Review

A systematic review and *meta*-analysis on the prevalence of infectious diseases of Duck: A world perspective

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ABSTRACT

The Indian poultry industry is one of the fast-growing sectors of which duck farming plays an important role. Duck population in India is 33.51 million that is concentrated towards north-east and southern parts of the country who rears mainly for eggs and meat. Duck diseases are of great concern as they badly affect the financial status of the small, landless farmers. Databases such as Google Scholar, PubMed, J gate were used to search articles between 2000 and 2019 that showed the prevalence of viral, bacterial, and parasitic duck diseases. R open source software was used to derive forest plots by statistical analysis. Pooled prevalence estimates of duck diseases worldwide was found to be 20% (95%-CI:15–26). Also, continent-wise analysis of all duck diseases has revealed highest prevalence in North America, followed by Asia, Africa, Europe,Oceania and South America. This prevalence of data would be helpful to the policymakers to develop appropriate intervention strategies to prevent and control diseases in their respective locations.

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1. Introduction

Ducks constitute a major part of the poultry industry worldwide. Very little information is available on the duck population in different countries. As per FAO, 2017 there were 1.15 billion ducks (*Anas* spp.) worldwide and 1.0 billion (88 percent) were in Asia. The largest duck populations are found in China, Vietnam, Bangladesh, and Indonesia (FAO, 2017). In India, the poultry industry is one of the fastest growing agricultural sectors today. Presently, the production of crops has been rising at a rate of 1.5 to 2% per annum while that of production of eggs and meat has been rising at a rate of 8 to 10% per annum (Indian mirror, 2019). According to the 20th Indian livestock census, the total poultry in India is 851.81 million, registered an increase of 16.8% over the previous census (DAHD, 2019). There are 33.51 million of ducks as per 20th livestock census against 23.53 million in 19th livestock census that shows a change of 42.36% which means that there is an increase in demand of duck and duck farming which further warrants the need for proper surveillance and monitoring of diseases affecting ducks thereby controlling them. Small, marginal farmers and nomadic tribes practice duck farming in India which is sometimes seasonal (Jeyathilakan et al., 2016). Ducks play an important role in rural livelihood as they cater to sustained meat and egg production. One of the important criteria is to keep the ducks healthy to prevent disease outbreaks and in cases where ducks encounter infection, administration of appropriate treatment is practiced to minimize the rate of mortality and morbidity.

The distribution and demographic dynamics of the duck population revealed that they are concentrated in East, North-East, and Southern states of the country. The leading states in the duck population are West Bengal, Assam, Kerala, Manipur, Jharkhand, Tripura, Bihar, Andhra Pradesh, Tamil Nadu, UP, and Orissa (DAHD, 2019). Traditionally, West Bengal and Kerala are the major consumer states for duck egg and meat and one of the reasons is that duck egg and meat highly suits and remain tastier for their fish based culinary preparations (Rajput et al., 2014). In India, farmers practice different systems of duck rearing viz., free range system, confined system, indoor system, integrated duck rearing system, duck keeping combined with paddy cultivation, duck keeping combined with fish ponds (Rajput et al., 2014)

Among the diseases affecting ducks in India, viral diseases have been known to have more serious repercussions to duck production. Farm workers are thus essential in ensuring that strict biosecurity are observed to reduce potential transmission of the disease. Of the most infectious include avian influenza (HPAI/LPAI), duck viral enteritis, West Nile disease, Japanese Encephalitis, Newcastle Disease, duck plague, duck viral hepatitis. Usually, ducklings between the age of 1–28 days are most susceptible to diseases and gradually become immune as they grow older. It would be mandatory to establish and maintain good and viable biosecurity programs that will prevent the invasion of disease in the duck farms.

This study concentrates on estimating the prevalence of the infectious disease of duck in the world including India. The comprehensive information generated from this study would assist the policymakers to formulate prevention and control measures.

2. Methodology

2.1. Literature search

A comprehensive systematic literature search was conducted in electronic databases including PubMed, Google Scholar, Science Direct, Scopus, J gate, BioMed databases from 2000 to 2019 using a combination of keywords "Duck", "Disease", "prevalence", "India". Meanwhile, for the studies of different countries, the database was searched randomly without any restrictions imposed on year. Bibliographies/cross references of eligible studies were also manually searched to identify additional significant articles. The search was restricted to articles in English. Articles were extracted individually by two authors to avoid bias. All the search and scrutiny was conducted according to the PRISMA protocol (http://www.prisma-statement.org) (Table S1)

2.2. Study selection criteria

All the articles that described the prevalence rate of various Duck diseases were considered eligible and included in the study. A total of 1,163 articles were identified, of which 1,032 were excluded following the exclusion criteria described above. This comprehensive database searches returned 124 potential articles based on the search for combination of keywords. A total of 55 articles were selected suitable for the study including 80 studies for systematic review and *meta*-analysis (Fig. 1). Articles were restricted to the English language only. One of the major drawbacks of duck diseases are under-reporting; hence we have tried to pool data as much as possible.

2.3. Data extraction

The data was extracted from qualified studies that included first author, year of publication, total sample size, the location where the study was conducted, detection technique, and the type of
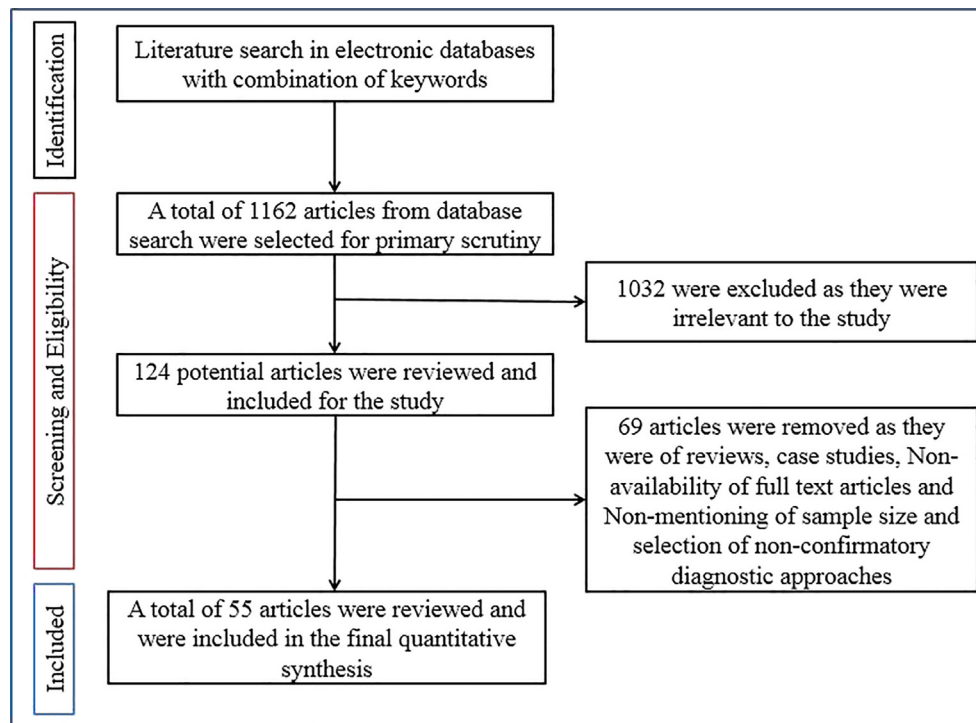
Fig. 1. Schematic diagram of selection of articles used for the systematic review of this study.

infection (viral, bacterial, or parasitic). Articles were stratified according to individual diseases including the studies from India and World. Continent-wise stratification of articles was also performed. Data was extracted independently from each selected article and inconsistency in data was rectified by double-checking the articles until consensus was reached.

2.4. Quality assessment

The quality assessment of different studies was done on a fixed rating scale (Suresh et al., 2019). The scoring was on a scale of 0 to 5, which included evaluation of author and year of study, representativeness of the sample used in the study, ascertainment of the exposure, comparability, and outcome, with each section having the maximum number of two stars. Hence, the overall quality assessment has a maximum score of 5 and a minimum score of 3 (Table 1).

