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Epidemiological status of bovine viral diarrhea virus in water buffalo (*Bubalus bubalis*): A global systematic review and meta-analysis

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ABSTRACT

Bovine viral diarrhea virus (BVDV) remains a neglected viral disease in water buffalo despite its significant economic impact in production systems. Although limited epidemiological studies have been reported worldwide, the serostatus and active infection in buffalo have not been systematically reviewed. A systematic review and meta-analysis were conducted to estimate BVDV prevalence in water buffalo and identify associated epidemiological factors. Relevant studies published up to January 31, 2026, were retrieved from five electronic databases. A total of 49 studies were identified from 15 different countries were found for inclusion. A random-effects model was used to estimate pooled-prevalence and assess heterogeneity among studies. A meta-analysis of 37 studies (9270 buffalo) estimated a pooled BVDV seroprevalence of 30.5%, while analysis of 16 studies (7189 animals) indicated an antigen prevalence of 16.5%. Continent-wise analysis revealed the highest BVDV seroprevalence in South-America (44.0%), while antigen prevalence was highest in Africa (21.2%) followed by Asia at 12.2%, and no BVDV data reported from North-America. Among the different countries, the highest BVDV seroprevalence was detected in Turkey (61.6%) and Argentina (59.0%), while antigen prevalence was highest in Egypt (21.2%), with lower estimates in Brazil (11.8%) and Iraq (11.3%). Notably, high heterogeneity ($I^2 > 90\%$) was observed in the all-pooled estimates, indicating variations in sampling period, age, sex, sample source and types, diagnostic methods, production-system, and study quality. These findings demonstrate the widespread presence of BVDV in water buffalo populations and indicate the need for targeted control strategies to mitigate its impact on health and productivity.

1. Introduction

Bovine viral diarrhea virus (BVDV) is a globally distributed pestivirus of the family *Flaviviridae* that causes significant economic losses in food animal production. BVDV belongs to the genus *Pestivirus* within the family *Flaviviridae* and possesses a positive-sense single-stranded RNA (ssRNA) genome. Under the previous nomenclature, *Pestivirus* species were designated as *Pestivirus A* (BVDV-1), *Pestivirus B* (BVDV-2), and *Pestivirus H* (HoBi-like pestivirus or BVDV-3) (Smith et al., 2017). However, based on genomic characteristics, antigenic relatedness, and host origin, International Committee on Taxonomy of Viruses (ICTV), revised the classification, and bovine pestiviruses are currently nomenclature as BVDV-1 (*Pestivirus bovis*), BVDV-2 (*Pestivirus tauri*), and HoBi-like virus (*Pestivirus brazilense*) (ICTV, 2025). Each species comprises multiple genetically diverse subgenotypes, with BVDV-1 consisting of 24 subgenotypes (1a–1×), BVDV-2 comprising five subgenotypes (2a–2e), and HoBi-like virus including four subgenotypes (BVDV-3a–3d) (Rana et al., 2025a; Rivas et al., 2022). These subgenotypes contribute to the virus's complex epidemiology and its variable pathogenicity across different hosts, ranging from acute clinical disease to subclinical or asymptomatic infection (Rana et al., 2026; Walz et al., 2010). Furthermore, BVDV exists in two biotypes, cytopathic and non-

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cytopathic (Walz et al., 2010). The cytopathic biotype is associated with life-threatening mucosal disease (MD), while the non-cytopathic biotype establishes persistent infections (PI) in various hosts (Rivas et al., 2022; Walz et al., 2010). Although cattle are the primary and natural host, BVDV can infect a wide range of domestic and wild mammals, including buffalo, sheep, goats, deer, yaks, bison, camels, llamas, and pigs (Rana et al., 2025b; Hause et al., 2021; Deng et al., 2015; Tao et al., 2013; Wentz et al., 2003). The virus causes diverse clinical conditions, ranging from asymptomatic infections to severe acute illness, including diarrhea, respiratory symptoms (like pneumonia), reproductive disorders (such as early embryonic death, abortion, stillbirth, foetal mummification, and teratogenicity), immunosuppression (leukopenia), and significant reduction in milk and meat production (Deng et al., 2015; Passler, 2014). PI animals can harbour the virus for prolonged periods without producing protective antibodies, thereby serving as a continuous source of infection and hindering effective prevention and control measures (Lindberg and Houe, 2005).

Water buffalo (*Bubalus bubalis*) is a major ruminant livestock species with a global population estimated at approximately 200–205 million head, contributing substantially to milk, meat, and leather production, supporting the livelihoods of millions of people, particularly in Asia and Africa (Food and Agriculture Organization of the United Nations (FAO), 2024; Deb et al., 2016). Buffalo farming boosts agricultural income, protects food security, and plays a crucial role in rural economic development in major buffalo-rearing countries such as India, Pakistan, Nepal, and Bangladesh (Deb et al., 2016; Gul et al., 2018). Buffalo are often considered less susceptible to overt clinical disease than other bovine species, as BVDV infection in buffalo is frequently mild or subclinical (Rana et al., 2025a; Deng et al., 2015). However, it has been documented that BVDV infection can cause reproductive disorders, including reduced fertility and abortion, as well as calf mortality, representing its impact on the health and productivity of buffalo herds (Martucciello et al., 2009). Water buffalo, often inhabiting semi-wild and wild ecosystems, may serve as important reservoirs of BVDV, facilitating viral persistence and transmission at the wildlife–livestock interface (Glidden et al., 2021). In addition, infected buffalo may act as carrier, contributing to virus circulation and posing a significant risk for cross-species transmission in mixed farming systems (Deng et al., 2015; Rana et al., 2025b). Moreover, water buffalo may act as secondary hosts, possibly due to conserved host receptor and virus interactions as well as cellular tropism that may facilitate BVDV infection (Rana et al., 2025b). BVDV poses a significant, often overlooked threat to the profitability and sustainability of buffalo farming, largely due to gaps in current knowledge of ongoing epidemics and limited understanding of effective control strategies. The epidemiological status of BVDV in water buffalo, including its distribution, infection status, genetic diversity, and associated management factors affecting production and reproductive performance, remains poorly characterized compared with cattle. Therefore, conducting systematic epidemiological studies on BVDV infection in buffalo, including comprehensive global, regional, and country-level pooled prevalence estimates, associated factors, and diagnostic approach are crucial for effective management and control measure worldwide. Due to the limited number of epidemiological studies on BVDV infection in water buffalo, this study integrates seroprevalence and antigen data with temporal distribution, animal demographic information, and production and management factors. These data are used to delineate the current infection status and epidemiological scenario, and to identify potential factors contributing to the spread of BVDV in buffalo-dense areas. To the best of the authors' knowledge, no systematic review and meta-analysis on the prevalence of BVDV in buffalo populations across countries has been conducted. Therefore, this review aimed to investigate BVDV infections in buffalo globally and conduct a meta-analysis to estimate pooled seroprevalence and antigen (active infection) prevalence based on published studies and evaluate potential variables influencing the variability of BVDV prevalence in water buffalo.

2. Materials and methods

2.1. Literature search and retrieval strategy

The systematic review and meta-analysis were conducted following PRISMA guidelines (Preferred Reporting Items for Systematic Reviews and Meta-Analyses) (Fig. 1). The PRISMA 2020 checklist was used to ensure standards across all sections, including the inclusion and exclusion criteria and quality assessment of relevant information (Supplementary File 1).

A systematic electronic search strategy was followed using five electronic databases: PubMed, Scopus, Science Direct, Web of Science and Google Scholar, with no time limitation, up to 31st January 2026 (Fig. 1). Predefined Boolean keywords and database-specific search strategies were used in various combinations for the initial screening of relevant articles across different databases, as presented in Table 1. Optimized keywords and search terms were adjusted to organize and avoid duplicate retrieval of articles across different search databases. The first author (EAR) independently performed the literature searches and retrieved all relevant studies. The reference lists of primarily extracted articles were searched individually in Google Scholar in three times to identify additional potential articles and ensure that the database search did not miss any relevant published reports. The overall study selection process for systematic review is illustrated in the PRISMA flowchart (Fig. 1).

2.2. Literature screening using inclusion and exclusion criteria

The published articles retrieved from five databases were assessed carefully by three authors (EAR, MSI, and BH). The titles and abstracts of articles relevant to BVDV infection in buffalo were screened and duplicate articles were removed manually as well as using the reference management software EndNote 21 (Clarivate Analytics, Murdoch University, WA). Any uncertainties or discrepancies that arose during the inclusion and exclusion of studies were discussed among all authors and specialists until a plenary solution or consensus was achieved.

The inclusion criteria were: (i) articles on BVDV infection or exposure in water buffalo and studies that included water buffalo as a sample population; (ii) studies estimating antigen prevalence or seroprevalence as a percentage, and/or reporting the total number of buffalo tested and the number of animals that tested BVDV positive; (iii) only original cross-sectional, and longitudinal studies; (iv) studies that diagnosed BVDV based on serological and molecular tests; (v) studies reporting results from any geographical area; and vi) full-text articles that were published in the English language (to ensure consistent data extraction, reliable interpretation, and uniform quality assessment). Subsequently, the exclusion criteria were: (i) studies not conducted on buffalo populations; (ii) studies reporting BVDV prevalence specifically in African buffalo (*Syncerus caffer*); (iii) studies in which prevalence data were not reported; (iv) case reports or studies describing only post-mortem findings or virus isolation and genetic diversity; (v) studies involving buffalo herds with a history of experimental trials; (vi) previous review articles; and (vii) non-English language articles.

2.3. Data curation

Based on inclusion and exclusion criteria, data from eligible studies were extracted and recorded in a spreadsheet as follows: the first author, year of publication, study period, location of the study (continent/country), study design, diagnostic technique, total number of tested buffalo and the number of BVD-positive buffalo, prevalence, production system, reported confirmed pestivirus species, study quality score and quality level (Table 2).

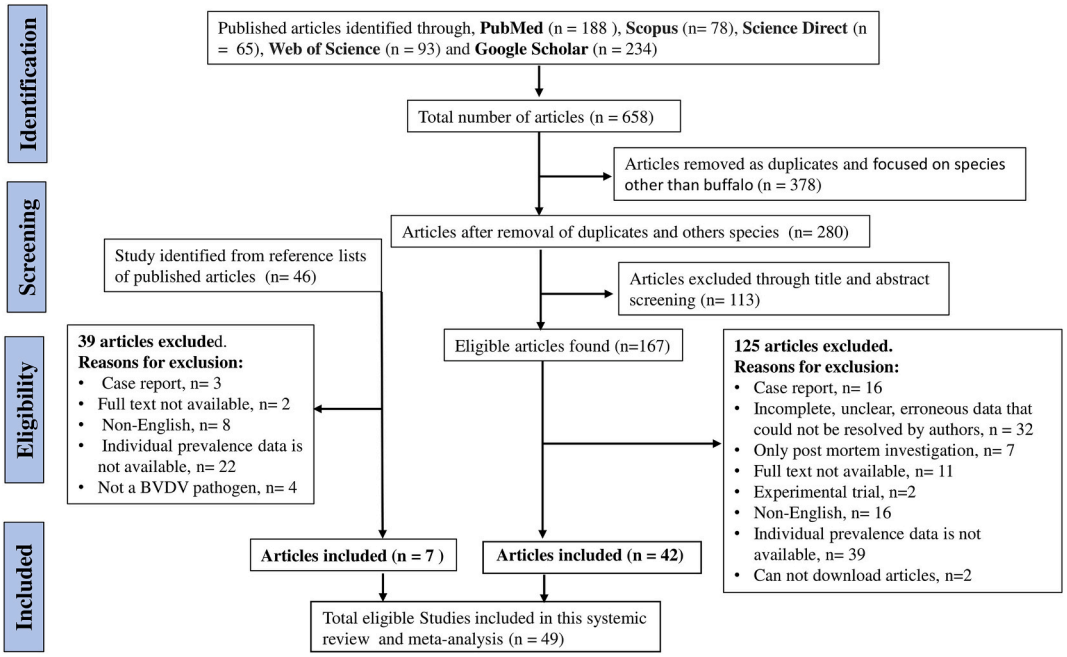


Fig. 1. The PRISMA flowchart illustrates the literature search and screening process, showing the inclusion and exclusion of articles analyzed in this systematic review and meta-analysis.

