

Epidemiology of ectoparasites in different domestic, peri-domestic, and wild animals in Bangladesh: A systematic review and meta-analysis

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ABSTRACT

Ectoparasites threaten animal health and productivity and may facilitate pathogen transmission, yet evidence on the burden of infestation across animal populations in Bangladesh remains fragmented. We conducted a systematic review and meta-analysis to estimate pooled infestation proportions of ectoparasites across diverse animal hosts in Bangladesh. Following systematic screening, we included 90 studies (1968–2024) containing relevant data. The random-effects model estimated highest pooled proportions in ticks 22.2% (95% CI: 16.6–29.0), followed by 16.6% (95% CI: 11.2–24.0) in lice, 16.2% (95% CI: 10.2–24.9) in flea, 13.0% (95% CI: 9.4–17.6) in mites, and 6.2% (95% CI: 3.8–9.8) in flies with high heterogeneity ($I^2 = 98\sim 99\%$). Tick infestation was predominant in livestock, particularly cattle (40%), whereas lice infestation was predominant in poultry, particularly ducks (98%). *Rhipicephalus* and *Haemaphysalis* were the most frequently observed genera, with *Rhipicephalus microplus* (19.5%) showing the highest pooled infestation proportion, followed by *Haemaphysalis bispinosa* (16.5%). Meta-regression explained 28.4%, 82.9%, and 39.9% of heterogeneity for ticks, lice, and mites, respectively. Sensitivity analyses supported the robustness of the findings. The study revealed Mymensingh (25.6%) as the most frequently represented study area, followed by Dhaka (24.4%) and Chattogram (15.6%). Research on ectoparasite fauna in Bangladesh is limited to cross-sectional studies with limited sample sizes, species, and geographical range, resulting in a knowledge gap about the overall ectoparasitic burden in animals across seasons and areas. Systematic studies across a broader animal species and geographic regions are necessary to better understand ectoparasite epidemiology in Bangladesh and to inform strategies for animal productivity and public health.

1. Introduction

Ectoparasites such as ticks, mites, fleas, flies, and lice are a diverse group of arthropods belonging to the class Arachnida (ticks and mites) and Insecta (flea, lice, and flies) that occupy the external body surfaces of vertebrates and feed on tissues and/or body fluids [1], causing

detrimental effects to the host body and overall health [2,3]. Ectoparasitic infestation is a common problem for the livestock industry as it causes various degrees of production losses [4]. It is a serious concern for human and animal health in developing countries. Ectoparasitic infestations are frequently observed in developing nations, particularly in Asia and Africa [5], due to poor hygienic practices and socioeconomic

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conditions [6–9]. Globally, ticks and Tick-Borne Diseases (TBDs) are estimated to cause annual economic losses of USD 22–30 billion [10]. In developing countries alone, the economic burden associated with TBDs is estimated at USD 14–19 billion annually [11]. In South Asia, substantial production losses have also been documented, including an estimated loss of approximately USD 787 million annually due to ticks and tick-borne diseases in cattle and buffaloes in India [12]. Similarly, a four-month study conducted on a Holstein Friesian dairy farm in Pakistan reported that tropical theileriosis, a tick-borne pathogen, alone resulted in an estimated economic loss of approximately USD 0.02 million, highlighting the substantial farm-level economic burden associated with tick-borne diseases [13]. Ectoparasite burdens are typically higher in tropical regions because the warm, humid climate creates ideal conditions to complete the life cycle of ticks, fleas, lice, and mites. In 2017, the World Health Organization (WHO) classified scabies and other ectoparasitic infections as Neglected Tropical Diseases (NTDs), highlighting the public health significance of ectoparasitic infections. This designation also underscores the One Health relevance of ectoparasitic infestations, as animal-associated ectoparasites can contribute to zoonotic transmission, pathogen dissemination, reduced livestock productivity, and increased risks at the human-animal-environment interface. A study in Kelantan, Malaysia, found that 60% of sampled small ruminants (sheep and goats) were infested with at least one species of ectoparasite, with lice and ticks being the most prevalent at 43.64% and 22.98%, respectively [14]. These findings are particularly relevant to the Bangladeshi context due to the shared tropical climatic conditions, including high humidity and temperatures, which facilitate year-round proliferation of similar ectoparasites. Moreover, both regions utilize comparable smallholder livestock management systems, in which similar host- and environment-related risk factors may contribute to high infestation rates. Ectoparasites can have several direct and indirect harmful effects on the host body, such as low weight gain and milk production, poor quality hides, reduced grazing time or rumination, rubbing and self-wounding, and pruritus [15–19]. Continuous irritation during biting or sucking blood by mites can cause emaciation, anemia, loss of production, and in severe cases, death among poultry [20–22]. Also, there are a few mite species like *Knemidocoptes mutans*, *Epidermoptes bilobatus*, and *Dermatophagoides* spp. etc., which do not suck blood; rather, they feed on the skin or tissues of the animal. An adult tick can suck blood 400–500 times its initial unfed body weight, and if three ticks are allowed to feed on a mouse, the animal may die due to severe anemia [23–25].

