rate was recorded in Egypt and Brazil, respectively. Dissimilarly, single study was reported from Hungary, Germany, Croatia, Belgium,

Czech Republic Japan, Thailand, Israel, Chile and Costa Rica, whereas Hungary possessed the highest prevalence rate.

From our analysis, it is concluded that viral pathogen (21%) is predominant than bacterial pathogen (17%) and protozoan pathogen (14%). This reason could be due to the robust disease reporting system available globally (Patil et al., 2021). Among the viral pathogen, Newcastle virus, Corona viruses (CoVs) and avian influenza were found more prevalent and recent study reported that, outbreaks of avian influenza continue to be a global public health concern due to ongoing circulation of various strains (H5N1, H5N2, H5N8, and H7N8), (OIE, 2021). On the other



**Table 5.** Prevalence viral, bacterial, and protozoal zoonotic disease from pigeon.

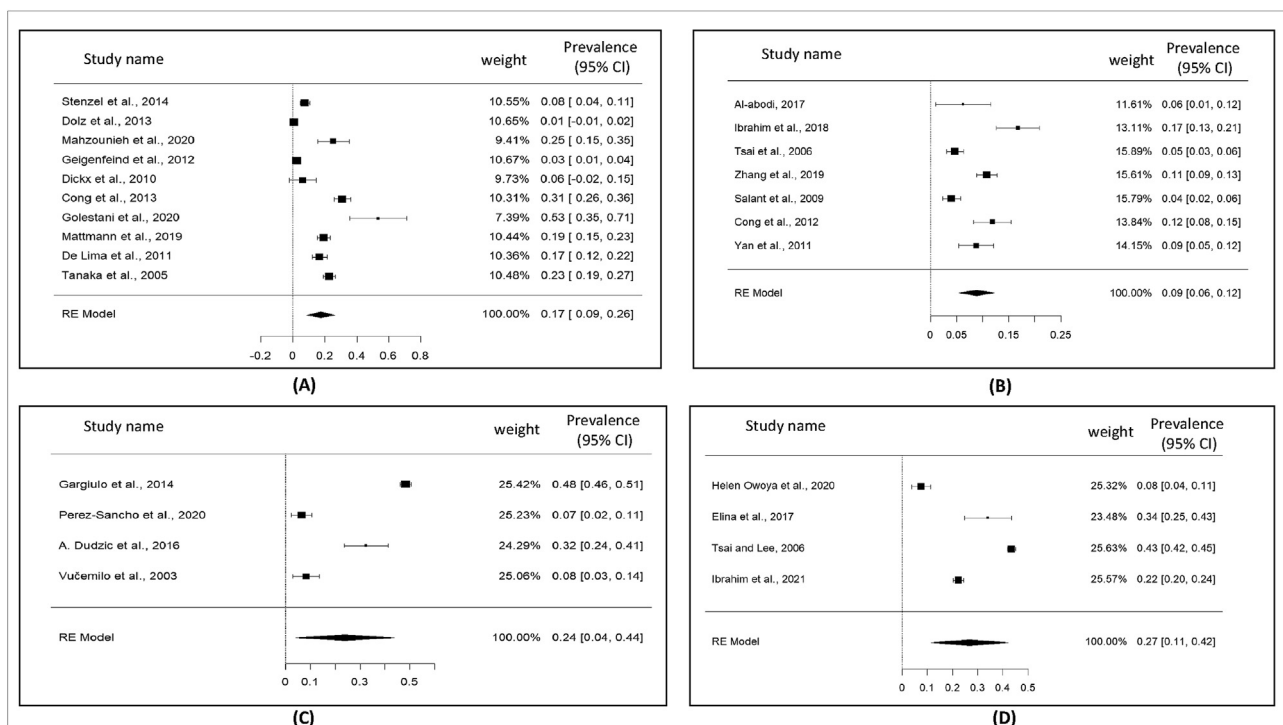
Type of causal agent	Random effect model					Fixed model
	No. of Studies	Prevalence (%) (95% CI)	I <sup>2</sup> (%)	H <sup>2</sup>	Tau <sup>2</sup>	Prevalence (%) (95% CI)
Virus	10	21 (10–32)	99.35	153.17	0.030	17 (16–17)
Bacteria	26	17 (12–23)	99.22	128.92	0.022	06 (05–06)
Protozoa	13	14 (10–19)	96.50	28.53	0.006	10 (09–11)