2.4. Quality assessment of the eligible studies

All eligible studies were subjected to quality assessment for reporting and selection bias using the standard Joanna Briggs Institute (JBI) Critical Appraisal checklist for prevalence studies, as described by Munn et al., 2015. The quality of each article was graded by using a scoring system based on a checklist with "yes", "no", "unclear", or "not applicable" options for each selected variable. Two authors (EAR and MSI) independently assessed and scored all of the articles, where a "yes" answer for each parameter was allocated a score of 1, whereas "no", "unclear", or "not applicable" responses were assigned a score of 0 (Supplementary Table 1). A total score was then calculated considering nine different parameters for each article and categorized as follows: low quality =1–3; moderate quality = 4–6; and high quality = 7–9 (Supplementary Table 1 and Fig. 1). The low-scored articles that met our minimum inclusion criterion were also included in the meta-analysis, although they may not provide complete information for subsequent analyses.

2.5. Statistical analysis

All selected relevant data were extracted and stored in a Microsoft Excel-2010 spreadsheet.

The pooled seroprevalence and antigen (virological) prevalence of BVDV infection in water buffalo, with 95% confidence intervals (CI) were calculated using a random effect weighted meta-analysis model with the restricted maximum likelihood (REML) estimation in STATA version 18.0 software (StataCorp LP, College Station, Texas, USA). Freeman–Tukey double arcsine transformation was applied during proportion meta-analysis to stabilize variance, particularly for studies reporting extreme prevalence estimates. The estimated weighted proportions, including 95% CIs for individual eligible studies, and the heterogeneity among studies were displayed in the forest plots prepared using STATA software. Additionally, prediction intervals (PI) were estimated to evaluate the expected range of true prevalence across different study populations under the random-effects model. The heterogeneity across studies was assessed using I^2 and Cochrane's Q statistics (represented as χ^2 and p-values) to estimate variations, where I^2 values of 25%, 50%, and $\geq$ 75% represented the low, medium, and high heterogeneity, respectively (Higgins and Thompson, 2002). Potential sources of heterogeneity were further assessed using subgroup analysis and meta-regression methods, where $P < 0.05$ was considered statistically significant. Moreover, τ^2 (tau-squared) was reported to quantify between-study variance in the random-effects meta-analysis. Subgroup analysis was performed across variables such as study region like continent and country, sampling period, and study duration, age, sex, diagnostic methods, source of samples, types of samples, production system, study design and quality. Publication bias was assessed using funnel plot symmetry and Egger's regression test (Egger et al., 1997). Symmetry of the funnel plot was interpreted as indicating the absence of publication bias, whereas asymmetry suggested potential publication bias and/or small-study effects. In addition, nonparametric trim-and-fill analysis under a random-effects model was performed to further evaluate potential publication bias and the robustness of the pooled estimates. The robustness of the meta-analysis results was evaluated through leave-one-out sensitivity analysis using a random-effects model fitted with REML method.

3. Results

3.1. Search results and included studies

A total of 658 articles were identified through an electronic database search. Of these, 378 articles were removed due to duplication or because they reported species other than buffalo. Subsequently, 113 studies were removed due to non-compliance with inclusion and exclusion criteria (Fig. 1). Moreover, 125 articles were excluded due to obvious reasons such as full text not available (n = 11), experimental trial (n = 2), case report (n = 16), prevalence data not available (n = 39), incomplete, or unclear that could not be resolved by the author's discussion (n = 32), only post-mortem investigation (n = 7), study not published on a BVDV pathogen (n = 4), article published in a language other than English (n = 16), and articles found in a systemic search but failed to download and access (n = 2). Additionally, seven studies were retrieved from the reference lists of 46 published articles that reported the prevalence of BVDV in water buffalo (Fig. 1). Finally, 49 eligible

Table 1
Database-specific search strategies and Boolean syntax used for systematic literature screening in the current study.

Database	Search field/ syntax used	Search implementation	Filters/ limitations
PubMed	Title/Abstract and keyword-based search	("Prevalence" OR "Seroprevalence" OR "Incidence" OR "Occurrence" OR "Active infection" OR "Antigen prevalence" OR "Frequency" OR "Investigation" OR "Survey" OR "Rate" OR "Epidemiology" OR "Detection" OR "Isolation" OR "Identification" OR "Characterization" OR Genetic diversity" OR "Genomic characterization" OR "Genotypes" OR "Subgenotypes" OR "Phylogenetic analysis") AND ("BVDV" OR "BVD" OR "bovine viral diarrhea virus" OR "bovine viral diarrhea virus" OR "Pestiviruses" OR "BVDV-1" OR "*Pestivirus bovis*" OR "BVDV-2" OR "*Pestivirus tauri*" OR "BVDV-3" OR "HoBi-like virus" OR "*Pestivirus brazilense*" OR "Mucosal disease" OR "Persistently infected" OR "Transiently infected") AND ("Buffalo" OR "Water buffalo" OR "*Bubalus bubalis*" OR "Swamp buffalo" OR "River buffalo")	English language; peer-reviewed articles
Scopus	TITLE-ABS-KEY (title, abstract, and keyword search)	TITLE-ABS-KEY ((Prevalence OR Seroprevalence OR Incidence OR Occurrence OR "Active infection" OR "Antigen prevalence" OR Frequency OR Investigation OR Survey OR Rate OR Epidemiology OR Detection OR Isolation OR Identification OR Characterization OR Genetic diversity OR Genomic characterization OR Genotypes OR Subgenotypes OR Phylogenetic analysis) AND (BVDV OR BVD OR "bovine viral diarrhea virus" OR Pestiviruses OR "BVDV-1" OR "*Pestivirus bovis*" OR "BVDV-2" OR "*Pestivirus tauri*" OR "BVDV-3" OR "HoBi-like virus") AND (Buffalo OR "Water buffalo" OR "*Bubalus bubalis*" OR "Swamp buffalo" OR "River buffalo"))	English language; research articles
ScienceDirect	Keyword-based full-text search	Same Boolean combinations were adapted according to ScienceDirect search requirements using keyword searches	English language
Web of Science	Topic search (TS)	TS = ((Prevalence OR Seroprevalence OR Incidence OR Occurrence OR "Active infection" OR "Antigen prevalence" OR Epidemiology OR Detection OR "Genetic diversity" OR Genomic characterization) AND (BVDV OR "bovine viral diarrhea virus" OR Pestiviruses OR "HoBi-like virus") AND (Buffalo OR "Water buffalo" OR "*Bubalus bubalis*"))	English language; articles only
Google Scholar	General keyword search	Simplified Boolean combinations and keyword searches were used due to platform search limitations	First several hundred relevant records screened manually

studies on BVDV infection in buffalo were included in the systematic review and meta-analysis (Table 2, Fig. 1). Among these, four studies (Deng et al., 2015; Al-Rubaye and Hasso, 2012; El-Mohamady et al., 2020; Assunção et al., 2022) reported both antigen and seroprevalence in water buffalo and were therefore included separately in the pooled antigen and seroprevalence analyses (Tables 2 and 3).

3.2. Continents and countries included

The eligible articles were retrieved from 15 different countries (Table 2) across 5 continents (Table 3). The highest number of studies (n = 21) were from Asia, covering 8 countries. In South America, 13 studies were conducted across three countries, while in Africa, 11 studies were reported from two countries. Likewise, only one country from Oceania, Australia (n = 1), and 3 studies from 2 European countries reported prevalence studies on BVDV in buffaloes (Tables 2 and 3). None of the North America countries reported prevalence studies on BVDV in buffaloes.

3.3. Study characteristics and quality assessment

Among the 49 eligible studies, 37 reported seroprevalence, while 16 reported active BVDV infection in water buffalo (Table 2), with four studies reporting both seroprevalence and antigen prevalence. Regarding sample origin, 41 studies were conducted on farms, 4 in abattoirs, and 4 involved laboratory-derived samples. For seroprevalence analysis, 36 studies used blood serum samples, while one study used milk samples. In contrast, for antigen detection, 11 studies used blood samples, whereas single studies used tissue samples (ear notch and lymph node), semen, follicular fluid, and faecal samples. Based on the diagnostic approaches, 37 studies utilized serological assays (Ab-ELISA, VNT, IFAT, AGID, MNT, and SNT) to determine serostatus, whereas 16 studies used RT-PCR and Ag-ELISA for the detection of active BVDV infection (Tables 2 and 3). Based on the quality score criteria, 31 studies were rated as medium quality, 17 studies as high quality, and only one study was categorized as low quality (Tables 2 and 3, Supplementary Table 1).

3.4. Publication Bias

Publication bias was assessed using funnel plots and Egger's regression test for BVDV seroprevalence and antigen prevalence studies (Fig. 2a and b). The funnel plot for seroprevalence studies was largely symmetrical (Fig. 2a), and Egger's test confirmed the absence of small-study effects (bias coefficient = −1.46, 95% CI: −6.18 to 3.27, SE = 2.33, p = 0.535). For antigen prevalence studies, slight asymmetry was observed in the funnel plot (Fig. 2b), but Egger's test indicated no

Table 2
Summary of studies reporting BVDV seroprevalence in Water buffaloes from various countries included in this systematic review.