In addition to the direct devastating effects, ectoparasites can also act as vectors for different pathogens of veterinary and human medical importance [26,27]. Crimean-Congo hemorrhagic fever virus, tick-borne encephalitis virus, *Coxiella burnetii*, *Rickettsia* spp., *Borrelia* spp. *Babesia* spp., *Anaplasma* spp., and *Theileria* spp. are transmitted by ticks [28–31]. Fleas are the vectors responsible for transmission of *Yersinia pestis* (plague) and *Rickettsia typhi* (murine typhus) from rats to humans [32]. In the past, both scrub typhus and murine typhus have been reported in Bangladesh. A study in Chittagong reported scrub typhus in 16.8% and murine typhus in 5.8% of febrile patients [33]. Similarly, *Rickettsia felis*, a flea-borne pathogen, has been detected at a high rate (46%) in sporadic patients with a fever of unidentified source in Bangladesh [34]. Cat fleas (*Ctenocephalides felis*) and dog fleas (*C. canis*) act as intermediate hosts of *Dipylidium caninum*, a zoonotic tapeworm commonly known as “flea tapeworm” or “cucumber tapeworm” [35].

Geographical location, tropical and subtropical climate, poor management and hygiene, host-parasite interactions, co-farming of various domestic animals and birds, co-endemicity, and easy entrance of peri-domestic and wild animals to farms and premises favor the multiplication and abundance of ectoparasites in Bangladesh [36]. Although ticks can infest many domestic and wild animals, only a few tick species that infest humans, cattle, dogs, goats, wild mammals, domestic fowls, and reptiles have been identified in Bangladesh [37]. A comprehensive and

robust study on ectoparasitic infestation in different species has not yet been performed in Bangladesh, but would provide a valuable reference for veterinary and human medicine. It is essential to know the host range, type, seasonal patterns, geographical range, and present research gaps to reduce the burden of ectoparasites in Bangladesh. This study presents a comprehensive systematic review and meta-analysis of the available literature on ectoparasites of domestic and wild animals, including poultry in Bangladesh, from 1968 to 2024.

2. Materials and methods

2.1. Study design and protocol

The study was carried out by the Preferred Reporting Items for Systematic Reviews and Meta-Analysis (PRISMA-2020) guidelines [38]. The outcome of interest of this study was to gather information regarding the infestation of different ectoparasites, such as ticks, lice, mites, fleas, and flies, across diverse animal hosts. Animal habitats were characterized as domestic and peri-domestic. The outcome measures were the prevalence or proportion of infestations of ectoparasites and their spatial and temporal distribution, based on peer-reviewed publications. All available published research articles on ectoparasitic infestation in domestic and peri-domestic animals were potentially helpful articles that may contain one or more datasets depending on the species, host, habitat, and geographic locations. The protocol of the systematic review and meta-analysis was registered in the Open Science Framework (OSF) registries (DOI: <https://doi.org/10.17605/OSF.IO/4VRT7>).