2.5. Meta-analysis

Meta-analysis was carried out using the R Open source scripting software (version 3.4.3, R Foundation for Statistical Computing, Vienna, Austria. https://www.R-project.org/). This analysis facilitates generating a weighted average proportion of prevalence of various studies that provides a way forward for proper planning. Metafor, metaprop, and Meta of R packages were used for statistical analysis. Tau square, I^2 (Higgin's I^2), and p value were computed to determine the percentage of variation due to heterogeneity among various reports included in this study. Both the random effect and fixed effect model were used to calculate the pooled prevalence of individual diseases since substantial heterogeneity was expected. The funnel plot generated with the y-axis showing the Standard Error (SE) of each study, with larger studies plotted on top of the y-axis indicates indicates publication bias and subsequently, the x-axis showed the effect of each study. The studies with high precision concentrate along the line of average when

the publication bias is almost nil, whereas those with low precision distribute evenly on either side of the average line, creating generally a funnel shaped scatter (Egger et al., 1997). The symmetry of the funnel plot was adjusted by the Trim-and-fill method. Graphical representation of the data was depicted in Forest Plot. The restricted maximum-likelihood estimator was used to determine between study variance τ^2. The prevalence estimates for duck diseases was expressed as a percentage with a Confidence Interval (CI) at the 95% level. Subgroup analysis was conducted based on species affected, a diagnostic method used, zones of India and continents of the world for determining the heterogeneity in each group and their comparison. In the present study, the data was stratified based on type of diseases and forest plots generated using the R software.

3. Results

3.1. Study details

Articles reporting the prevalence of duck diseases were thoroughly screened and irrelevant ones were excluded. A total of 55 articles were selected suitable for the study including 80 studies for systematic review and *meta*-analysis. All the articles described the prevalence of various duck diseases of bacterial, viral, and parasitic infections. Systematic Review was conducted to study the reported duck diseases worldwide including those in India. Articles retrieved were from countries belonging to Asia, Europe, Africa, North America, South America, and Oceania regions. All articles used in our study were restricted to the English language only and the study period selected was between 2000 and 2019.

3.2. Meta-analysis of the prevalence of Duck diseases

The worldwide percentage prevalence of different duck diseases was estimated statistically using R software to generate forest and funnel plots, of which, the viral diseases were found to be the most

Table 1
Risk of bias and quality assessment of studies included.

Sl. No.	Author and year of publication	Selection		Comparability	Outcome	Overall Quality Assessment score
		Representativeness of the sample	Ascertainment of exposure		Assessment of outcome	
1	AbouLaila et al., 2011	*Truly representative serum samples	*Identification of *T. gondii* infection confirmed by MAT	Study did not control for other factors	*Independent blind assessment	4
2	Adzitey et al., 2012a	*Truly representative fecal swabs, cloacal swabs, intestinal tissue and other environmental samples	**Identification of *Campylobacter* spp. by mPCR	Study did not control for other factors	*Independent blind assessment	3
3	Adzitey et al., 2012b	*Truly representative fecal swabs, cloacal swabs, intestinal tissue and other environmental samples	*Identification of *Salmonella* isolates by Gram staining, LATEX agglutination test and Biochemical tests	Study did not control for other factors	*Independent blind assessment	4
4	Ahamed et al., 2015	*Truly representative cloacal swabs & visceral organs samples	**Identification of DPV isolates by AGIT, PHA test and PCR	Study did not control for other factors	*Independent blind assessment	4
5	Cha et al., 2013a	*Truly representative sample of bursa of Fabricious and other tissue samples	**Identification of duck Circovirus by PCR	Study did not control for other factors	*Independent blind assessment	3
6	Cha et al., 2013b	*Truly representative cloacal swabs and tissue swabs	*Identification of the *Salmonella* by isolation and testing by Latex test kit and API 20E	Study did not control for other factors	*Independent blind assessment	4
7	Cha et al., 2015	*Truly representative Pharyngeal and cloacal swabs	**Identification of Riemerella by PCR, API-20NE and API-ZYM tests	Study did not control for other factors	*Independent blind assessment	4
8	Chen et al., 2016	*Truly representative cloacal swabs and serum samples	**Identification of goose parvovirus-related parvovirus was detected by PCR, ELISA and IFA	Study did not control for other factors	*Independent blind assessment	3
9	Cong et al., 2012	*Truly representative blood samples	*Identification of *T. gondii* infection by MAT test	Study did not control for other factors	*Independent blind assessment	3
10	Das et al., 2005	*Truly representative samples of poultry birds	*Identification of Colibacillosis, Duck Cholera, DEV/DP, DHAV, Coccidiosis and Salmonellosis by post-mortem lesions and microscopic examination	Study did not control for other factors	*Independent blind assessment	4
11	Douglas et al., 2007	*Truly representative sample of cloacal swabs	**Identification of Avian Influenza virus and Newcastle disease virus by virus isolation and RT-PCR	Study did not control for other factors	*Independent blind assessment	4
12	El-Massry et al., 2000	*Truly representative serum samples	Identification of *T. gondii* infection by MAT test	Study did not control for other factors	*Independent blind assessment	3
13	Erfan et al., 2015	*Truly representative tissue samples	**Identification of DHAV by RT-PCR assays	Study did not control for other factors	*Independent blind assessment	4
14	Ferenczi et al., 2016	*Truly representative fecal samples	**Identification of Avian Influenza by PCR	Study did not control for other factors	*Independent blind assessment	4
15	Germundsson et al., 2010	*Truly representative cloacal and tracheal swabs	**Identification of Avian Influenza confirmed by RT-PCR	Study did not control for other factors	*Independent blind assessment	4
16	Ghersi et al., 2009	*Truly representative sample of fecal swabs	**Identification of Avian Influenza virus by virus isolation, antigen capture tests, Haemagglutination and RT-PCR	Study did not control for other factors	*Independent blind assessment	4
17	Gonzalez-Reiche et al., 2012	*Truly representative sample of cloacal and tracheal swabs	**Identification of Avian Influenza virus by RRT-PCR	Study did not control for other factors	*Independent blind assessment	3
18	Houque et al., 2011	*Truly representative tissue samples	*Identification of DEV/DP, Duck cholera, Colibacillosis, DHAV by microscopicexamination, biochemical test	Study did not control for other factors	*Independent blind assessment	4
19	Islam et al., 2009	*Truly representative tissue samples	**Identification of DEV/DP, Duck cholera, Coccidiosis, Colibacillosis and Salmonellosis by histo-pathological examinations and PCR	Study did not control for other factors	*Independent blind assessment	4
20	Jamali et al., 2014	*Truly representative tissue samples	*Identification of Listeriosis, Salmonellosis and Yersiniosis by API 20E, Kirby-Bauer disc diffusion method and USDA method	Study did not control for other factors	*Independent blind assessment	3
21	Jamali et al., 2015	*Truly representative tissue samples	*Identification of Campylobacteriosis by Kirby Bauerdisc diffusion method	Study did not control for other factors	*Independent blind assessment	4
22	Kalaiyarasu et al., 2016	*Truly representative sera, oral and cloacal swabs	*Identification of West Nile virus and Japanese encephalitis virus by ELISA and Virus Neutralization test	Study did not control for other factors	*Independent blind assessment	5
23	Kamomae et al., 2017	*Truly representative tissue samples	*Identification of DHAV Histological, Bacteriological and biochemical tests	Study did not control for other factors	*Independent blind assessment	4
24	Karki et al., 2014	*Truly representative serum samples	*Identification of Avian Influenza by IDEXX Influenza A Ab test kit	Study did not control for other factors	*Independent blind assessment	3

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Table 1 (*continued*)