Study ID	Sampling period	Country	Study design	Diagnostic method	Total number examined	Total positive number	Overall prevalence (%)	Quality score	Quality level	Detection of BVDV species
Asia										
Deng et al. (2015)	2010–2013	China	Cross sectional	SNT	134	19	14.18	7	High	Yes
Lotfi et al. (2016)	Not mentioned	Iran	Cross sectional	Ab-ELISA	513	167	32.60	7	High	No
HajiHajikolaei et al. (2010)	Not mentioned	Iran	Cross sectional	IFAT	310	105	33.90	8	High	No
Al-Rubaye and Hasso (2012)	Not mentioned	Iraq	Cross sectional	Ab-ELISA	210	83	39.52	5	Medium	No
Alsaad et al. (2012)	Not mentioned	Iraq	Cross sectional	Ab-ELISA	92	20	21.70	8	High	No
Narayan Sarangi et al. (2023)	Not mentioned	India	Cross sectional	Ab-ELISA	234	76	32.29	5	Medium	No
Khaneja et al. (2021)	Not mentioned	India	Cross sectional	Ab-ELISA	220	84	38.18	4	Medium	No
Naveena et al. (2022)	June 2019 to December 2019.	India	Cross sectional	VNT	71	3	3.50	7	High	No
Sood et al. (2007)	Not mentioned	India	Cross sectional	Ab-ELISA	498	115	23.0	5	Medium	No
Sudharshana et al. (1999)	January 1996 and December 1997	India	Cross sectional	Ab-ELISA	112	26	23.21	6	Medium	No
Selvaraj et al. (2007)	Not mentioned	India	Cross sectional	Ab-ELISA	168	46	27.40	4	Medium	No
Olmo et al. (2018)	Not mentioned	Laos	Cross sectional	Ab-ELISA	61	3	4.91	7	High	No
Shabbir et al. (2013)	April to June 2011	Pakistan	Cross sectional	Ab-ELISA	47	3	6.40	9	High	No
Akhtar and Asif (1996)	Not mentioned	Pakistan	Cross sectional	MNT	36	11	30.60	6	Medium	No
Raheem et al. (2020)	3 months	Pakistan	Cross sectional	VNT	68	6	8.22	6	Medium	No
Ozan et al. (2012)	Not mentioned	Turkey	Cross sectional	Immunodiffusion in agar gel	82	56	68.30	4	Medium	No
Guer and Akca (2008)	Not mentioned	Turkey	Cross sectional	VNT	452	257	56.80	4	Medium	No
Europe										
Roncoroni et al. (2007)	2004–2005	Italy	Cross sectional	SNT	465	102	22.0	8	High	No
Julia Victoria (2017)	Not mentioned	Switzerland	Cross sectional	Ab-ELISA	48	5	5.40	4	Medium	No
El-Mohamady et al. (2020)	Not mentioned	Italy	Cross sectional	VNT	40	12	30	6	Medium	No
South America										
Craig et al. (2015)	Not mentioned	Argentina	Cross sectional	Ab-ELISA	38	32	84.20	5	Medium	Yes
Pecora et al. (2017)	Not mentioned	Argentina	Cross sectional	Ab-ELISA	130	42	32.31	4	Medium	Yes
Assunção et al. (2022)	Not mentioned	Brazil	Cross sectional	Ab-ELISA	89	18	20.22	5	Medium	No
Viana et al. (2016)	Not mentioned	Brazil	Cross sectional	Ab-ELISA	225	122	54.22	8	High	No
Fernandes, 2018	Not mentioned	Brazil	Cross sectional	Ab-ELISA	136	12	8.80	7	High	No
Soares et al. (2017)	Not mentioned	Brazil	Cross sectional	Ab-ELISA	244	239	97.90	4	Medium	No
Paixão et al. (2018a)	Not mentioned	Brazil	Cross sectional	IFAT	305	110	36.10	6	Medium	No
Lage et al. (1996)	1989 and 1990	Brazil	Cross sectional	Ab-ELISA	220	116	52.70	6	Medium	No
Silva et al. (2016)	Not mentioned	Brazil	Cross sectional	VNT	805	113	14.0	6	Medium	No
Leite et al. (2020)	Not mentioned	Brazil	Cross sectional	Ab-ELISA	241	185	76.70	6	Medium	No
García et al. (2022)	Not mentioned	Colombia	Cross sectional	Ab-ELISA	1100	302	27.50	6	Medium	No
Pastrana et al. (2022)	first semester 2019	Colombia	Cross sectional	MNT	861	186	21.70	9	High	No

(*continued on next page*)

Table 2 (*continued*)

Study ID	Sampling period	Country	Study design	Diagnostic method	Total number examined	Total positive number	Overall prevalence (%)	Quality score	Quality level	Detection of BVDV species
Africa										
Lotfy et al. (2020)	2018–2019	Egypt	Cross sectional	VNT	50	13	26.0	8	High	No
Zaghawa (1998)	Not mentioned	Egypt	Cross sectional	Ab-ELISA	150	78	51.3	5	Medium	No
Ghazy et al. (2007)	2004–2006	Egypt	Cross sectional	Ab-ELISA	360	44	12.20	7	High	No
Ghazi et al. (2008)	Not mentioned	Egypt	Cross sectional	MNT	210	53	25.0	3	Low	No
Oceania										
Evans et al. (2016)	between 1993 and 2001	Australia	Cross sectional	Ab-ELISA	245	11	4.50	6	Medium	No

Where, Ab-ELISA: Antibody-capture enzyme linked immunosorbent assay, VNT: Virus neutralization test; Ag-ELISA: Antigen-capture enzyme linked immunosorbent assay, AGID: Agarose gel immunodiffusion, FAT = Fluorescent antibody technique, RT-PCR: Reverse transcription polymerase chain reaction; SNT: serum neutralization test; MNT: Microneutralization test.

Table 3
Summary of studies reporting BVDV active infection in water buffaloes from various countries included in this systematic review.

Study ID	Sampling period	Country	Study design	Diagnostic method	Total number examined	Total positive number	Overall prevalence (%)	Quality score	Quality level	Detection of BVDV species
Asia										
Safarpoor Dehkordi, 2011	Not mentioned	Iran	Cross sectional	Ag-ELISA	372	139	37.36	5	Medium	No
Deng et al. (2015)	2010–2013	China	Cross sectional	Ag-ELISA	134	26	19.4	7	High	yes
Wahid and Al-Saad, (2020)	January to December 2020	Iraq	Cross sectional	RT-PCR	980	168	17.14	7	High	No
Al-Rubaye and Hasso (2012)	Not mentioned	Iraq	Cross sectional	RT-PCR	210	13	6.1	5	Medium	Yes
Mishra et al. (2007)	2001–2005	India	Cross sectional	RT-PCR	183	4	2.18	6	Medium	No
Brar et al. (2023)	Not mentioned	India	Cross sectional	RT-PCR	300	50	16.67	4	Medium	No
Mingala et al. (2009)	Not mentioned	Philippine	Cross sectional	RT-PCR	445	42	9.40	4	Medium	No
Europe										
El-Mohamady et al. (2020)	Not mentioned	Italy	Cross sectional	RT-PCR	40	14	35.0	6	Medium	No
South America										
Assunção et al. (2022)	Not mentioned	Brazil	Cross sectional	RT-PCR	89	8	8.9	5	Medium	No
Paixão et al. (2018b)	Not mentioned	Brazil	Cross sectional	RT-PCR	44	7	15.90	8	High	No
Africa										
Soltan et al. (2015)	Not mentioned	Egypt	Cross sectional	RT-PCR	108	10	9.25	7	High	Yes
Amin et al. (2014)	2011–2012	Egypt	Cross sectional	Ag-ELISA	372	63	16.94	7	High	No
Sharawi et al. (2016)	2013–2014	Egypt	Cross sectional	Rt-PCR	400	88	22.0	6	Medium	No
Emran et al. (2014)	Not mentioned	Egypt	Cross sectional	RT-PCR	1602	135	8.40	5	Medium	No
Ahmed and Zaher (2008)	2004–2008	Egypt	Cross sectional	RT-PCR	1850	824	44.5	6	Medium	Yes
Abd El-Hafeiz et al. (2005)	Not mentioned	Egypt	Cross sectional	RT-PCR	60	21	35.0	6	Medium	No

Where, Ag-ELISA: Antigen-capture enzyme linked immunosorbent assay, RT-PCR: Reverse transcription polymerase chain reaction.

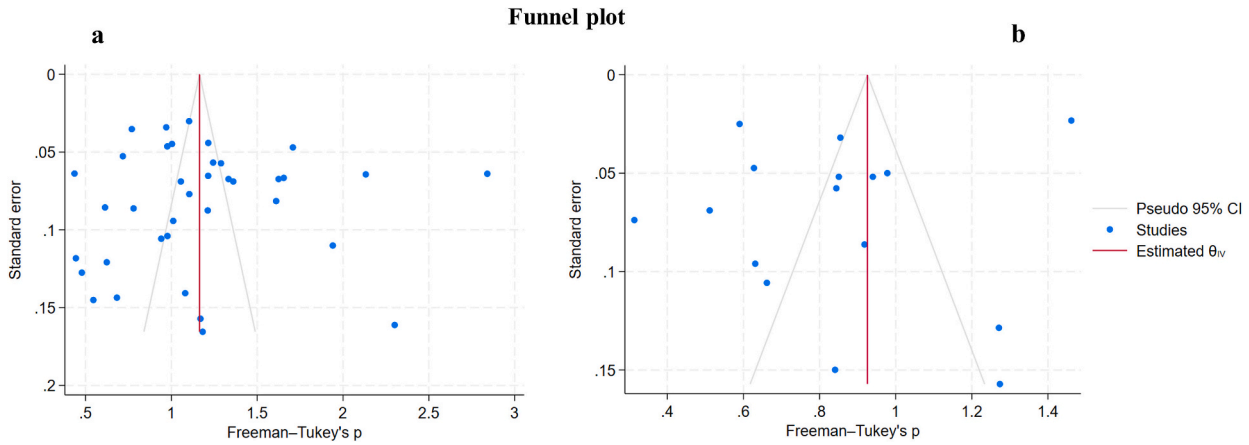


Fig. 2. Funnel plots with pseudo 95% confidence limits used to assess potential publication bias in studies reporting BVDV prevalence in water buffalo. Panel (2a) represents seroprevalence studies, while panel (2b) depicts antigen (active infection) prevalence studies. Each point corresponds to an individual study, and the vertical red line indicates the pooled effect estimate. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

significant small-study effects (bias coefficient = 0.93, 95% CI: −3.28 to 5.14, SE = 1.96, $p = 0.642$). Moreover, the nonparametric trim-and-fill analysis using a linear estimator identified no potentially missing studies for either the seroprevalence or antigen prevalence studies included in the meta-analysis (imputed studies = 0). The pooled estimates remained unchanged before and after adjustment for both seroprevalence studies ($\theta = 1.173$; 95% CI: 1.002–1.343) and antigen prevalence studies ($\theta = 0.843$; 95% CI: 0.695–0.990), suggesting no substantial evidence of publication bias. Random-effects models were applied for both seroprevalence ($I^2 = 98.53\%$) and antigen studies ($I^2 = 97.28\%$), with results visualized in forest plots (Figs. 3 and 4). Detailed bias assessment scores for individual studies are provided in Supplementary Table 1. These findings suggest that while some visual asymmetry exists in antigen studies, overall, there is no statistically significant evidence of publication bias in the included datasets.

3.5. Pooled seroprevalence and active infection of BVDV in water buffalo

A total of 9270 water buffalo from 37 studies were screened for BVDV seroprevalence across various geographical regions, of which 2876 animals tested seropositive. The random-effects meta-analysis estimated an overall pooled seroprevalence of 30.5% (95% CI: 22.6–38.9%), with a high degree of heterogeneity among studies ($\chi^2 = 1886.10$, $I^2 = 98.52\%$, $p < 0.0001$) (Table 4, Fig. 3). For active BVDV infection, 7189 animals from 16 studies were tested for antigen presence, of which 1550 were viremic. The random-effects meta-analysis indicated a pooled antigen (virological) prevalence of 16.50% (95% CI: 10.9–22.9%), also showing substantial heterogeneity ($\chi^2 = 894.56$, $I^2 = 97.15\%$, $p < 0.0001$) (Table 4, Fig. 4). The wide 95% prediction intervals (PI) for both seroprevalence (1.26–81.20%) and active infection (viremia) studies (1.01–45.70%) indicated substantial variability in BVDV prevalence across different buffalo populations, geographical regions, and epidemiological settings (Table 4).

3.6. Distribution and pooled estimate of BVDV in different continents

The continent-wise pooled prevalence estimates of BVDV in water buffalo are presented in Table 5. Among the continents, the highest pooled seroprevalence was observed in South America at 44.0% (95% CI: 23.8–65.4%), followed by Europe at 37.1% (95% CI: 15.9–61.3%) and Africa at 27.7% (95% CI: 6.1–57.2%). All regions exhibited significant heterogeneity ($I^2 > 95\%$, $p < 0.001$). In contrast, the highest pooled antigen (viremic) prevalence was reported in Africa at 21.2% (95% CI: 8.3–38.0%), followed by Asia at 12.2% (95% CI: 6.0–20.1%), both with high heterogeneity ($I^2 > 94\%$, $p < 0.001$). No data on active BVDV infection (antigen prevalence) were reported from North America and Oceania continent (Table 5).