hand, *Campylobacter* species, *Escherichia coli*, *Chlamydia psittaci*, *Salmonella* species, were found as main causal agent for the bacterial diseases occurring in pigeon and all of these pathogens have a dreadful effect on public health concern. Going more deeper, pigeons are the potential carrier for zoonotic pathogens, including *Campylobacter* species and *Salmonella* species that are mainly associated with severe acute gastroenteritis, *Coxiella burnetii*, the causal agent of Q fever and *Chlamydia psittaci* is responsible for respiratory tract infection in humans (Gabriele-Rivet et al., 2016; Weygaerde et al., 2018). In term of parasitic pathogens, *Toxoplasma gondii* was found more prevalent; whereas, single study reported for *Enterocytozoon bieneus*, *Haemoproteus columbae*, and *Neospora caninum*. Previous study revealed that *Toxoplasma gondii* is one of the most serious coccidian parasites, which infect human because of

consuming raw and poorly cooked pigeon meat with *Toxoplasma* oocysts. Consequently, these birds may represent a public health problem for humans (Ibrahim et al., 2018). However, our analysis has few limitations, such as the dearth of multiple studies from every continent of the world and the risk of missing some studies to include. Given the limitations, our findings may vary slightly from the actual prevalence rate. Thus, we recommended that more rigorous molecular research should be performed for the finding of accurate global prevalence rate.

## 5. Conclusion

The current meta-analysis analyzed 49 articles with a total of 18,589 samples and revealed that the global prevalence of pigeon-borne zoonotic pathogens was 17%; analyzing the continent-wise result of all zoonotic pathogens from pigeon, the highest prevalence rate was found in Asia 20%, followed by Europe 16% and Africa 16%, the difference rate may be due to poor hygiene practices in developing countries in Asia rather than developed European countries. Besides, our result showed that the prevalence rate of viral pathogens is higher than bacterial and protozoal pathogens. This could be due to the new geographic areas being swiftly filled by rising human populations; as a result, people are more likely to live in close proximity to wild and pet birds, including pigeons. Therefore as a result, understanding the global epidemiological

**Figure 10.** Forest plot showing the pooled prevalence rate based on causal agent; A) *Chlamydia psittaci*; B) *Toxoplasma gondii*; C) *Campylobacter* spp., and D) Newcastle Disease Virus.**Table 6.** Prevalence of zoonotic diseases categorized by causal agent.

Type of causal agent	Random effect model					Fixed model
	No. of Studies	Prevalence (%) (95% CI)	I <sup>2</sup> (%)	H <sup>2</sup>	Tau <sup>2</sup>	Prevalence (%) (95% CI)
<i>Campylobacter</i> species	04	24 (04–44)	98.79	82.89	0.040	35 (33–36)
<i>Chlamydia psittaci</i>	10	17 (09–26)	98.76	80.37	0.018	05 (05–06)
<i>Escherichia coli</i>	04	18 (-09–44)	99.77	428.91	0.069	02 (01–02)
Newcastle Disease	04	27 (11–42)	99.20	124.86	0.023	33 (32–34)
<i>Salmonella</i> species	05	17 (06–28)	95.98	24.88	0.014	07 (06–09)
<i>Toxoplasma gondii</i>	07	09 (06–12)	91.47	11.72	0.001	07 (06–08)

prevalence for intervention against these zoonoses is crucial for global public health. Moreover, raising public awareness about disease reporting to their local veterinary practitioners, as well as adopting prevention, control, and biosecurity techniques, can significantly reduce pigeon mortality.

## Declarations

### Author contribution statement

Md. Mukthar Mia and Mahamudul Hasan: Conceived and designed the experiments; Analyzed and interpreted the data; Wrote the paper; M. Rashed Hasnath: Analyzed and interpreted the data.

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The authors declare no conflict of interest.

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