Sl. No.	Author and year of publication	Selection		Comparability	Outcome	Overall
		Representativeness of the sample	Ascertainment of exposure		Assessment of outcome	Quality Assessment score
25	Karlsson et al., 2013	*Truly representative sample of cloacal and fecal swabs	**Identification of Avian Influenza virus by RRT-PCR	Study did not control for other factors	*Independent blind assessment	4
26	Khatun et al., 2013	*Truly representative cloacal swabs and serum samples	**Identification of Avian influenza by RT-PCR and ELISA	Study did not control for other factors	*Independent blind assessment	4
27	Li et al., 2017	*Truly representative tissue samples	**Identification of Goose parvovirus by RT-PCR and ELISA	Study did not control for other factors	*Independent blind assessment	4
28	Liu et al., 2010	*Truly representative serum and tissue samples	**Identification of Duck Circovirus by ELISA, PCR and Western Blot	Study did not control for other factors	*Independent blind assessment	4
29	Liu et al., 2018	*Truly representative tissue samples	**Identification of DHAV, Avian influenza, DEV/DP, Duck Parvovirus and Respiratory enteric orphan virus by PCR	Study did not control for other factors	*Independent blind assessment	3
30	Madsen et al., 2013	*Truly representative Serum, tracheal, and cloacal swabs	**Identification of Newcastle disease, Infectious laryngotracheitis, *M. gallisepticum* and *Salmonella* by PCR and ELISA	Study did not control for other factors	*Independent blind assessment	3
31	Mandal et al., 2017	*Truly representative tissue samples	**Identification of DEV/DP by PCR	Study did not control for other factors	*Independent blind assessment	5
32	Mbuko et al., 2010	*Truly representative serum and tissue samples	*Identification of Infectious Bursal Disease by Histological, and biochemical tests	Study did not control for other factors	*Independent blind assessment	4
33	Mishra et al., 2012	*Truly representative tracheal swabs, cloacal swabs, serum and tissue samples	**Identification of West Nile virus by ELISA and RT-PCR	Study did not control for other factors	*Independent blind assessment	5
34	Molia et al., 2017	*Truly representative blood samples	*Identification of NDV by ELISA	Study did not control for other factors	*Independent blind assessment	4
35	Mondal et al., 2008	*Truly representative cloacal swabs	*Identification of *Salmonella* by biochemical test	Study did not control for other factors	*Independent blind assessment	4
36	Montalvo-Corral et al., 2011	*Truly representative sample of cloacal and oropharyngeal swabs	**Identification of Avian Influenza virus by RRT-PCR	Study did not control for other factors	*Independent blind assessment	4
37	Neher et al., 2019	*Truly representative blood samples, cloacal andtracheal swabs	**Identification of DEV/DP by PCR	Study did not control for other factors	*Independent blind assessment	5
38	Ninvilai et al., 2019	*Truly representative tissue samples	**Identification of Duck Tembusu virus by RT-PCR	Study did not control for other factors	*Independent blind assessment	3
39	OIE report., 2015a	*Truly representative cloacal swabs and serum samples	*Identification of Avian Influenza by Antigen detection test.	Study did not control for other factors	*Independent blind assessment	5
40	OIE report., 2015b	*Truly representative cloacal swabs and serum samples	*Identification of Avian Influenza by Antigen detection test.	Study did not control for other factors	*Independent blind assessment	5
41	Rimondi et al., 2011	*Truly representative sample of cloacal swabs	**Identification of Avian Influenza virus by RRT-PCR	Study did not control for other factors	*Independent blind assessment	4
42	Slemons et al., 2003	*Truly representative cloacal swabs	*Identification of Avian influenza by virus isolation and typing of HA and NA genes	Study did not control for other factors	*Independent blind assessment	4
43	Soliman et al., 2015	*Truly representative tissue samples	**Identification of DHAV by RT-PCR assays	Study did not control for other factors	*Independent blind assessment	3
44	Spackman et al., 2006	*Truly representative sample of cloacal swabs	**Identification of Avian Influenza virus by RRT-PCR	Study did not control for other factors	*Independent blind assessment	4
45	Tarnagda et al., 2011	*Truly representative tracheal and cloacal swabs	**Identification of Infectious bronchitis and Newcastle disease virus by PCR	Study did not control for other factors	*Independent blind assessment	3
46	Wang et al., 2010	*Truly representative fecal samples	**Identification of *Cryptosporidium* by PCR	Study did not control for other factors	*Independent blind assessment	4
47	Wei et al., 2016	*Truly representative tissue samples	**Identification of *Campylobacter* by bacterial isolation and confirmation by PCR	Study did not control for other factors	*Independent blind assessment	4
48	Wille et al., 2016	*Truly representative fecal samples and cloacal swabs	**Identification of Avian Coronavirus by RT-PCR	Study did not control for other factors	*Independent blind assessment	4

Table 1 (continued)

Sl. No.	Author and year of publication	Selection		Comparability	Outcome	Overall Quality Assessment score
		Representativeness of the sample	Ascertainment of exposure		Assessment of outcome	
49	Wilson et al., 2013	*Truly representative serum samples and cloacal swabs	**Identification of Avian Influenza by RT-PCR and ELISA	Study did not control for other factors	*Independent blind assessment	4
50	Wojnarowicz et al., 2007	*Truly representative tissue samples	*Identification of West Nile virus by Histo-pathological Examination	Study did not control for other factors	*Independent blind assessment	3
51	Yang et al., 2012	*Truly representative serum samples	*Identification of *T. gondii* infection by MAT	Study did not control for other factors	*Independent blind assessment	4
52	Yeh et al., 2017	*Truly representative tissue samples	*Identification of *E. coli* infection by API 20E system	Study did not control for other factors	*Independent blind assessment	4
53	Yun et al., 2015	*Truly representative liver samples	*Identification of Novel Duck Reovirus by Western Blot	Study did not control for other factors	*Independent blind assessment	3
54	Zhang et al., 2011	*Truly representative serum samples	**Identification and confirmation of New castle disease by HA and HI test and RT-PCR	Study did not control for other factors	*Independent blind assessment	4
55	Zhao et al., 2013	*Truly representative cloacal swabs	**Identification and confirmation of Avian Influenza by HI test and RT-PCR	Study did not control for other factors	*Independent blind assessment	4

RT-PCR: Reverse Transcriptase Polymerase Chain Reaction; MAT: Modified agglutination test, IFA: Indirect Immunofluorescence Assay, (*) Stars represent the number of points awarded for the category; * = 1, ** = 2.

Table 2
Continent-wise stratification of studies.

Continent/Region with total prevalence	Country	Articles	Disease(s)/Infection
Asia (23%)	South Korea	Cha et al., 2013a, 2013b, 2015;Soliman et al., 2015Wei et al., 2016	Duck Circovirus, Salmonellosis, *Riemerella*, DHAV, Campylobacteriosis
	China	Wang et al., 2010 Zhang et al., 2011 Cong et al., 2012; Yang et al., 2012 Zhao et al., 2013 Yun et al., 2015; Chen et al., 2016 Yeh et al., 2017 Li et al., 2017Liu et al., 2010, 2018	Duck Parvovirus, *T. gondii*, Duck Parvovirus, Duck Circovirus, DHAV, Avian Influenza, DEV/DP, Respiratory enteric orphan virus, Cryptosporiodiosis, Colibacillosis, Duck Reovirus, Newcastle disease
	Nepal	Karki et al., 2014	Avian Influenza
	Japan	Kamomae et al., 2017	DHAV
	Bangladesh	Mondal et al., 2008Islam et al., 2009; Hoque et al., 2011; Khatun et al., 2013; Das et al., 2005; Ahmed et al., 2015	Colibacillosis, Duck Cholera, DEV/DP, DHAV, Coccidiosis, Salmonellosis, avian Influenza
	India	Mishra et al., 2012; OIE, 2015a, 2015b; Kalaiyarasu et al., 2016; Mandal et al., 2017; Neher et al., 2019	West Nile Virus, DEV/DP, Avian Influenza, West Nile Virus, Japanese encephalitis, DEV/DP
	Bangkok	Ninvilai et al., 2019	Duck Tembusu virus
	Iran	Jamali, et al., 2014, 2015	Listeriosis, Salmonellosis, Yersiniosis
	Malaysia	Adzitey et al., 2012aAdzitey et al., 2012bAhmed et al., 2015	Salmonellosis, Campylobacteriosis, DEV/DP
Europe (16%)	Norway	Germundsson et al., 2010	Avian Influenza
	Sweden	Wille et al., 2016	Avian Coronavirus
Africa (23%)	Mali	Molia et al., 2017	Newcastle disease
	Egypt	AboouLaila, 2011Erfan et al., 2015El-Massry et al., 2000	*T. gondii*, DHAV
	Burkina Faso	Tarnagda et al., 2011	Newcastle disease
	Nigeria	Mbuko et al., 2010	Infectious Bursal Disease
North America (29%)	Canada	Wojnarowicz et al., 2007	West Nile virus
	Maryland	Madsen et al., 2013Slemons et al., 2003	Avian Influenza Newcastle disease, *M. gallisepticum*, Infectious laryngotracheitis
	Alaska	Wilson et al., 2013	Avian Influenza
South America (2%)	Mexico	Montalvo-Corral et al., 2011	Avian Influenza
	West Indies	Douglas et al., 2007	Avian Influenza, Newcastle disease
	Peru	Ghersi et al., 2009	Avian Influenza
	Guatemala	Gonzalez-Reiche et al., 2012	Avian Influenza
	Columbia	Karlsson et al., 2013	Avian Influenza
	Argentina	Rimondi et al., 2011	Avian Influenza
	Bolivia	Spackman et al., 2006	Avian Influenza
Oceania (5.43%)	Australia	Ferenczi et al., 2016	Avian Influenza