2.2. Literature search strategy

We conducted a comprehensive electronic and manual search of literature published from 1968 through 2024. The electronic search was performed using online databases such as PubMed, CAB Abstracts, Scopus, Web of Science, Google Scholar, and ResearchGate. The search strategy was developed using combinations of Boolean operators (AND, OR), Medical Subject Headings (MeSH), and free-text terms related to ectoparasites, host animals, epidemiological outcomes, and geographical locations. For PubMed, both MeSH terms and free-text keywords were applied to improve search sensitivity and specificity, whereas database-compatible keyword combinations were used for the remaining databases. The search keys were (“prevalence” OR “incidence” OR “occurrence” OR “identification” OR “isolation” OR “characterization”) AND (“ectoparasite*” OR “tick*” OR “lice” OR “louse” OR “mite*” OR “fly” OR “flies” OR “flea*” OR “mange”) AND (“cattle” OR “cow*” OR “buffalo*” OR “goat*” OR “sheep” OR “horse*” OR “pig*” OR “dog*” OR “cat*” OR “poultry” OR “bird*” OR) AND (“Bangladesh” OR “Dhaka” OR “Chittagong” OR “Sylhet” OR “Mymensingh” OR “Rajshahi” OR “Rangpur” OR “Barisal” OR “Khulna”). Full-text articles that could not be accessed online were identified from the library of the Bangladesh Agricultural University, Mymensingh, Bangladesh. Database-specific search syntaxes are provided in the Supplementary File 1. All the included studies are cited in the study characteristics table (Supplementary Table 1), and their corresponding full references are provided in the main manuscript's reference list, including studies not individually cited in the main text.

2.3. Eligibility criteria

Articles were included in this study based on seven criteria: 1) availability of the full-text article, 2) clear report on ectoparasitic infestation, 3) geographic location includes Bangladesh or any district or sub-district of Bangladesh, 4) clear statement of animal host species, 5) descriptive (survey, case report, case series) or observational study (cross-sectional, case-control, and cohort), 6) English as the language of the article, and 7) diagnostic method of ectoparasite detection: studies were included based on diagnostic approaches used in the original

publications for ectoparasite detection. Eligible studies were those that employed one or more of the following approaches: morphological identification by conventional microscopic examination based on taxonomic characteristics, following established guidelines; molecular confirmation using nucleic acid-based methods, such as PCR assays; immunodiagnostic techniques, such as ELISA or antigen/antibody detection; and clinical examination and visual inspection. Articles excluded from this study included experimental studies and randomized controlled trials, studies conducted outside of Bangladesh, those that did not report outcomes of interest, inconsistent data, book chapters, review articles, unpublished studies, conference proceedings, duplicate articles, and unrelated titles. Duplications were eliminated using the web-based software Covidence (<https://www.covidence.org/>). Two reviewers independently screened all titles and abstracts applying inclusion and exclusion criteria in Covidence, and a third reviewer resolved any conflicts regarding articles. EndNote version 21 was used to manage references and insert articles into Covidence.

2.4. Quality appraisal

All included studies were independently assessed for methodological quality by two authors (Debnath K and Raquib A) using the Joanna Briggs Institute (JBI) critical appraisal checklist for prevalence studies [39] and case reports [40]. The assessment was conducted using a Microsoft Excel-based spreadsheet. Any disagreements in scoring were cross-checked by the authors and resolved through discussion. Each study was assessed for the appropriateness of the sampling frame and method, the clarity of study population and setting descriptions, and the adequacy of data analysis for the reported sample. In addition, studies were assessed for the validity of diagnostic methods used to detect ectoparasitic infections, the reliability of outcome measurement across participants, the appropriateness of statistical analyses, and the adequacy and management of the response rate. Each item was scored as “1” for yes, “0” for no/unclear/NA (not applicable). The total quality scores were then used to categorize studies into three groups: low quality (0-3), moderate quality (4-6), and high quality (7-9).

2.5. Outcome definition

The primary outcome was the infestation proportion, defined as the proportion of examined animals found to be infested with a specified ectoparasite taxon or species. For each study, the infestation proportion was calculated as the number of animals infested with the respective ectoparasite divided by the total number of animals examined, and was expressed as a percentage. Where reported, infestation proportions were extracted at the ectoparasite taxon, genus, or species level. For studies reporting multiple ectoparasite taxa or species, each estimate was treated as a separate outcome according to the corresponding taxon or species. The term “infestation proportion” was used as the overall outcome measure because the included studies differed in their sampling frameworks and populations. In population-based cross-sectional studies, the infestation proportion is the proportion of infested animals in the sampled population, whereas in hospital registry-based studies, it is the proportion of animals infested among those examined or registered. Accordingly, the pooled estimates were interpreted as infestation proportions rather than as population-level prevalence estimates across all study designs.