3.7. Distribution and pooled prevalence of BVDV in different countries

Country-wise pooled prevalence estimates of BVDV in water buffalo are presented in Table 6. Among Asian countries, the highest seroprevalence was reported in Iran (33.0%, 95% CI: 14.5–54.9%), whereas Iraq showed a comparable estimate (30.7%, 95% CI: 0.0–100%). In South America, Argentina showed the highest seroprevalence (59.0%, 95% CI: 0.0–100%), followed by Brazil (45.7%, 95% CI: 17.2–75.8%). In Europe, Turkey reported the highest estimate (61.6%, 95% CI: 2.7–100%), whereas Italy demonstrated a lower prevalence (23.3%, 95% CI: 0.0–70.9%) (Table 6). For active BVDV infection, Egypt reported the highest pooled antigen prevalence (21.2%, 95% CI: 8.3–38.0%). Brazil and Iraq showed lower estimates of 11.8% (95% CI: 0.0–62.5%) and 11.3% (95% CI: 0.0–98.3%), respectively. Notably, antigen prevalence estimates for several countries, including China (19.4%), Iran (20.4%), Italy (35.0%), and the Philippines (9.4%) were derived from single studies (Table 6).

3.8. Reported distribution of Pestivirus species in water buffalo populations

Pestivirus species identification was limited across the included studies (Table 7). BVDV-1 was reported in six studies from three countries (China, Argentina, and Egypt), whereas BVDV-2 was identified in three studies from two countries (Argentina and Egypt). No studies reported HoBi-like pestivirus in buffalo. Notably, the majority of studies ($n = 43$) did not specify Pestivirus species (Table 7).

3.9. Subgroup analysis of factors associated with BVDV seroprevalence

Subgroup analyses were conducted to explore potential sources of heterogeneity in pooled BVDV seroprevalence, including study duration and period, age, sex, sample source and type, diagnostic methods, production systems, as well as study quality. The results are summarized in Table 8 and Fig. 5a. Based on study duration, seroprevalence was highest (24.0%; 95% CI: 11.90–38.60, $I^2 = 96.32$, $p < 0.001$)) in studies conducted between 6 to ≤12 months. Temporal analysis indicated a decreasing trend in seroprevalence, with estimates of 39.9% (95% CI: 17.2–65.0%; $I^2 = 91.33$; $p < 0.001$) before 2000, and 23.8% (95% CI: 9.0–42.9; $I^2 = 97.70$; $p < 0.001$) in the period 2021–2025. Age-wise

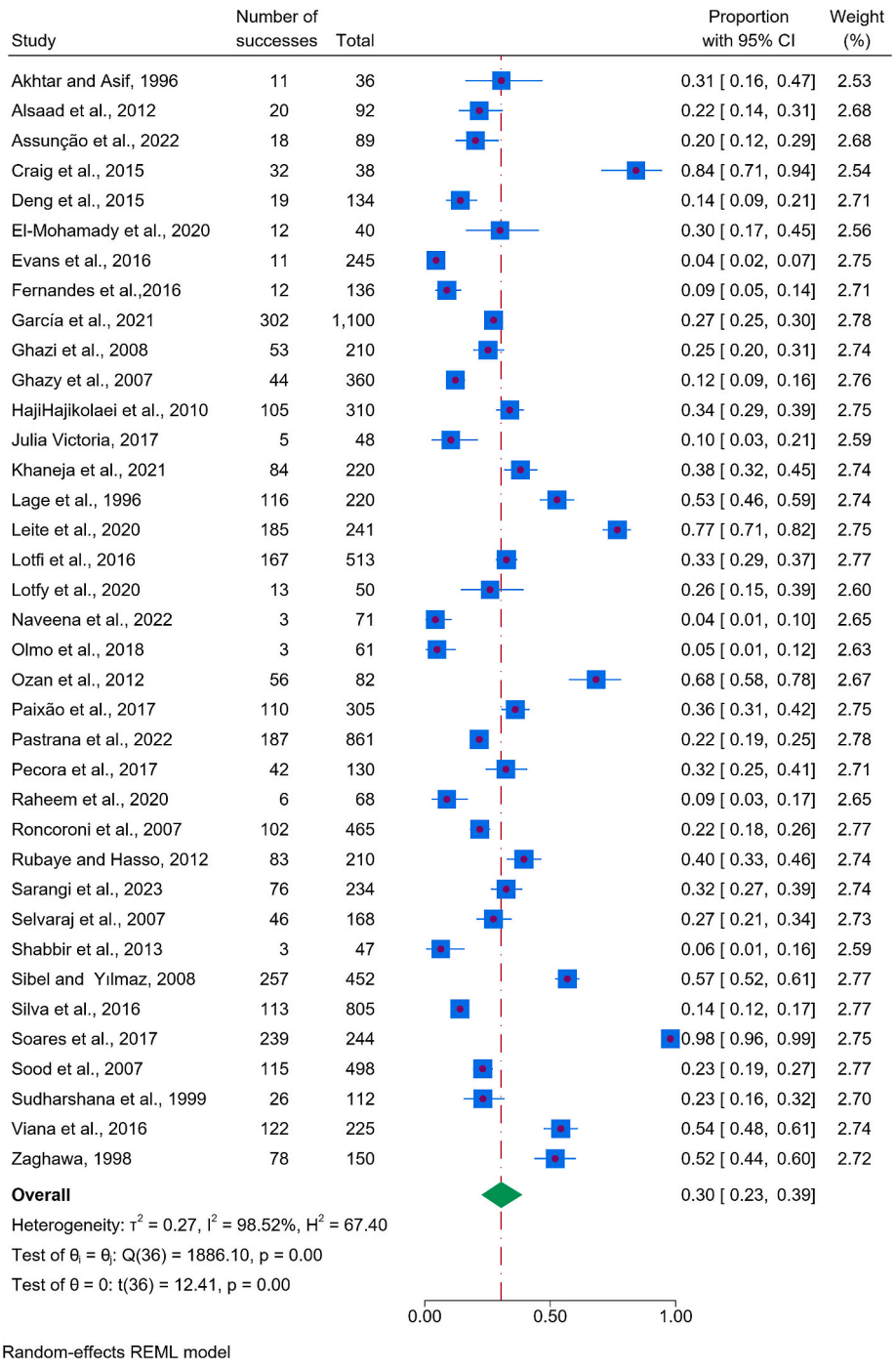


Fig. 3. Forest plot illustrating the random-effects meta-analysis of BVDV seroprevalence in water buffalo across studies conducted in various regions of the globe. This plot represents the study ID, number of BVDV-positive cases, total sample size, prevalence point estimate (blue box sized by study weight), 95% confidence interval (horizontal lines), and the weight assigned to each study in the analysis. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

subgroup analysis revealed that the pooled seroprevalence higher in young buffalo was 27.8% (95% CI: 18.5–38.1; $I^2 = 28.39$; $p = 0.161$) compared to adults (19.9%, 95% CI: 8.0–35.3; $I^2 = 91.92$; $p < 0.001$). Sex-wise analysis estimated a higher prevalence in females (36.0%, 95% CI: 18.4–55.8; $I^2 = 98.90$; $p < 0.001$) compared to males (25.4%, 95% CI: 17.2–34.5; $I^2 = 58.28$; $p = 0.016$), with studies lacking sex-specific data reporting 31.7% (95% CI: 20.4–44.2; $I^2 = 98.65$; $p < 0.001$). Regarding sample source, abattoir-based studies showed a markedly higher seroprevalence (52.5%, 95% CI: 6.6–95.8; $I^2 = 98.88$; $p < 0.001$) compared to farm-based (27.9%, 95% CI: 19.9–36.6; $I^2 = 98.40$; $p < 0.001$) and laboratory-based samples (29.3%, 95% CI: 0.0–93.2%; $I^2 = 97.73$; $p < 0.001$). Seroprevalence estimates were primarily derived from serum samples (31.2%, 95% CI: 23.3–39.8; $I^2 = 98.53$; $p < 0.001$), whereas milk-based estimates were limited (6.4%, 95% CI: 1.3–17.5%) in the water buffalo. Among the different serological diagnostic methods, Ab-ELISA (33.1%, 95% CI: 21.0–46.5; $I^2 = 98.81$; $p < 0.001$) also reported relatively higher estimates, whereas VNT (22.2%, 95% CI: 8.1–40.6%; $I^2 = 96.96$; $p < 0.001$), MNT (23.0%, 95% CI: 15.6–31.4; $I^2 = 25.20$; $p = 0.277$), and SNT (18.4%, 95% CI: 0.0–76.6; $I^2 = 75.22$; $p = 0.045$) yielded comparatively lower values. Production system analysis

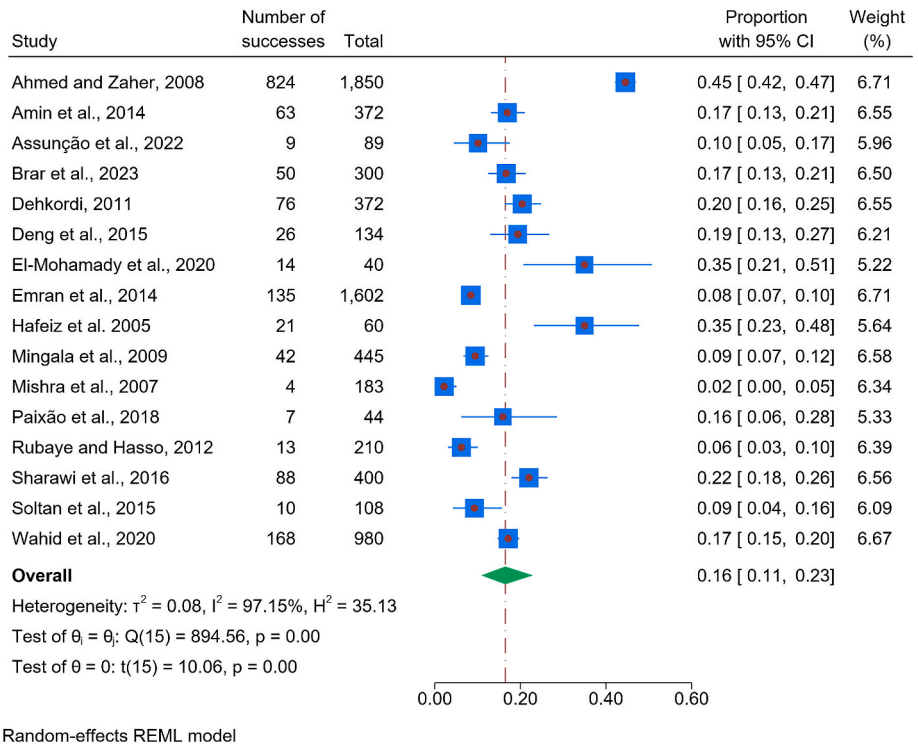


Fig. 4. Forest plot represents the random-effects meta-analysis of BVDV antigen prevalence (active infection) in water buffalo across studies conducted in various regions of the world. This plot represents the study ID, number of BVDV-positive cases, total sample size, prevalence point estimate (blue box sized by study weight), 95% confidence interval (horizontal lines), and the weight assigned to each study in the analysis. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

Table 4
Pooled prevalence estimates of BVDV in water buffalo based on serological and antigen detection methods across the globe.

BVDV Detection approach	No. of study	No. of buffalo sampled	No. of BVDV Positive buffalo	Estimated Pooled prevalence, %; (95% CI)	Heterogeneity					95% Prediction Interval
					Chi-square ($\chi 2$)	I^2%	H^2	tau^2 (τ^2)	*p*-value	
BVDV antibody detection	37	9270	2876	30.50 (22.60–38.90)	1886.10	98.52	67.40	0.272	< 0.001	1.26–81.20%
BVDV antigen detection	16	7189	1550	16.50 (10.90–22.90)	894.56	97.15	35.13	0.084	< 0.001	1.01–45.70%

Abbreviations: CI: confidence interval; I2: inverse variance index; $\chi 2$: Cochran's Q chi-square.

Table 5
Estimated pooled prevalence of BVDV in water buffalo across different continents of the world.