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prevalent. Articles retrieved were from the countries belonged to Asia (9 countries), Europe (2 countries), Africa (4 countries), North America (3 countries), South America (7 countries), and Oceania (Australia) regions (Table 2). The pooled prevalence of duck diseases worldwide was found to be 20% (95%-CI: 15–26%), I^2 = 100%, and τ^2 value was 0.0990, p = 0 (Fig. 2). Continent-wise analysis of all duck diseases has revealed highest prevalence in North America 29% (95% CI = 13–49%) , followed by Asia 23% (95% CI = 16–31%) , Africa 23% (95% CI = 8–41%) , Europe 16% (95% CI = 10–25%) , Oceania 5.43% and South America 2% .(Fig. 3) The total number of studies included for *meta*-analysis was 55 with 438,518 samples for the period 2000–2019. The *meta*-analysis indicated that the heterogeneity was high between studies, I^2 = 100% (τ^2 = 0.0990 with P = 0), and hence the random effect model was considered. With the available reports on the prevalence of duck diseases from India, the pooled prevalence of various diseases of duck were also calculated. The prevalence rate of duck diseases reported in India during 2000–2019 was found to be 22% (95%-CI: 4–48%), with I^2 = 99% and τ^2 value 0.1357, p < 0.01 (Fig. 4).

3.2.1. Viral diseases

The prevalence avian influenza was 9% (95%-CI: 4–15%), I^2 = 100%, τ^2 value was 0.0387p = 0 (Fig. 5), Meanwhile, studies on duck tembusu virus infection revealed a prevalence of 23% (95%-CI: 18–28%) in Bangkok. Whereas, prevalence of Newcastle Disease was found to be 23% (95%-CI: 7–46%), I^2 = 97%, τ^2 value was 0.0737, p < 0.01 (Fig. 6). Prevalence of West Nile virus infection was found to be 13% (95%-CI: 0–40%), I^2 = 97%, τ^2 value was = 0.0725, p < 0.01 as shown in Fig. 7. Two articles of duck circovirus from South Korea and China showed 52% (95%-CI: 3–98%) prevalence (Fig. 8). Duck parvovirus infection from China (3 articles) revealed a prevalence of 49% (95%-CI: 2–97%) (Fig. 9), whereas the duck hepatitis A virus infection showed a prevalence of 28% (95%-CI: 3–63%) (Fig. 10). In the case of duck plague infection in Asian countries showed a prevalence of 35% (95%-CI: 14–59%) (Fig. 11). A single article on Japanese encephalitis from India showed a 10% prevalence (95%-CI: 6–15%). Infectious bursal disease and infectious laryngotracheitis showed a prevalence estimate of 6% (95%-CI: 3–9%) and 52% (95%-CI: 7–94%) respectively.
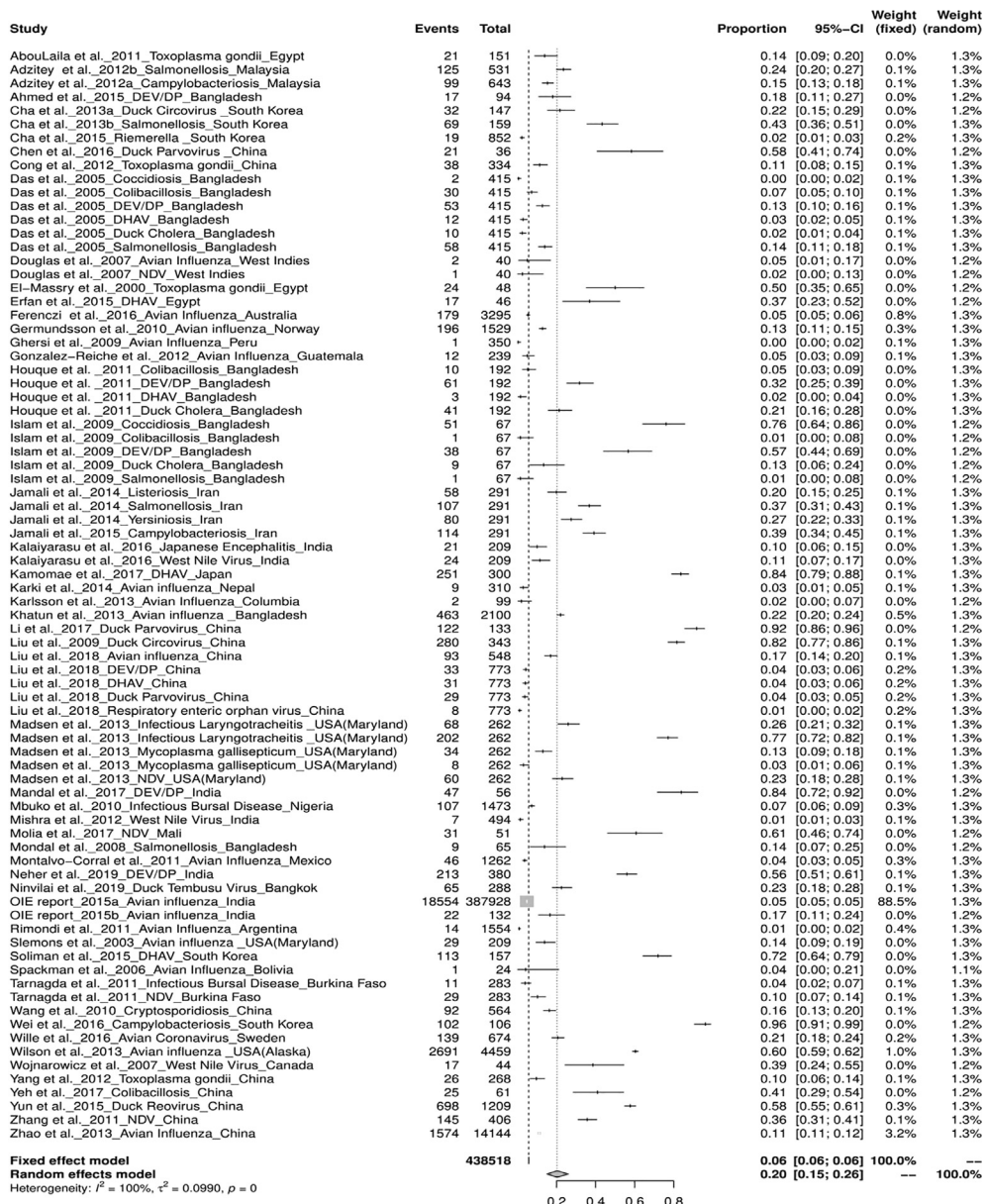