2.6. Data extraction, study characteristics, and descriptive analysis

From the selected articles, we extracted the data systematically in a standardized spreadsheet. The extracted information included the name of the first author, publication year, study design, sampling method/type, geographic location (district), ectoparasite taxon and species, host species, prevalence/infestation proportion/occurrence of different ectoparasites, population size, infested animal, seasonal infestation, and

diagnostic methods in an Excel spreadsheet. Three authors (Debnath K, Sarker BS, and Siddique SS) conducted the study selection and data extraction independently to minimize bias and ensure accuracy. In case of discrepancy, the article or extracted data were assessed and resolved through a discussion or consultation with a fourth reviewer (Islam A).

Descriptive characteristics of the included studies were summarized as frequencies and percentages. To describe the variation in reported ectoparasite infestation among host species, the minimum and maximum infestation proportions reported across individual studies were summarized for each host species. These observed infestation proportion ranges were calculated separately at the ectoparasite taxon and species levels across host species. The overall infestation proportion range was summarized from studies that explicitly reported an overall ectoparasite infestation proportion and was not calculated by summing taxon- or species-specific proportions, because individual animals could have been concurrently infested by more than one ectoparasite taxon or species. Studies that reported the presence or identification of ectoparasite taxa/species but did not provide sufficient data to calculate infestation proportions were included in the descriptive systematic review but excluded from quantitative meta-analysis.

2.7. Data analysis

The apparent ectoparasitic infestations by different taxa were estimated as a proportion of the infested animals among the total number of animals examined. Forest plots were used to visualize the variation in the estimated proportion of infestation. Between-study variation was identified using Cochran's Q test to measure the heterogeneity, indicating whether the variation in the studies was more than the expected level by chance ($P < 0.05$ was considered significant heterogeneity). Higgins's I^2 value was used to determine the percentage of total variance in effect estimates attributable to heterogeneity rather than chance among the studies. I^2 values of 25%, 50%, and 75% were considered low, moderate, and high heterogeneity, respectively [41]. A random-effect meta-analysis was carried out to estimate the proportion of ectoparasite infestation in Bangladesh with 95% confidence intervals (CI) to represent heterogeneity.

Genus- and species-level infestation proportions were summarized separately within each major ectoparasite taxon (tick, lice, mite, flea, and fly). For each genus or species, the observed infestation proportion range was defined as the minimum and maximum infestation proportions reported across eligible studies. Separate random-effects meta-analyses were then conducted for each genus and species to obtain pooled infestation proportion estimates with corresponding 95% confidence intervals. Estimates were pooled across all eligible host species without stratification by host species.

A subgroup meta-analysis was conducted on different subsets of data to estimate the infestation proportions of ectoparasite taxa (ticks, lice, mites, fleas, and flies) across animal host species (cattle, buffalo, goats, sheep, dogs, cats, horses, pigs, and poultry). The test for subgroup differences was based on Cochran's Q value, which indicates the presence of heterogeneity among subgroups. The infestation proportion estimates of different datasets were pooled using the DerSimonian-Laird random-effect method [42]. All analyses were performed using R version 4.3.2 and RStudio version 2024.04.2 + 764, using the “meta” package. Pooled proportion estimates were calculated using the “metaprop” function, and Forest plots were generated using the “forest” function within the same “meta” package.

Univariable and multivariable random-effects meta-regression analyses were conducted separately for each ectoparasite taxon to further investigate the source of between-study heterogeneity in reported infestation proportions. The logit-transformed infestation proportion was used as the outcome. Categorical moderators included study design, sampling type, diagnostic method, host, host order, host category, and study quality, while publication year and sample size were evaluated as continuous moderators. Sample size was expressed per 100 animals to

facilitate interpretation of the regression coefficient. Moderator categories with fewer than 3 studies were excluded from both univariable and multivariable meta-regression analyses due to sparse data, which can lead to unstable estimates. Each moderator was initially assessed in a univariable meta-regression model to identify predictors of heterogeneity. Moderators with $p < 0.20$ were considered candidates for multivariable analyses. Associations among categorical moderators were assessed using Cramér's V, and multicollinearity was evaluated using generalized variance inflation factors (GVIFs). Moderators that were highly correlated were not included simultaneously in the multivariable meta-regression. Multivariable models were fitted when candidate moderators were suitable for simultaneous inclusion without substantial collinearity, subject to the number of available studies and model parsimony. The meta-regression model was fitted using restricted maximum likelihood (REML) estimation. Residual heterogeneity was evaluated using I^2 and τ^2 statistics, while R^2 was used to estimate the proportion of heterogeneity.