Variables	BVDV detection type	No. studies	No. of buffalo tested	No. of buffalo positive	Pooled estimate prevalence (%)	95% CI	Heterogeneity				
							Chi square ($\chi 2$)	I^2%	H^2	tau^2 (τ^2)	*p*-value
Asia	Antibody	15	2774	767	21.90	15.20–29.40	148.14	93.85	16.25	0.086	<0.001
	Antigen	7	2624	379	12.20	6.0–20.10	83.65	94.58	18.44	0.051	<0.001
Europe	Antibody	5	1087	432	37.10	15.90–61.30	174.88	98.30	58.89	0.202	<0.001
	Antigen	1	40	14	35.0	20.62–51.68	–	–	–	–	–
South America	Antibody	12	4394	1478	44.0	23.80–65.40	1257.92	99.35	153.76	0.451	<0.001
	Antigen	2	133	16	11.80	0.0–62.50	0.95	0.0	1.0	0.00	0.329
North America	Antibody	N/A	–	–	–	–	–	–	–	–	–
	Antigen	N/A	–	–	–	–	–	–	–	–	–
Africa	Antibody	4	770	188	27.70	6.10–57.20	85.81	95.83	23.95	0.134	<0.001
	Antigen	6	4392	1141	21.20	8.30–38.0	688.45	98.59	70.69	0.118	<0.001
Oceania	Antibody	1	245	11	4.50	2.26–7.89	–	–	–	–	–
	Antigen	0	–	–	–	–	–	–	–	–	–

Abbreviations, CI: confidence interval; I^2: inverse variance index; $\chi 2$: Cochran's Q chi-square; N/A: No BVDV prevalence data reported for water buffalo.

Table 6
Estimated pooled seroprevalence and virological prevalence of BVDV in water buffalo in different countries of the world.

Country	BVDV detection type	No. of study	No. of buffalo sampled	No. of BVDV Positive buffalo	Estimated pooled prevalence (%)	95% CI	Heterogeneity ($\chi 2$)	I^2%	H^2	tau^2 (τ^2)	*p*-value
Argentina	Antibody	2	168	74	59.0	0.00–100	35.26	97.16	35.26	0.576	< 0.001
	Antigen	N/A	–	–	–	–	–	–	–	–	–
Australia	Antibody	1	245	11	*4.50	2.26–7.89	–	–	–	–	–
	Antigen	N/A	–	–	–	–	–	–	–	–	–
Brazil	Antibody	8	2265	915	45.70	17.20–75.80	1089.47	99.32	146.25	0.554	< 0.001
	Antigen	2	133	16	11.80	0.0–62.50	0.95	0.00	0.000	1.0	0.329
China	Antibody	1	134	19	*14.18	8.76–21.25	–	–	–	–	–
	Antigen	1	134	26	*19.40	13.08–27.12	–	–	–	–	–
Colombia	Antibody	2	1961	489	24.60	0.09–65.40	8.56	88.31	8.56	0.007	0.003
	Antigen	N/A	–	–	–	–	–	–	–	–	–
Egypt	Antibody	4	770	188	27.70	6.10–57.20	85.81	95.83	23.95	0.134	< 0.001
	Antigen	6	4392	1141	21.20	8.30–38.0	688.45	98.59	70.69	0.118	< 0.001
India	Antibody	6	350	1303	24.0	12.20–38.30	50.87	94.09	16.91	0.080	< 0.001
	Antigen	2	483	54	8.0	0.0–100	32.06	96.88	32.06	0.136	< 0.001
Iran	Antibody	2	823	272	33.0	14.50–54.90	0.16	0.01	1.0	0.000	0.693
	Antigen	1	372	76	*20.43	16.45–24.89	–	–	–	–	–
Iraq	Antibody	2	302	103	30.70	0.00–100	9.44	89.41	9.44	0.065	0.002
	Antigen	2	1190	181	11.30	0.00–98.30	20.42	95.10	20.42	0.056	< 0.001
Italy	Antibody	2	505	114	23.30	0.0–70.90	1.39	28.28	1.39	0.005	0.238
	Antigen	1	40	14	*35.0	20.63–51.68	–	–	–	–	–
Laos	Antibody	1	61	3	*4.91	1.02–13.71	–	–	–	–	–
	Antigen	N/A	–	–	–	–	–	–	–	–	–
Pakistan	Antibody	2	151	20	13.50	0.00–52.0	9.87	81.95	5.54	0.092	0.007
	Antigen	N/A	–	–	–	–	–	–	–	–	–
Philippines	Antibody	N/A	–	–	–	–	–	–	–	–	–
	Antigen	1	445	42	*9.40	6.89–12.54	–	–	–	–	–
Switzerland	Antibody	1	48	5	*10.40	3.47–22.66	–	–	–	–	–
	Antigen	N/A	–	–	–	–	–	–	–	–	–
Turkey	Antibody	2	534	313	61.60	2.70–100	3.77	73.50	3.77	0.020	0.052
	Antigen	N/A	–	–	–	–	–	–	–	–	–

* Represents a single-study prevalence estimate. N/A: BVDV seroprevalence or antigen detection data were not reported for this country. Abbreviations: CI: confidence interval; I2: inverse variance index; $\chi 2$: Cochran's Q chi-square.

indicated lower prevalence in dairy buffalo (18.3%, 95% CI: 0.0–55.5; $I^2 = 81.01$; $p = 0.009$) compared to studies with unspecified production systems (31.4%, 95% CI: 22.9–40.5; $I^2 = 98.52$; $p < 0.001$). Study quality influenced prevalence estimates, with medium-quality studies reporting higher seroprevalence (38.0%, 95% CI: 26.4–50.3; $I^2 = 98.68$; $p < 0.001$) compared to high-quality studies (19.0%, 95% CI: 11.3–28.0%; $I^2 = 96.47$; $p < 0.001$). All included studies were cross-sectional in design, with an overall pooled seroprevalence of 30.5% (95% CI: 22.6–38.9), accompanied by substantial heterogeneity ($I^2 >$ 90% in most subgroups, $p < 0.001$) (Table 8, Fig. 5a).

3.10. Subgroup analysis of factors associated with active infection of BVDV

Subgroup analyses were performed to explore potential sources of heterogeneity in pooled BVDV antigen prevalence across study duration, sampling period, age, sex, sample source and type, diagnostic methods, production systems, and study quality (Table 7, Fig. 5b). Based on study duration, antigen prevalence ranged from 20.4% (95% CI: 16.4–24.9%) in studies ≤6 months to 18.5% (95% CI: 12.3–25.5%; $I^2 = 58.98\%$, $p = 0.091$) in studies conducted for >6 to ≤12 months. Studies exceeding 12 months showed comparable estimates (18.8%, 95% CI: 0.0–84.7%) but with substantial heterogeneity ($I^2 = 98.93\%$, $p < 0.001$). Temporal analysis indicated a decreasing trend in antigen prevalence, from 19.4% (95% CI: 0.0–60.3%; $I^2 = 99.06\%$) during 2001–2010 to 14.0% (95% CI: 0.0–66.3%; $I^2 = 56.43\%$) in 2021–2025. Based on the Age group analysis showed higher viremic prevalence in adult buffalo (>2 years) (26.3%, 95% CI: 5.9–54.3%; $I^2 = 96.40\%$, $p < 0.001$) compared to young animals (<2 years) (18.4%, 95% CI: 11.2–26.9%; $I^2 = 57.60\%$, $p = 0.106$). Sex-wise analysis demonstrated higher prevalence in females (41.8%, 95% CI: 2.2–90.2%; $I^2 = 52.84\%$, $p = 0.145$) compared to males (14.0%, 95% CI: 0.0–100%; $I^2 = 96.73\%$, $p < 0.001$), although estimates were based on a limited number of studies. Regarding sample source, abattoir-based studies showed higher prevalence (21.0%, 95% CI: 0.0–100%; $I^2 = 92.55\%$, $p < 0.001$) compared to farm-based studies (15.9%, 95% CI: 10.1–22.8%; $I^2 = 97.42\%$, $p < 0.001$). Among sample types, tissue samples (ear notch and lymph node) yielded 20.7% (95% CI: 0.0–100%; $I^2 = 90.43\%$), while blood-based detection showed 17.2% (95% CI: 11.1–24.4%; $I^2 = 97.07\%$). Lower prevalence was observed in semen (9.4%, 95% CI: 6.9–12.5%) and faecal samples (2.2%), whereas follicular fluid showed higher detection (35.0%, 95% CI: 23.1–48.4%), though based on single studies. Regarding diagnostic methods, comparable prevalence estimates were observed using Ag-ELISA (16.0%, 95% CI: 7.8–26.3%; $I^2 = 41.08\%$, $p = 0.157$) and RT-PCR (16.8%, 95% CI: 9.9–25.0%; $I^2 = 97.91\%$, $p < 0.001$). Production system analysis indicated higher prevalence in dairy buffalo (32.9%, 95% CI: 0.0–100%; $I^2 = 98.70\%$, $p < 0.001$) compared to studies with unspecified systems (14.2%, 95% CI: 9.4–19.7%; $I^2 = 94.60\%$, $p < 0.001$). Study quality had minimal influence on prevalence estimates, with 16.5% (95% CI: 14.0–19.1%; $I^2 = 0.0\%$, $p = 0.216$) in high-quality studies and 17.0% (95% CI: 8.8–27.0%; $I^2 = 98.17\%$, $p < 0.001$) in medium-quality studies. All included studies were cross-sectional, with an overall pooled antigen

Table 7
Subgroup analysis of different variables and their contribution to heterogeneity in the prevalence (active infection) of BVDV in water buffalo.

Variables	*No. studies	No. of buffalo tested	No. of buffalo positive	Pooled estimate prevalence (%)	95% CI	Heterogeneity				
						chi square ($\chi 2$)	I^2%	H^2	tau^2 (τ^2)	*p*-value
Study duration										
≤6 months	1	372	76	20.43	16.44–24.89	–	–	–	–	–
>6 to ≤12	3	1752	319	18.50	12.30–25.50	4.80	58.98	2.44	0.003	0.091
>12	3	2167	854	18.80	0.0–84.70	244.38	98.93	93.75	0.328	<0.001
Not mentioned	9	2898	301	14.20	7.70–22.30	62.10	93.61	15.64	0.062	<0.001
Sampling period										
before 2000	0	–	–	–	–	–	–	–	–	–
2001–2010	4	2538	891	19.40	0.0–60.30	414.98	99.06	105.82	0.286	<0.001
2011–2020	10	4262	600	15.80	10.80–21.40	118.39	92.69	13.68	0.034	<0.001
2021–2025	2	389	59	14.0	0.0–66.30	2.30	56.43	2.30	0.009	0.130
Age										
Young (less than 2 year)	4	1452	259	18.40	11.20–26.90	4.50	57.60	2.36	0.004	0.106
Adult (more than 2 year)	4	2224	886	26.30	5.90–54.30	137.66	96.40	27.76	0.122	<0.001
Not mentioned	10	4161	603	16.60	11.90–21.90	110.99	90.82	10.90	0.028	<0.001
Sex										
Male	2	223	18	14.0	0.0–100	30.58	96.73	30.58	0.446	<0.001
Female	2	1910	845	41.80	2.20–0.902	2.12	52.84	2.12	0.010	0.145
Not mentioned	12	4700	637	13.60	8.80–19.20	152.55	94.45	18.0	0.049	<0.001
Source of sample										
Farm	14	7040	1520	15.90	10.10–22.80	881.10	97.42	38.77	0.083	<0.001
Abattoir	2	149	30	21.0	0.0–100	13.42	92.55	13.42	0.172	<0.001
Type of sample										
Blood	11	6372	1460	17.20	11.10–24.40	759.30	97.07	34.19	0.064	<0.001
Tissue sample (Ear notch, Lymph node)	2	129	23	20.70	0.0–100	10.45	90.43	10.45	0.169	<0.001
Semen	1	445	42	9.44	6.89–12.54	–	–	–	–	–
Follicular fluid	1	60	21	35.0	23.13–48.40	–	–	–	–	–
Faeces	1	183	4	2.19	5.99–5.50	–	–	–	–	–
Methods of detection										
[#]Ag-ELISA	3	595	98	16.0	7.80–26.30	3.70	41.08	1.70	0.004	0.157
[#]RT-PCR	13	6594	1452	16.80	9.90–25.0	885.79	97.91	47.82	0.103	<0.001
Production system										
Diary buffalo	2	2250	912	32.90	0.0–100	76.92	98.70	76.92	0.115	<0.001
Not specify	14	4939	638	14.20	9.40–19.70	155.01	94.60	18.53	0.056	<0.001
Study Quality										
High	5	1638	274	16.50	14.0–19.10	5.79	0.00	1.0	0.000	0.216
Medium	11	5551	1276	17.0	8.80–27.0	874.52	98.17	54.70	0.123	<0.001
Low	0	–	–	–	–	–	–	–	–	–
Study design										
Cross sectional	16	7189	1550	16.50	10.90–22.90	894.56	97.15	35.13	0.084	< 0.001
Survey	0	–	–	–	–	–	–	–	–	–
Longitudinal	0	–	–	–	–	–	–	–	–	–
Pilot study	0	–	–	–	–	–	–	–	–	–
Detection of pestivirus species										
BVDV-1	Only 6 studies from 3 different countries such as China, Argentina and Egypt reported BVDV-1.									
BVDV-2	Only 3 studies from two different countries such as Argentina and Egypt reported BVDV-2.									
HoBi like pestivirus	None of the study or country reported HoBi like pestivirus in buffalo.									
Not mentioned	Remaining 41 studies were not identified any BVDV species.									