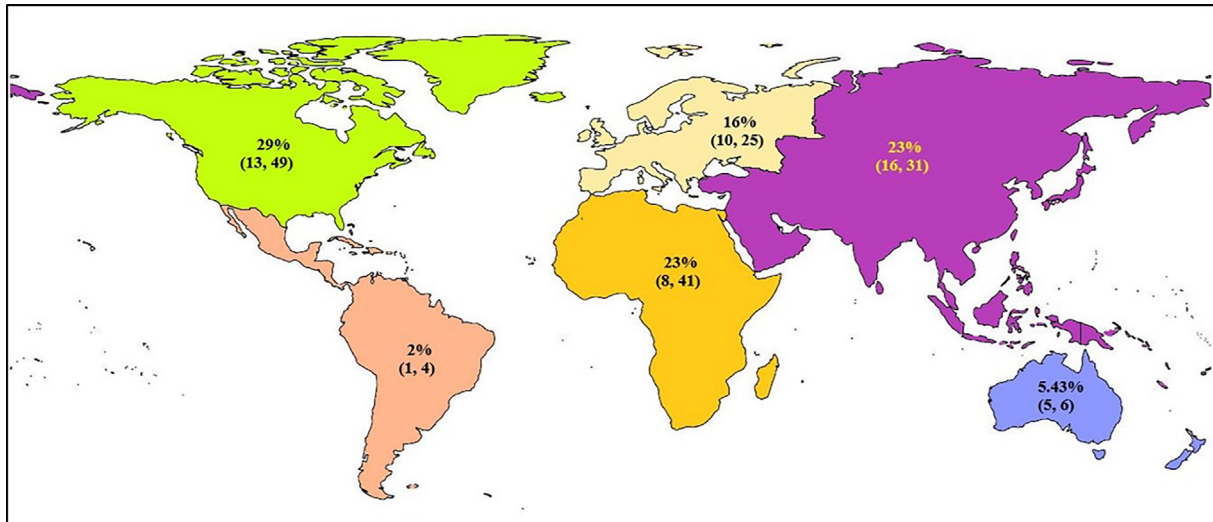Fig. 2. Forest plot of prevalence of duck diseases world-wide.

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Fig. 3. Continent-wise pooled prevalence of infectious disease of ducks. Figures in bracket indicate the range at 95% Confidence Interval.
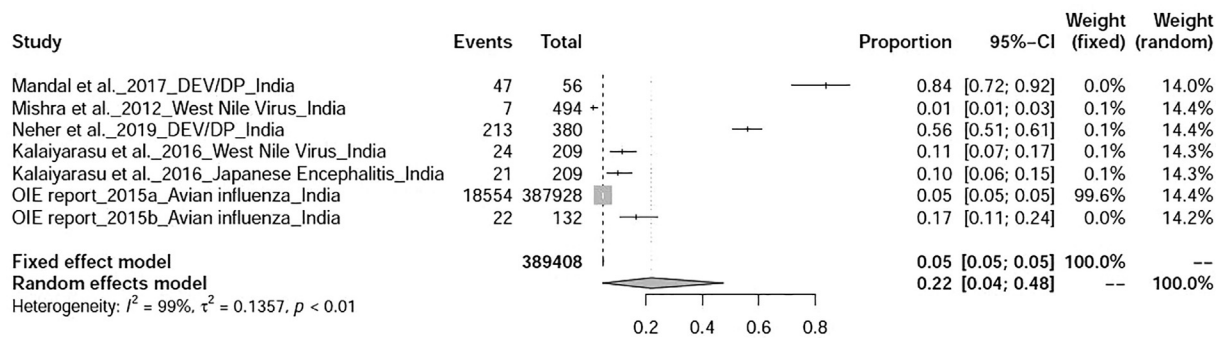

Fig. 4. Forest plot of pooled prevalence of duck diseases in India.
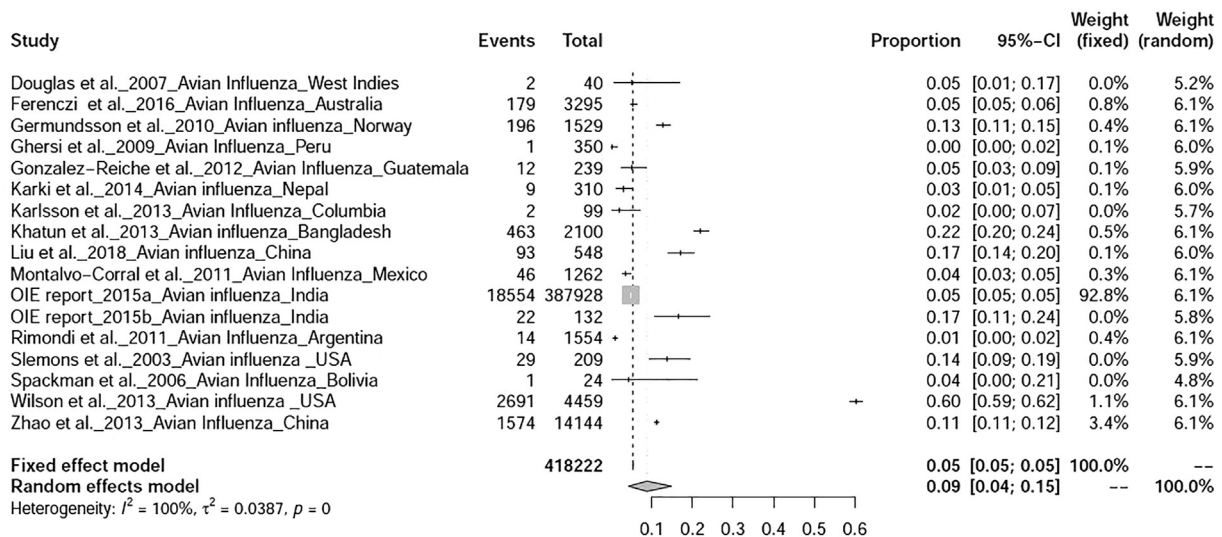

Fig. 5. Forest plot of prevalence of avian influenza.

Duck respiratory enteric orphan virus infection and duck reovirus infection, both articles from China showed a prevalence of 1% and 58% respectively, while avian coronavirus infection showed 21% prevalence in ducks from Sweden.

3.2.2. Bacterial diseases

Six bacterial diseases of ducks were analysed in this study. Prevalence of salmonellosis in ducks was found to be 20% (95%-CI: 8–35%) with heterogeneity I^2 = 96%, τ^2 value was 0.0432,
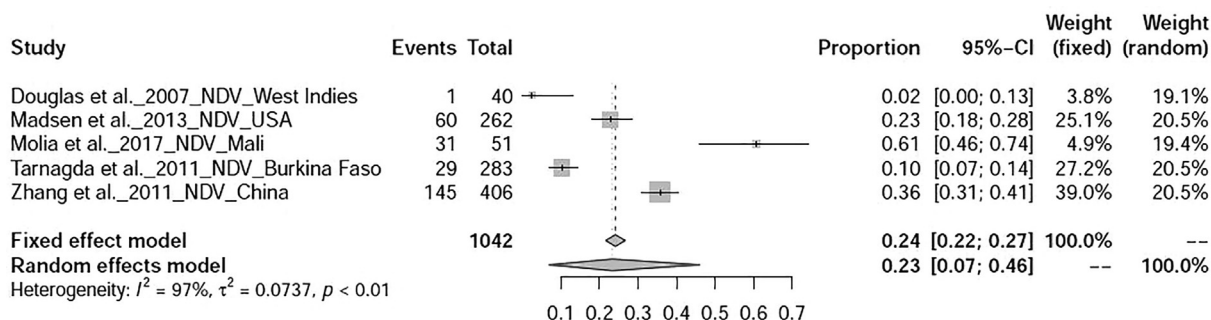
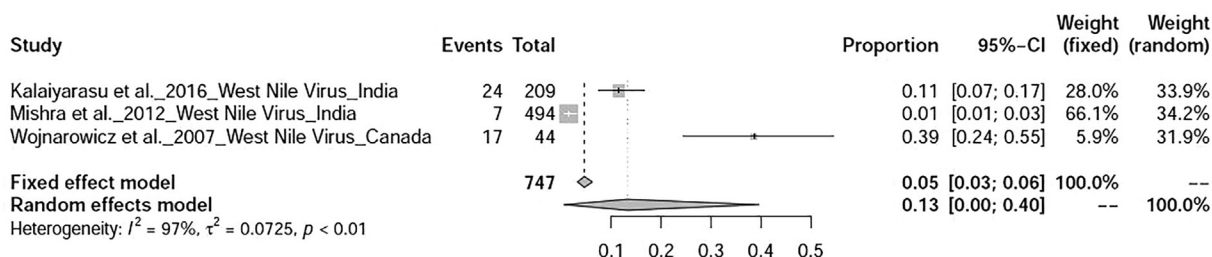**Fig. 6.** Forest plot of prevalence of Newcastle disease.

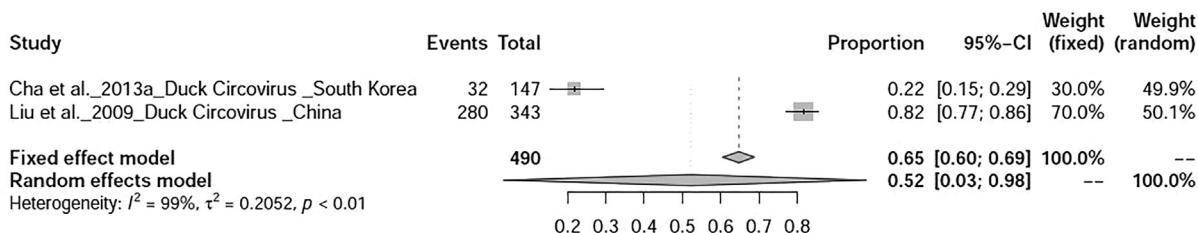**Fig. 7.** Forest plot of prevalence of West Nile fever infection.

Fig. 8. Forest plot of prevalence of duck circovirus infection.
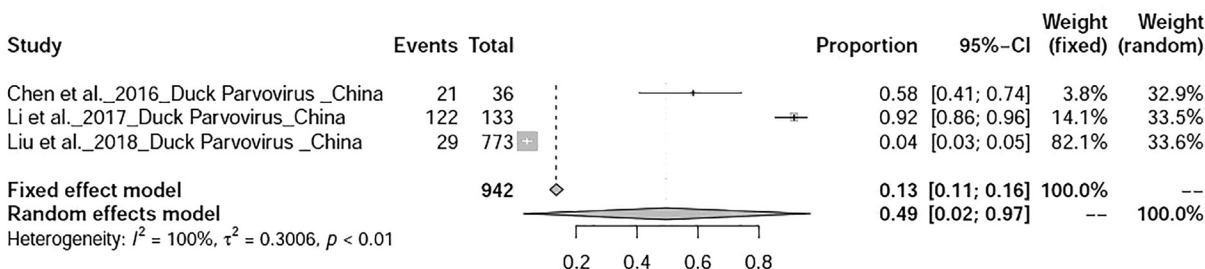

Fig. 9. Forest plot of prevalence of duck parvovirus infection.

$p < 0.01$ (Fig. 12), whereas duck campylobacteriosis showed prevalence of 53% (95%-CI: 6–97%) with heterogeneity $I^2 = 99\%$, τ^2 value was 0.2493, $p < 0.01$ (Fig. 13). Duck colibacillosis revealed the prevalence of 10% (95%-CI: 1–29%) with heterogeneity $I^2 = 94\%$, τ^2 value was 0.0579, $p < 0.01$ (Fig. 14). A total of three articles on duck cholera reported from Bangladesh showed a prevalence of 11% (95%-CI: 2–25%) with heterogeneity $I^2 = 97\%$, τ^2 value was 0.0273, $p < 0.01$ (Fig. 15). Prevalence of duck *Mycoplasma gallisepticum* infection was found to be 7% (95%-CI: 1–20%). Prevalence of a single study on three bacterial diseases viz., *Riemerella* infection, listeriosis, and yersiniosis was found to be 2%, 20%, and 27% respectively.

3.2.3. Parasitic diseases

Two studies on parasitic diseases of ducks were selected in this study viz., toxoplasmosis, and coccidiosis whose prevalence was found to be 17% (95%-CI: 6–31%) and 29% (95%-CI: 0–1%) respectively (Figs. 16-17).

To assess the heterogeneity between-study reports, a Galbraith plot was generated (Fig. 18). The standardized effect estimates against inverse standard error were shown as scattered points in the plot. The points representing the study reports outside confidence bounds may be contributing to the heterogeneity. In the absence of heterogeneity, all points (reports) are expected to lie within the confidence limits centring around the line.
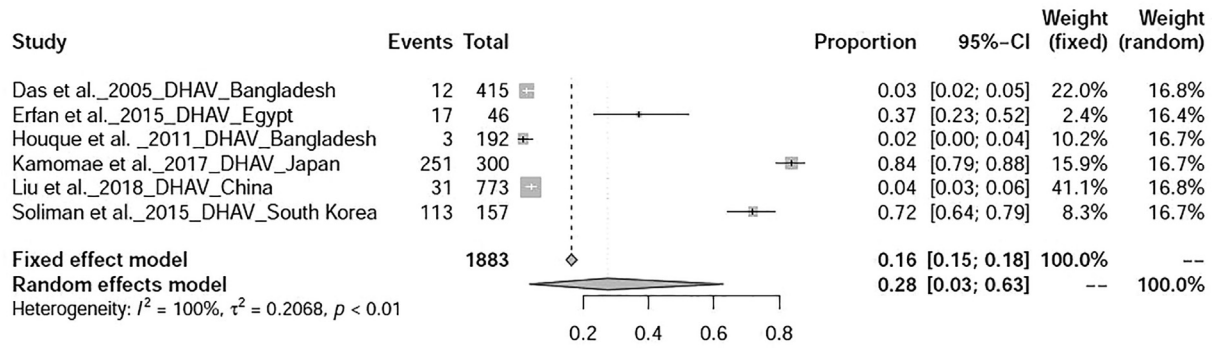
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Study	Events	Total		Proportion	95%-CI	Weight (fixed)	Weight (random)
Das et al._2005_DHAV_Bangladesh	12	415		0.03	[0.02; 0.05]	22.0%	16.8%
Erfan et al._2015_DHAV_Egypt	17	46		0.37	[0.23; 0.52]	2.4%	16.4%
Houque et al. _2011_DHAV_Bangladesh	3	192		0.02	[0.00; 0.04]	10.2%	16.7%
Kamomae et al._2017_DHAV_Japan	251	300		0.84	[0.79; 0.88]	15.9%	16.7%
Liu et al._2018_DHAV_China	31	773		0.04	[0.03; 0.06]	41.1%	16.8%
Soliman et al._2015_DHAV_South Korea	113	157		0.72	[0.64; 0.79]	8.3%	16.7%
Fixed effect model		1883		0.16	[0.15; 0.18]	100.0%	--
Random effects model				0.28	[0.03; 0.63]	--	100.0%
Heterogeneity: I^2 = 100%, τ^2 = 0.2068, p < 0.01							

Fig. 10. Forest plot of prevalence of duck hepatitis A virus infection.

Study	Events	Total		Proportion	95%-CI	Weight (fixed)	Weight (random)
Ahmed et al._2015_DEV/DP_Bangladesh	17	94		0.18	[0.11; 0.27]	4.8%	14.2%
Das et al._2005_DEV/DP_Bangladesh	53	415		0.13	[0.10; 0.16]	21.0%	14.5%
Houque et al. _2011_DEV/DP_Bangladesh	61	192		0.32	[0.25; 0.39]	9.7%	14.4%
Islam et al._2009_DEV/DP_Bangladesh	38	67		0.57	[0.44; 0.69]	3.4%	14.1%
Liu et al._2018_DEV/DP_China	33	773		0.04	[0.03; 0.06]	39.1%	14.5%
Mandal et al._2017_DEV/DP_India	47	56		0.84	[0.72; 0.92]	2.8%	14.0%
Neher et al._2019_DEV/DP_India	213	380		0.56	[0.51; 0.61]	19.2%	14.5%
Fixed effect model		1977		0.20	[0.18; 0.22]	100.0%	--
Random effects model				0.35	[0.14; 0.59]	--	100.0%
Heterogeneity: I^2 = 99%, τ^2 = 0.1071, p < 0.01							

Fig. 11. Forest plot of prevalence of duck plague.