[#] RT-PCR: Reverse transcription polymerase chain reaction; Ag-ELISA: Antigen-capture enzyme linked immunosorbent assay. BVDV-1: bovine viral diarrhea virus 1 (*Pestivirus bovis*); BVDV-2: bovine viral diarrhea virus 2 (*Pestivirus tauri*); HoBiPeV: HoBi-like pestivirus (*Pestivirus brazilense*); CI: confidence interval. *Estimate based on a single study and only represents the prevalence.

Table 8
Subgroup analysis of different variables and their contribution to heterogeneity in the seroprevalence of BVDV in water buffalo.

Variables	*No. studies	No. of buffalo tested	No. of buffalo positive	Pooled estimate prevalence (%)	95% CI	Heterogeneity				
						chi square ($\chi 2$)	I^2%	H^2	tau^2 (τ^2)	*p*-value
Study duration										
≤6 months	2	115	9	7.80	0.0–60.10	0.17	0.00	1.0	0.000	0.680
>6 to ≤12	7	1989	500	24.0	11.90–38.60	107.22	96.32	27.16	0.108	<0.001
>12	4	1237	189	12.80	3.0–27.80	55.46	93.82	16.19	0.0524	<0.001
Not mentioned	24	5929	2178	38.40	27.40–50.0	1369.85	98.58	70.60	0.294	<0.001
Sampling period										
before 2000	4	518	231	39.90	17.20–65.0	34.91	91.33	11.53	0.089	<0.001
2001–2010	7	2463	722	28.0	16.20–4.15		96.95	32.81	0.092	<0.001
2011–2020	21	3803	1271	31.40	18.40–46.0	1477.82	98.63	72.99	0.417	<0.001
2021–2025	5	2486	652	23.80	9.0–42.90	58.01	97.70	43.48	0.102	<0.001
Age										
Young (less than 2 year)	4	600	181	27.80	18.50–38.10	5.16	28.39	1.40	0.006	0.161
Adult (more than 2 year)	8	630	130	19.90	8.0–35.30	79.99	91.92	12.37	0.149	<0.001
Not mentioned	28	6532	2154	33.80	24.0–44.40	1635.83	98.54	68.33	0.297	<0.001
Sex										
Male	6	596	149	25.40	17.20–34.50	14.0	58.28	2.40	0.017	0.016
Female	14	2912	950	36.0	18.40–55.80	1119.50	98.90	90.58	0.454	<0.001
Not mentioned	22	5074	1709	31.70	20.40–44.20	1256.15	98.65	73.82	0.326	<0.001
Source of sample										
Farm	30	7927	2346	27.90	19.90–36.60	1520.20	98.40	62.36	0.2397	<0.001
Abattoir	4	912	365	52.50	6.60–95.80	257.95	98.88	89.42	0.457	<0.001
Laboratory	3	431	165	29.30	0.0–93.20	56.22	97.73	43.99	0.332	<0.001
Type of sample										
Blood serum	36	9223	2873	31.20	23.30–39.80	1867.81	98.53	68.17	0.269	<0.001
Milk	1	47	3	6.38	1.34–17.54	–	–	–	–	–
Methods of detection										
#Ab-ELISA	22	5213	1783	33.10	21.0–46.50	1413.43	98.81	84.21	0.3664	<0.001
VNT	7	1654	450	22.20	8.10–40.60	299.17	96.96	32.89	0.171	<0.001
IFAT	2	615	215	35.0	13.40–60.30	0.32	0.01	1.0	0.00	<0.001
MNT	3	1107	251	23.0	15.60–31.40	2.57	25.20	1.34	0.002	0.277
SNT	2	599	121	18.40	0.00–76.60	4.03	75.22	4.03	0.015	0.045
AGID	1	82	56	68.29	57.08–78.13	–	–	–	–	–
Production system										
Diary buffalo	3	175	34	18.30	0.0–55.50	9.43	81.01	5.27	0.079	0.009
Not specify	34	8087	2560	31.40	22.90–40.50	1862.66	98.52	67.45	0.285	<0.001
Study Quality										
High	13	3325	800	19.0	11.30–28.0	244.50	96.47	28.32	0.114	<0.001
Medium	23	5735	2023	38.0	26.40–50.30	1503.35	98.68	75.98	0.315	<0.001
Low	1	210	53	25.23	19.51–31.68	–	–	–	–	–
Study design										
Cross sectional	37	9270	2876	30.50	22.60–38.90	1886.10	98.52	67.40	0.272	<0.001
Survey	0	–	–	–	–	–	–	–	–	–
Longitudinal	0	–	–	–	–	–	–	–	–	–
Pilot study	0	–	–	–	–	–	–	–	–	–

[#] Ab-ELISA: Antibody-capture enzyme linked immunosorbent assay; VNT: Virus neutralization test; IFAT = Fluorescent antibody technique; AGID: Agar gel immunodiffusion assay; MNT: Microneutralization Test; SNT: serum neutralization test. CI: confidence interval. *Estimate based on a single study and only represents the prevalence.

prevalence of 16.5% (95% CI: 10.9–22.9%), accompanied by high heterogeneity (I^2 = 97.15%, $p < 0.001$) (Table 7, Fig. 5b).

3.11. Sensitivity analysis of pooled prevalence estimates

The leave-one-out sensitivity analysis was performed for both seroprevalence (37 studies) and antigen prevalence (16 studies) to assess the robustness of the pooled estimates (Figs. 6 and 7). Sequential exclusion of individual studies resulted in minimal variation in the pooled seroprevalence estimates, ranging approximately from 28% (95% CI: 22–35%; p < 0.001) to 31% (95% CI: 23–39%; p < 0.001), while antigen prevalence estimates varied between 15% (95% CI:

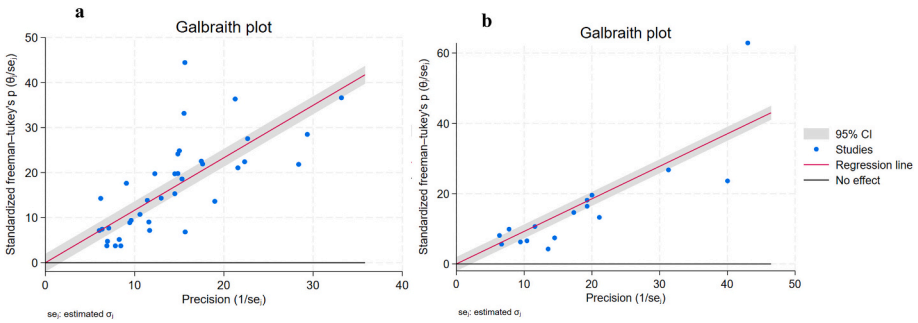


Fig. 5. Galbraith plots illustrating heterogeneity among studies included in the meta-analysis of BVDV prevalence in water buffalo. Panel (5a) represents seroprevalence studies, and panel (5b) represents antigen (active infection) prevalence studies. Each point corresponds to an individual study, plotted against its precision (1/SE). The central regression line indicates the pooled effect, and points lying outside the 95% confidence limits suggest potential outliers and sources of heterogeneity.

10–19%; $p < 0.001$) to 18% (95% CI: 13–23%; $p < 0.001$), with consistent overlap of the corresponding 95% confidence intervals across all iterations. Furthermore, all pooled estimates remained statistically significant ($p < 0.001$) following each exclusion, demonstrating that no individual study disproportionately affected the overall prevalence estimates (Figs. 6 and 7).

3.12. Sensitivity analysis across diagnostic methods

Leave-one-out sensitivity analyses stratified by diagnostic methods demonstrated minimal variation in the pooled prevalence estimates for both BVDV seroprevalence and active infection studies (Supplementary Figs. 1 and 2). Across antibody detection methods, including Ab-ELISA, VNT, IFAT, MNT, SNT, and AGID, the pooled seroprevalence estimates ranged from 28% (95% CI: 22–35%; $p < 0.001$) to 31% (95% CI: 23–39%; $p < 0.001$). Similarly, analyses based on BVDV antigen or viral RNA detection methods, including Ag-ELISA and RT-PCR, showed consistent active infection (viremia) prevalence estimates ranging from 15% (95% CI: 10–19%; $p < 0.001$) to 18% (95% CI: 13–23%; $p < 0.001$). The consistency of the pooled estimates across exclusions, with all *p*-values remaining significant ($p < 0.001$), indicated that sequential exclusion of individual diagnostic methods did not substantially influence the overall pooled estimates.