Study	Events	Total		Proportion	95%-CI	Weight (fixed)	Weight (random)
Adzitey et al._2012b_Salmonellosis_Malaysia	125	531		0.24	[0.20; 0.27]	34.8%	17.2%
Cha et al._2013b_Salmonellosis_South Korea	69	159		0.43	[0.36; 0.51]	10.4%	16.8%
Das et al._2005_Salmonellosis_Bangladesh	58	415		0.14	[0.11; 0.18]	27.2%	17.1%
Islam et al._2009_Salmonellosis_Bangladesh	1	67		0.01	[0.00; 0.08]	4.4%	16.0%
Jamali et al._2014_Salmonellosis_Iran	107	291		0.37	[0.31; 0.43]	19.0%	17.0%
Mondal et al._2008_Salmonellosis_Bangladesh	9	65		0.14	[0.07; 0.25]	4.3%	15.9%
Fixed effect model		1528		0.23	[0.21; 0.25]	100.0%	--
Random effects model				0.20	[0.08; 0.35]	--	100.0%
Heterogeneity: I^2 = 96%, τ^2 = 0.0432, p < 0.01							

Fig. 12. Forest plot of prevalence of salmonellosis.

Study	Events	Total		Proportion	95%-CI	Weight (fixed)	Weight (random)
Adzitey et al._2012a_Campylobacteriosis_Malaysia	99	643		0.15	[0.13; 0.18]	61.8%	33.4%
Jamali et al._2015_Campylobacteriosis_Iran	114	291		0.39	[0.34; 0.45]	28.0%	33.4%
Wei et al._2016_Campylobacteriosis_South Korea	102	106		0.96	[0.91; 0.99]	10.2%	33.2%
Fixed effect model		1040		0.30	[0.27; 0.33]	100.0%	--
Random effects model				0.53	[0.06; 0.97]	--	100.0%
Heterogeneity: I^2 = 99%, τ^2 = 0.2493, p < 0.01							

Fig. 13. Forest plot of prevalence of campylobacteriosis.

4. Discussion

Information on the world duck population is very scanty in general and reports on disease prevalence is very less in particular. As per FAO, 2017 there were 1.15 billion ducks (*Anas* spp.) worldwide and 1.0 billion (88 percent) were in Asia. The largest duck populations are found in China, Vietnam, Bangladesh, and Indonesia FAO, 2017). India has 33.5 million of ducks and the majority of them are domesticated in the northeast including the West Bengal state of India. Duck farming is becoming a popular one and is usually

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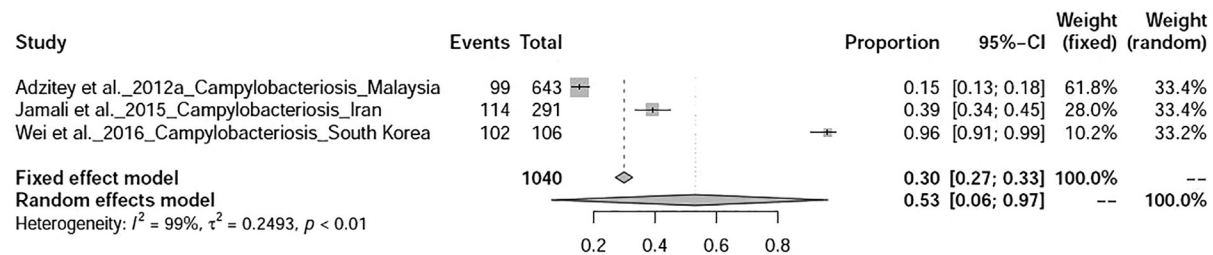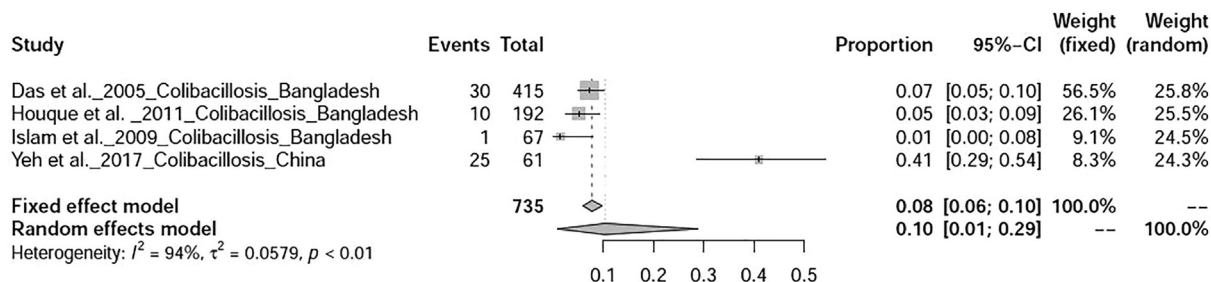*Saudi Journal of Biological Sciences 28 (2021) 5131–5144*

Fig. 14. Forest plot of prevalence of Colibacillosis.
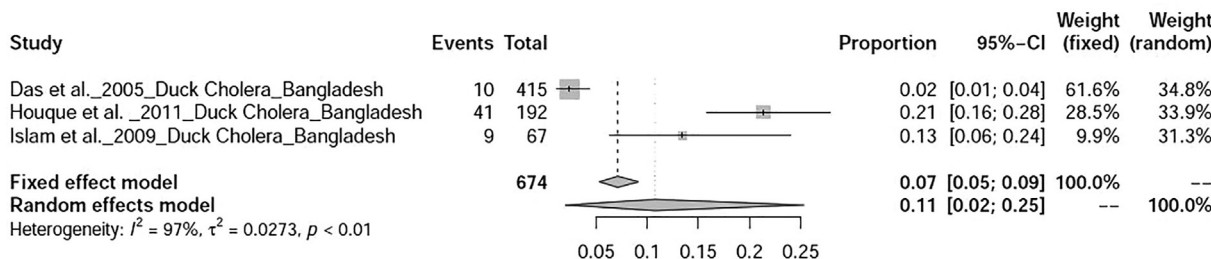

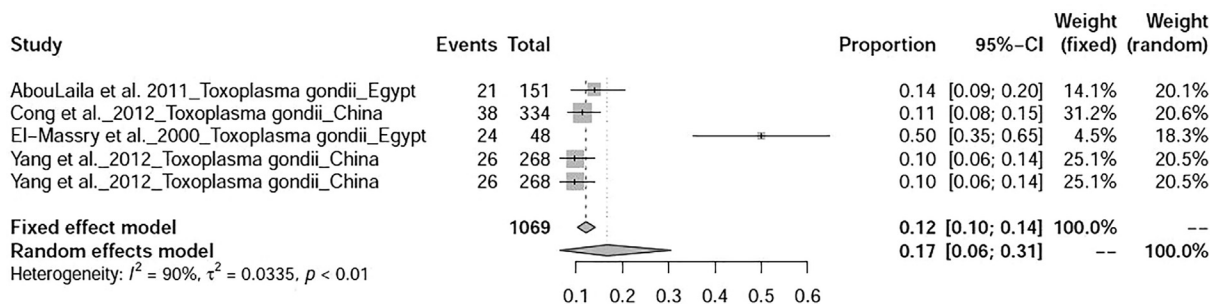**Fig. 15.** Forest plot of prevalence of duck cholera.

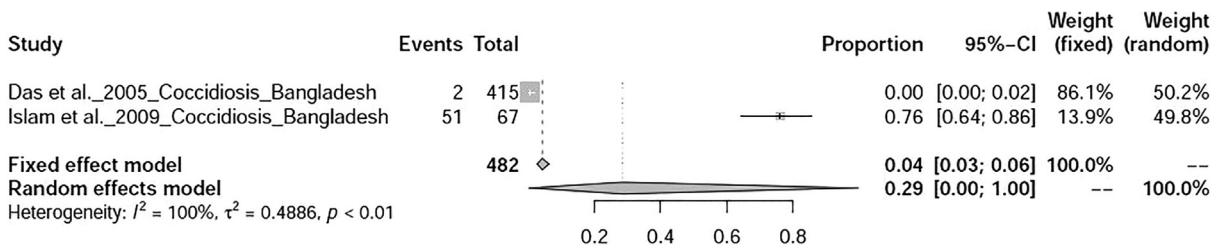**Fig. 16.** Forest plot of prevalence of *T. gondii*.