4. Discussion

This study represents the first meta-analysis on the prevalence and epidemiology of BVDV in domesticated water buffalo populations. This meta-analysis revealed that the overall pooled seroprevalence and antigen prevalence of BVDV in water buffalo was 30.50% and 16.50%, respectively. The pooled serostatus observed in this study is closely aligned with the detection rates reported studies from various countries, such as Iran (32.60%), Pakistan (30.60%), Brazil (30.33%), Colombia (27.50%), and India (27.40%) (Lotfi et al., 2016; Akhtar and Asif, 1996; Assunção et al., 2022; García et al., 2022; Selvaraj et al., 2007). Additionally, BVDV antigen prevalence exhibits considerable regional variation worldwide, ranging from 2.18% to 44.5%; however, the limited number of surveillance studies conducted across countries constrains the accurate estimation of true prevalence (Rana et al., 2025a). Additionally, the wide prediction intervals observed for both seroprevalence and active infection estimates indicate considerable between-study variability, suggesting that BVDV occurrence in water buffalo populations is strongly influenced by regional epidemiological conditions, herd management practices, diagnostic approaches, and study characteristics. Despite this heterogeneity, the leave-one-out sensitivity analysis showed only minor changes in pooled estimates after sequential exclusion of individual studies, demonstrating that the overall findings were not disproportionately driven by any single study. Therefore, the consistency of the results across all iterations confirms the stability and robustness of the meta-analysis. The consistent statistical significance and overlapping confidence intervals across all iterations further support the reliability of the pooled estimates. Nevertheless, the persistently high heterogeneity indicates that the pooled prevalence values should be interpreted cautiously, as they may not fully reflect the epidemiological situation across all buffalo production systems and geographic settings. However, BVDV prevalence in water buffalo remains unreported in many countries where the virus is known to circulate in cattle population. Since commercial BVDV vaccination in water buffalo has not yet been implemented anywhere, the detection of BVDV-specific antibodies and RNA suggests natural exposure to circulating wild strains. Current analysis indicates considerable variations in BVDV infection rates, with seroprevalence ranging from 3.50% (Naveena et al., 2022) to 97.90% (Soares et al., 2017). This discrepancy may be attributed to differences in study regions, herd management and husbandry practices, BVDV detection methods, and research designs. Notably, BVDV seroprevalence was higher in South America (44.0%) and Europe (37.1%) compared to Asia (21.9%) and Africa (27.7%), whereas antigen prevalence was greatest in Africa (21.2%) and Asia (12.2%), reflecting regional differences in infection dynamics within the buffalo population. However, water buffalo are not established as a production population in North America and are limited to small, non-commercial herds for research or zoological exhibition purposes (Martínez-Burnes et al., 2024). Consequently, they are not included in routine livestock disease surveillance, which primarily targets cattle. The absence of eligible studies therefore reflects a genuine lack of published data on BVDV in water buffalo in this region. Additionally, several countries reported high seroprevalence estimates, including Turkey (61.60%), Argentina (59.0%), Brazil (45.70%), Iran (33.0%) and Iraq (30.70%). The high serostatus BVDV in water buffalo may be attributed to their wide geographic distribution, close contact with naturally infected hosts, unrestricted animal movement, inadequate quarantine practices, and limited access to routine diagnostic facilities (Deng et al., 2015; Deb et al., 2016; Hause et al., 2021). Furthermore, the high infection rate observed in these regions is likely associated with extensive or mixed production systems, frequent introduction of new animals into buffalo herds, and close interspecies interactions between cattle and buffalo, all of which facilitate active viral transmission and persistence within populations. Epidemiological studies on BVDV infection in domesticated water buffalo remain limited, and consequently, the true prevalence and impact of the virus are not well understood, potentially due to the species' relatively aggressive and elusive behaviour (Rana et al., 2025a). Moreover, country-level pooled prevalence estimates for Argentina, Brazil, Italy, Colombia, India, Iraq, and Pakistan showed extremely wide confidence intervals, indicating limited precision and instability of the estimated prevalence due to sparse data availability and the limited number of studies. The limited data might be due to the practical

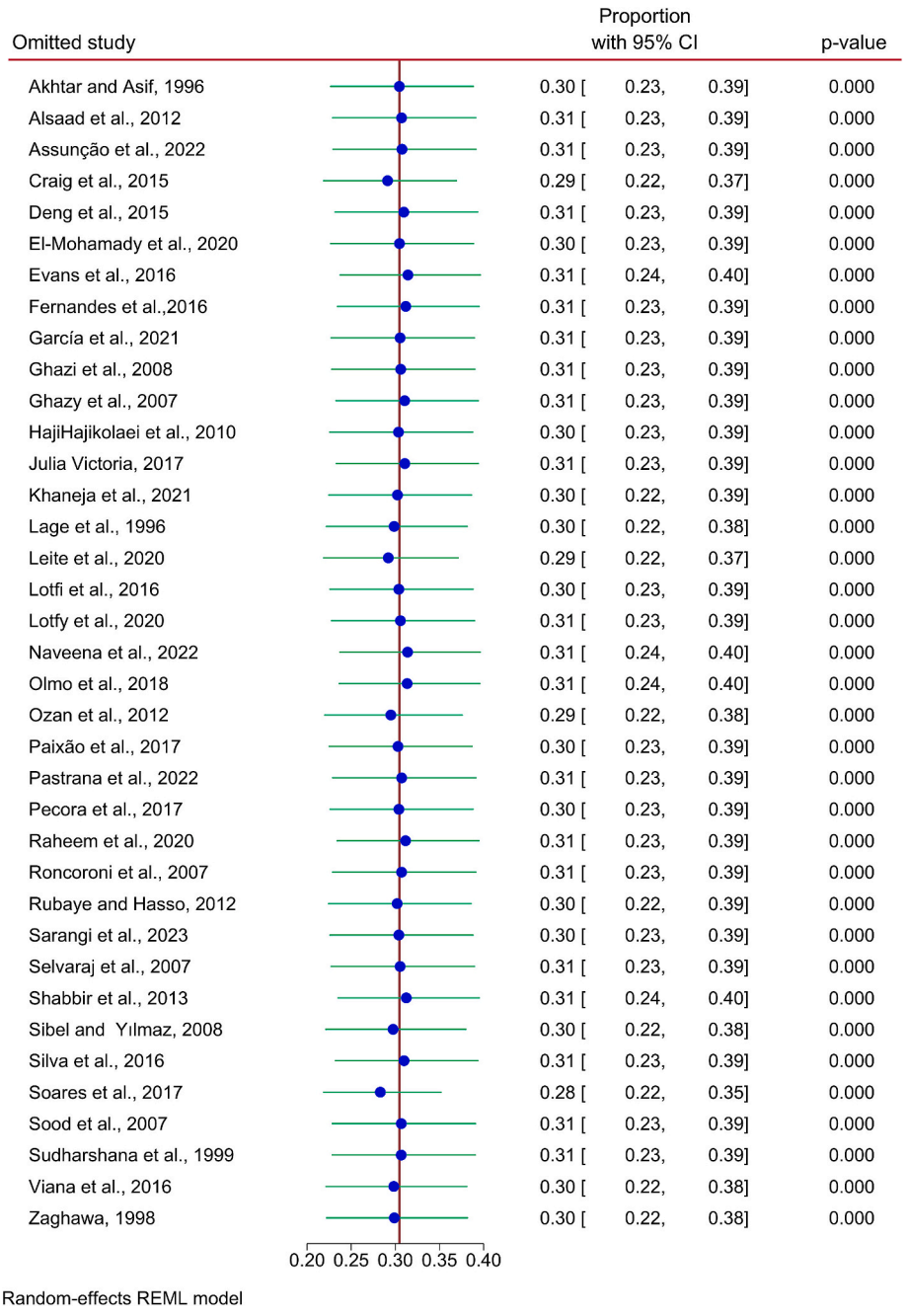


Fig. 6. The forest plot illustrates the leave-one-out sensitivity analysis of BVDV seroprevalence studies included in the pooled prevalence estimate.

difficulties associated with inherent challenges of restraining and sampling free-ranging or semi-managed buffalo populations. These constraints directed the need for long-term surveillance and systematic monitoring programs to better elucidate infection dynamics, epidemiological patterns, and the potential role of buffalo in BVDV transmission. Other contributing factors including free-grazing practices of buffalo in humid climatic conditions that aggravate disease transmission, presence of PI buffalo, absence of vaccine, and poor knowledge, limited funding, and lack of policies for BVDV monitoring and eradication (Deb et al., 2016; Ran et al., 2019). It is well documented that PI cattle are the major source of the infective virus, as they shed large quantities of infectious viral particles to maintain the BVDV infection within the herd (Walz et al., 2010; Dow et al., 2015). It is believed that cross-species spillover of BVDV contributes to the rising prevalence among buffalo, depending on the farming practices and endemic situation (Walz et al., 2010; Deng et al., 2015).

To date, fewer studies have reported the circulation of BVDV-1 and BVDV-2 in buffalo herds, with no reports of HoBi-like pestivirus in buffalo. While a broader genetic diversity of BVDV has been documented in cattle populations across various countries (Rana et al., 2025a; Rivas et al., 2022; Glotov et al., 2022), research on the genetic diversity of BVDV in buffalo remains scarce. Although differences in pathogenicity among Pestivirus species and BVDV subgenotypes have been primarily reported in cattle, experimental and pathological evidence in water buffalo is still limited. Moreover, the near-complete absence of detailed BVDV genetic characterization in the majority of included studies represents a critical epidemiological gap, as 43 of 49 studies did not report any genetic diversity data. This substantial evidence deficit severely limits robust inference on circulating Pestivirus diversity, evolutionary dynamics, and host–virus adaptation processes

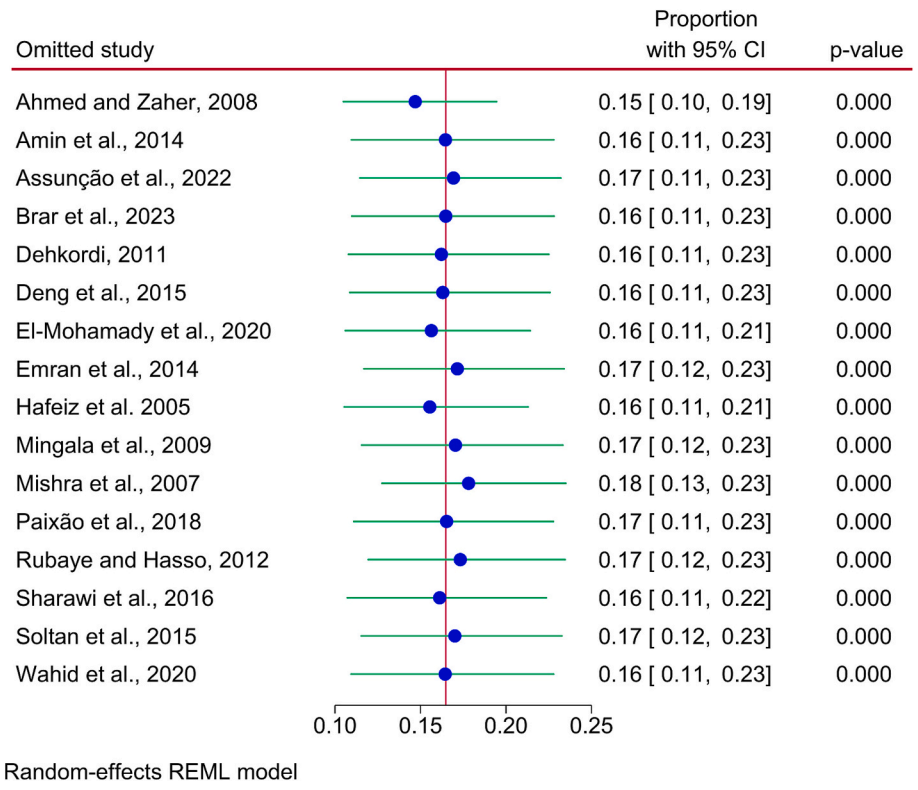


Fig. 7. Forest plot showing leave-one-out sensitivity analysis of BVDV antigen (active infection) studies included in the pooled antigen prevalence estimate.

in water buffalo populations. Furthermore, the lack of molecular data undermines the ability to conduct meaningful comparative phylogeographic analyses across regions and restricts assessment of genotype-specific transmission dynamics, differences in virulence potential, and possible impacts on diagnostic sensitivity and vaccine cross-protection. Therefore, it demands the immediate necessities for epidemiological surveys and laboratory investigations to better understand the genetic diversity of BVDV in buffalo herds. Such studies are also pivotal for designing effective intervention measures, including movement restrictions for PI animals, practicing culling strategies, as well as development and implementation of vaccination programs to curb the burden of BVDV. Although confirmatory clinical data on BVDV infection in buffalo are limited, experimentally infected buffalo calves have exhibited clinical signs comparable to those observed in cattle, including pyrexia, nasal and lacrimal discharge, diarrhea, erosive and ulcerative stomatitis with congestion of the nasal mucosa and gums, and leukopenia (Martínez-Burnes et al., 2024). Furthermore, Martucciello et al. (2009) isolated BVDV from clinically aborted buffalo, confirming natural infection and its reproductive impact in this species. Additionally, the pathological and characteristic clinical conditions such as gastrointestinal and respiratory disorders, immunosuppression, teratogenic effects, and economic impacts remain poorly documented in buffalo. However, due to limited diagnostic confirmation and under-recognition in the field, BVDV infection in buffalo remains a neglected disease in buffalo farming systems. There are limited quantitative data estimating the direct economic losses arising from production and reproductive losses associated with BVDV infection in water buffalo herds. Therefore, longitudinal economic studies are warranted to better quantify the production and reproductive impacts attributable to BVDV in buffalo populations.