Fig. 17. Forest plot of coccidiosis.

practiced by economically disadvantaged people of the society in some countries. Duck meat contributes to food security in low and middle-income countries. Vast majority of the ducks are raised in households or subsistence-based production system (backyard or small flocks) There are no systematic reports of the occurrence of infectious diseases in ducks in India and elsewhere. Hence the efforts were made to gather information on prevalence of duck disease available in public domains. The information on duck diseases was reviewed and analysed using different statistical tools/methods including *meta*-analysis. A *meta*-analysis combines the results from two or more studies conducted by different individuals to

provide a single value with high statistical power. In the present study, a systematic review of scientific publications on the prevalence of duck diseases was conducted for 19 years (2000–2019). After the screening of articles, data was extracted from 55 cross-sectional studies published in peer-reviewed journals that reported the prevalence of various duck diseases, reviewed systematically, and conducted a *meta*-analysis. Meta-analysis showed high heterogeneity, I = 100%, τ^2 = 0.0990 indicating a true heterogeneity among the studies. Further, asymmetry in the funnel plot showed heterogeneity of studies since very few studies on the pre-
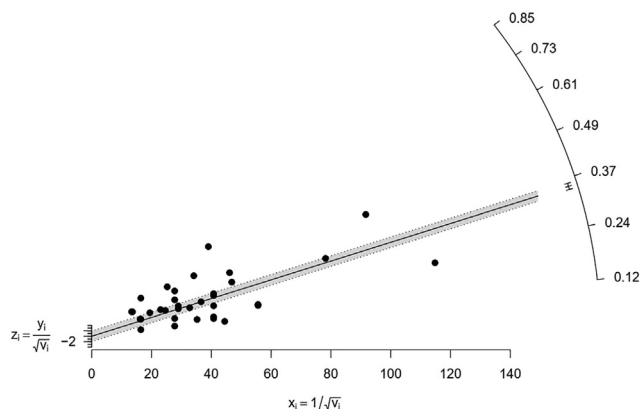
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Fig. 18. Galbraith Plot showing heterogeneity between-study reports.

valence of different duck diseases were available in a limited number of countries within the continents.

In the present study, articles on the prevalence of infectious diseases of duck in different countries between 2000 and 2019 were analysed. The reports were scanty. The continent-wise analysis revealed a diversified prevalence of duck diseases. In the Asian continent (23% prevalence), China reported the majority of duck diseases that may be due to the highest population of ducks in that country, followed by India, Bangladesh, South Korea, Malaysia, Bangkok. India and Bangladesh have reported a maximum of duck diseases. West Bengal and Assam states of India shares border with Bangladesh which is porous in nature. There is no restriction of movement of men and materials hence there are possibilities of transboundary movement of ducks without proper health records in these borders. Meanwhile, only one report per country was retrieved from Nepal, Japan, and Iran. The articles from Norway and Sweden reporting on the prevalence of Avian influenza in ducks were from Europe (16% prevalence). In Africa (23% prevalence), reports on the prevalence of duck diseases were from Mali, Egypt, Burkina Faso, and Nigeria. North America reported a 29% prevalence of duck diseases from Canada, Maryland, and Alaska, whereas South America including Latin America reported a 2% prevalence of duck diseases from Peru, Columbia, Argentina, Bolivia, Mexico, Guatemala, and West Indies. There was only a report on prevalence (5.43%) of avian Influenza from Australia (Oceania continent).

During 2000–2007, duck diseases were under reported and gradually a number of reports on disease prevalence showed an increasing trend from 2008 to 2015 that may be due to adoption of more precise tools in disease diagnosis (Fig. 19), thereafter a declining trend was observed 2016 onwards that may be due to better health care management.

From the analysis, it is evident that the viral disease remains predominant when compared to bacterial, and parasitic infections. It was found that the viral disease incidence is highly concentrated towards the eastern countries such as China, Korea, Japan and Bangladesh. This may be due to the robust disease reporting system available. However, under reporting of the disease is one of the major drawbacks. During our study, we observed that the reports of duck disease are very scanty which causes the poor availability of previous references. This causes hindrance in evaluating out a strategic plan to control the diseases.

Despite being an important factor in the poultry industry, duck diseases often tend to bring great economic loss to the farmers. Hence, it is important to take precautionary measures by vaccination, better health management practices and also other farm related biosecurity procedures to avoid infections.

Further to *meta*-analysis, barring selection bias, systematic reviews helps the revision of all the scientific evidence on a given topic. Based on the output, the summarized information can be used to propose hypotheses that explain the behaviour of the data and to identify areas of gaps where further research is needed (Afanador-Villamizar et al., 2017; Moher et al., 2010). However, it is a controversial tool because several conditions are critical and even small violations of these can lead to misleading conclusions. While designing and performing a *meta*-analysis, several decisions concerning personal judgment and expertise need to be made that may eventually create bias or expectations that influence the result (Greco et al., 2013).

5. Conclusion

This *meta*-analysis indicated that pooled prevalence of various duck diseases worldwide during the period 2000–2019 was found to be 20% (95% CI = 15–26%) and the pooled prevalence estimate for India was found to be 22% (95% CI: 4–48%) which might be due to increased reporting of duck disease during recent years using precise tools for disease diagnosis. Concerning viral diseases, it was observed that the disease occurrence was concentrated towards the Asian subcontinent especially countries like India,
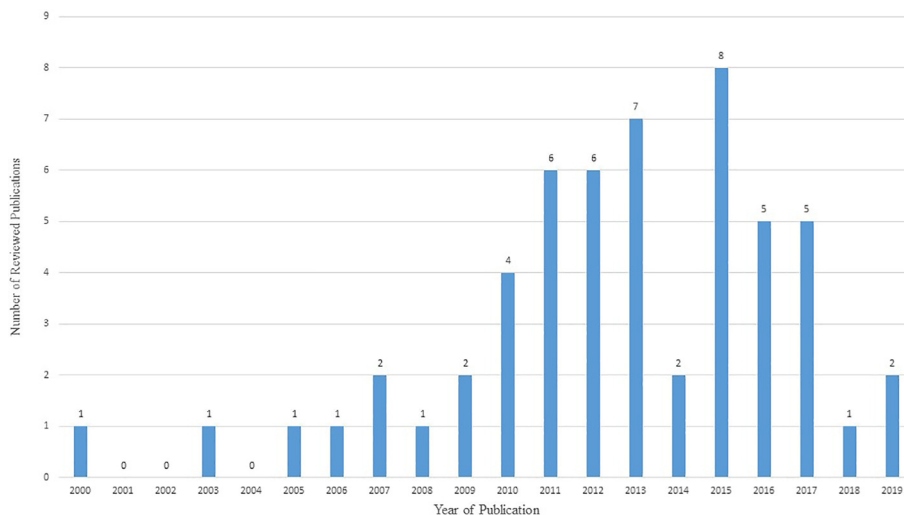

Fig. 19. Details of year-wise number of publications reviewed in the study.

China, and Korea as they have a high number of ducks. Among the viral diseases reported, Avian Influenza was found to be the most predominant followed by Duck Plague and Duck Hepatitis Viral Infections. In the case of bacterial infections in ducks, Salmonellosis was the most prevalent in Bangladesh, North Korea, China, and Malaysia. Among Parasitic diseases, *Toxoplasma gondii* infection was found to be most prevalent in China. Very little information is available concerning parasitic infection of ducks. Although there is an increase in the total duck population, India still faces a high threat of economic loss due to infectious diseases. Furthermore, awareness amongst farmers about disease reporting to their nearest veterinary doctors, following prevention, control measures, and biosecurity practices can drastically help to reduce duck mortality.

Ethical approval

Not applicable as the study utilised the published data available in the web.

7. Data availability statement

Not applicable since the data used in this study was from peer-reviewed published articles and are available in the public domain for which DOI is mentioned against each reference.

Funding

Not applicable since the entire study utilised the published data available in the internet.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Appendix A. Supplementary material

Supplementary data to this article can be found online at https://doi.org/10.1016/j.sjbs.2021.05.034.

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