The subgroup meta-analysis estimated that pooled BVDV seroprevalence was higher in young buffalo (27.8%), whereas antigen prevalence was higher in adult buffalo (26.3%). This result is in agreement with several previous studies reporting the seroprevalence rates at 32.6% in Iran (Lotfi et al., 2016), 23.38% in Egypt (Amin et al., 2014), 21.7% in Colombia (Pastrana et al., 2022), and 17.4% in Iraq (Wahid and Al-Saad, 2020) among young buffaloes. This might be due to the presence of PI animals among young buffaloes or exposure to the virus during an early stage of life (Glotov et al., 2022; Dow et al., 2015). However, the relationship between age and susceptibility to BVDV infection warrants further investigation to better understand the transmission dynamics and host tropism. Nevertheless, BVDV active infection in older buffalo is also noteworthy, as they are more likely to be exposed to BVDV infection over time in positive herds (Soltan et al., 2015; Paixão et al., 2018a). Specifically, PI animals continuously shed the virus, acting as a persistent source of infection for susceptible individuals and contributing to increased BVDV prevalence within herd populations (Soltan et al., 2015; Pecora et al., 2017).

Moreover, the estimated pooled virological prevalence of BVDV is higher in female buffalo than in male animals. This could be due to buffalo cows being typically retained longer in herds for reproduction and milk production, increasing their likelihood of exposure to BVDV over time (Paixão et al., 2018a; Martínez-Burnes et al., 2024). In contrast, male buffalo are sold for meat purposes at an early age, except for a few selected buffalo bulls used only for breeding purposes. Additionally, the close contact and interactions associated with reproductive management practices, such as natural breeding, artificial insemination, and calving, may further increase the risk of BVDV transmission among buffalo cows (Rana et al., 2026; Olmo et al., 2018; Albayrak et al., 2012). These findings suggest the importance of control measures focusing on breeding animals to effectively reduce the BVDV infection in entire buffalo populations.

The subgroup meta-analysis revealed that BVDV prevalence varied based on study duration, sampling period, sample source and types, detection methods, target components (antigen or antibody), buffalo production system and study quality. Overall, BVDV prevalence was higher in samples from abattoirs and farms, with the highest detection in tissue samples (Abd El-Hafeiz et al., 2005; Mingala et al., 2009). This may be because abattoir animals often include cull stock, sick animals, or those with reproductive issues and infectious disease history,

increasing the likelihood of BVDV detection rates (Abd El-Hafeiz et al., 2005; Paixão et al., 2018b). Although blood serum and milk samples are commonly used for serological detection of BVDV (Paixão et al., 2018a; Dubovi, 2013), tissue samples such as ear notch, lymphoid, reproductive, and respiratory tissues may yield higher detection rates, as they often contain higher concentrations of viral RNA or antigen compared to other sample types (Saliki and Dubovi, 2004; Al-Rubaye and Hasso, 2012).These findings highlight the importance of abattoir-based surveillance in identifying BVDV-positive animals and monitoring the virus's epidemics in buffalo populations within that geographical area. Moreover, 36 studies included in the meta-analysis used serum samples for various serological assays as diagnostic tests. Notably, serological assays are comparatively cheaper, easier and faster, to test the infection status of BVDV in a large animal population. Furthermore, 13 studies confirmed active BVDV infection through the detection of viral RNA, representing the true existence of circulating virus in buffalo herds with relatively moderate prevalence (16.80%). This is because PCR detected only active infections, while majorities of serological tests were performed to detect the BVDV-specific antibody which indicated the viral exposure. Moreover, the molecular method is typically utilized in relatively small sample sizes because of higher cost and technical challenges (Diao et al., 2021). Among the detection methods, serological assay such as Ab-ELISA was performed in the majority of studies. This is because ELISA is a sensitive, cost-effective, rapid, easy, and reliable test for screening larger animal herds compared to other methods (Tignon et al., 2017). Furthermore, the VNT, MNT and IFAT detected a higher seroprevalence rate in buffalo samples. It is important to note that the VNT and MNT are highly specific as it detects virus-specific neutralizing antibodies circulating in the host. Additionally, VNT might be more sensitive at detecting past exposure in cases where the sensitivity of Ab-ELISA is compromised due to antigenic variation of particular viruses or lower antibody titers in the host body (Tignon et al., 2017). Unlike PCR, which detects only active infections targeting particular nucleic acid sequences, ELISA could identify both previous exposure (Ab-ELISA) and current infections (Ag-ELISA) by detecting antibodies and antigens, respectively leading to higher prevalence estimates (Tignon et al., 2017; Werid et al., 2023). In the sensitivity analysis, the minimal variation in pooled prevalence estimates across different diagnostic methods indicates that the overall findings were not substantially influenced by the type of assay performed, supporting the robustness and methodological consistency of the meta-analysis. Nevertheless, variations in diagnostic sensitivity, specificity, and detection targets among serological and molecular assays may still have contributed to the residual heterogeneity observed between studies. However, none of the articles reported the sensitivity and specificity of the diagnostic tests, which are critical parameters for accurately estimating the true seroprevalence or active infection status of animals under field conditions. Studies involving buffalo under two years of age reported higher seroprevalence, which may be influenced by sampling bias and study design, as epidemiological investigations often preferentially include younger animals due to the practical challenges associated with restraining adult buffalo (Sarrazin et al., 2013). Additionally, young animals are more susceptible to BVDV infection, which may contribute to an overestimation of seropositivity. This increased susceptibility is likely due to their immunologically naïve status and greater exposure risk during early life, particularly through close contact with infected dams, including existing PI animals. Moreover, the prolonged retention of older animals in herds for production and reproductive purposes may increase the risk of active infection and seropositivity (Rana et al., 2026). Within the buffalo production system, only a limited number of studies specifically reported BVDV in dairy buffalo production systems, while the majority did not clearly define production types within buffalo populations. This lack of detailed classification constrains the ability to accurately assess the influence of production systems on BVDV epidemiology. Therefore, future studies should incorporate clearly defined production system categories to better elucidate their impact on BVDV prevalence and support the development of targeted control strategies.

In the current meta-analysis, all included studies were cross-sectional in design, the pooled prevalence estimates of BVDV should be interpreted within the context of this study type, which may be influenced by variations in sampling strategies, study objectives, and diagnostic approaches. Cross-sectional studies typically use direct, highly sensitive diagnostic testing within a defined timeframe, capturing a broader snapshot of infection. Although no longitudinal or pilot studies were identified in this analysis, such study designs typically involve smaller sample sizes, more specific inclusion criteria, and follow-up over time, which may influence prevalence estimates (Ran et al., 2019). These findings highlight the critical role of study design in determining disease estimates and suggest that standardized, large-scale studies are essential for accurate epidemiological understanding of BVDV in buffalo populations. Nevertheless, this review and meta-analysis highlight the importance of study duration in interpreting prevalence estimates in epidemiological research.

The current review provides strong evidence that buffaloes can be naturally infected with BVDV and potentially act as spillover hosts that may exhibit clinical manifestations, incur economic losses, and play a major role in BVDV transmission dynamics. Notably, BVDV vaccines are widely used in cattle populations, but no specific vaccination programs have been recommended for water buffalo worldwide. This gap may result from the under recognition of BVDV as a prevalent pathogen in buffalo herds. The lack of vaccination programs not only leaves buffalo populations susceptible to infection but may also undermine broader control strategies, particularly in mixed-species farming systems where buffaloes and cattle are raised together (Rana et al., 2025a). Therefore, targeted vaccination strategies or at least evaluations of existing bovine BVDV vaccines for their efficacy and safety in buffalo are urgently needed to mitigate the impact of BVDV in these animals and reduce the risk of spillover events.

Despite estimating the pooled prevalence and highlights the widespread distribution of BVDV infection in buffalo, this study encounters several limitations that should be acknowledged. In particular, the meta-analysis is limited by the significant heterogeneity among various factors related to BVDV infection in buffalo. Although limited publication bias was detected in this study, the current analysis excluded case reports, non-peer reviewed articles, studies lacking prevalence data, and results of experimental trials. These limitations are inevitable due to the lack of access to these studies. Many studies seemed to follow a cross-sectional design, but the absence of a clearly stated study design limits the assessment of methodological quality. Moreover, there were a limited number of studies or in some cases, only a single study with small sample sizes, reported from a geographical location. Therefore, the actual prevalence of BVDV among the buffalo population may not have been truly represented for that particular region. Another limitation is the inclusion of only English-language studies, which may have affected the accuracy of the prevalence estimates, as the exclusion of non-English articles may introduce language bias and limit comprehensive epidemiological assessment due to challenges in data extraction and interpretation. Additionally, the quality score of the included articles was uneven, indicating that the studies may not fully reflect the prevalence of buffalo BVDV across all regions, thus affecting the statistical analysis and results. Nevertheless, clear gaps existed in prior studies, as sufficient data on the epidemic nature of BVDV in buffalo, including associated risk factors and management practices influencing its epidemiology, were not provided. Therefore, meta-regression analysis was not performed, which limited the identification of associated risk factors of BVDV in water buffalo. Finally, it is recommended to conduct well-designed and detailed epidemiological studies in buffalo-rich areas to elucidate the true infection rate and transmission dynamics of BVDV. Such efforts will provide valuable and essential guidance for developing targeted intervention strategies as well as policies to effectively control BVDV in buffalo populations.

5. Conclusion

The present study demonstrates that BVDV infection is widely distributed in water buffalo populations, particularly in regions with high buffalo density. The pooled seroprevalence and active infection (antigen) prevalence were estimated at 30.5% and 16.5%, respectively. Higher prevalence was observed in South America, Africa, and Asia, with notable country-level estimates in Turkey, Argentina, and Egypt, indicating substantial geographical variation in BVDV distribution. The findings further indicate a higher infection burden in younger animals and female buffalo, underscoring the role of host demographic factors in disease epidemiology. These results emphasize the need for region-specific surveillance using sensitive diagnostic approaches to accurately assess infection status in buffalo and other susceptible hosts. Finally, standardized, species-specific epidemiological studies are essential to generate robust evidence for livestock producers, veterinarians, and policymakers, and to support the planning of future intervention efforts aimed at reducing the epidemics of BVDV in water buffalo populations.

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Authors' contribution

Eaftekhar Ahmed Rana: Conceptualization, Study design, Data curation, Investigation, Methodology, Resources, Validation, Statistical analysis, Software, Visualization, writing – original draft, Writing – review & editing. Md Saiful Islam, Belayet Hossain: Data curation, Methodology. Mieghan Bruce, Subir Sarker, Jully Gogoi-Tiwari: Validation, Writing – review & editing, Jasim Uddin: Conceptualization, Resources, Validation, Writing – review & editing and Supervision. All authors read and endorsed the final version.

CRediT authorship contribution statement

Eaftekhar Ahmed Rana: Writing – review & editing, Writing – original draft, Visualization, Validation, Software, Resources, Project administration, Methodology, Investigation, Funding acquisition, Formal analysis, Data curation, Conceptualization. **Md Saiful Islam:** Methodology, Data curation. **Belayet Hossain:** Methodology, Data curation. **Mieghan Bruce:** Writing – review & editing, Validation. **Subir Sarker:** Writing – review & editing, Validation. **Jully Gogoi-Tiwari:** Writing – review & editing, Validation. **Jasim M. Uddin:** Writing – review & editing, Validation, Supervision, Resources, Conceptualization.

Declaration of competing interest

The authors declare no competing interests.

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Data availability

The generated datasets and analyses of the present study are available from the corresponding author upon request.

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