Sensitivity analyses were conducted to assess the robustness of the pooled infestation proportion estimates to study quality and the influence of individual studies. For study-quality sensitivity analysis, studies were categorized as high quality (HQ), moderate quality (MQ), or low quality (LQ) based on the JBI quality-assessment criteria. A sequential study-quality sensitivity analysis was performed by first excluding low-quality studies (HQ+MQ), then restricting the analysis to high-quality studies only (HQ). Changes in the pooled proportions from these analyses were compared with those from the primary analysis (HQ+MQ+LQ) to assess the robustness of the findings to study quality. In addition, the leave-one-out sensitivity analysis was conducted to evaluate the robustness of the pooled infestation proportion and to determine whether any individual study disproportionately influenced the overall meta-analysis. The analysis was performed using the “metainf” function in the R package ‘meta’ within RStudio. Prior to analysis, unique study identifiers were generated using the “make.unique” function to distinguish multiple datasets reported by the same author in the same publication year. The results were visualized using an influence forest plot scaled to percentage infestation proportion values.

Potential small-study effects may influence the pooled effect estimate. Therefore, funnel plots were generated to visually assess funnel-plot asymmetry. Additionally, the asymmetry of the plot was tested and quantified using Egger's test [43].

A choropleth map was created using RStudio to depict the spatial pattern of the study locations throughout the country and to visualize the temporal distribution of ectoparasitic infestation proportion and yearly publication numbers in Bangladesh. Additional analyses were conducted to assess whether the lead research institutions of each study showed a tendency to conduct research within or near their respective base regions, and these detailed analytical methods and institution-specific findings are provided in the [Supplementary Methods](#) (Supplementary File 2).

3. Results

3.1. Study selection

Fig. 1 shows the overall selection process used in this systematic review and meta-analysis. A total of 674 articles were identified through database searches in PubMed, Scopus, Web of Science, CAB Abstracts, Google Scholar, and ResearchGate, and 18 additional articles were collected from the BAU library archive and included. After removing duplicates, 314 articles remained for title and abstract screening. Following the initial screening process, 164 articles were selected for full-text assessment. During full-text evaluation, studies were excluded if they were conducted outside Bangladesh, did not focus on ectoparasites, lacked animal-level infestation data, involved only human populations, were review articles, or contained insufficient or unclear data. Finally, 90 articles met the inclusion criteria and were included in the systematic

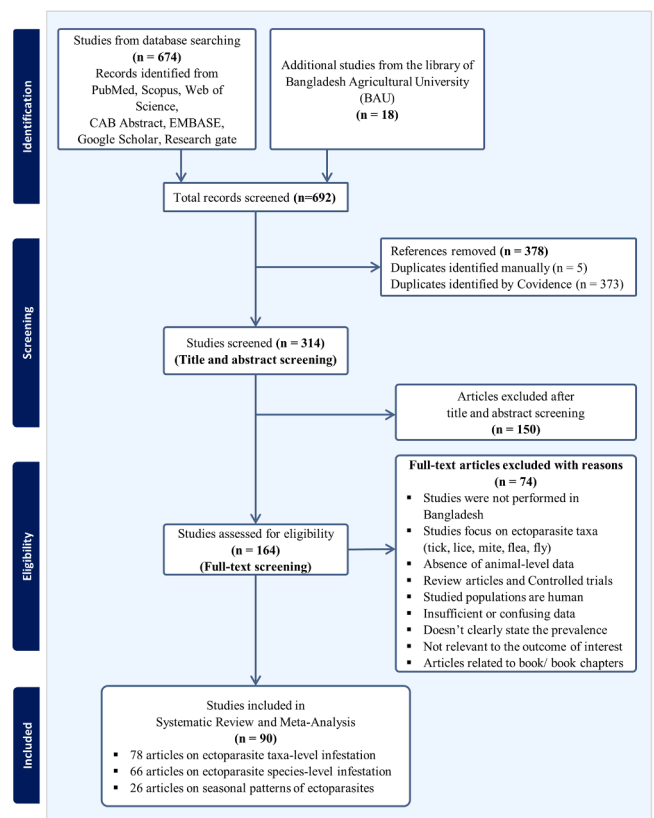


Fig. 1. PRISMA flow diagram of the study selection process for the systematic review and meta-analysis of the epidemiology of ectoparasites in Bangladesh, 1968-2024.

review and meta-analysis to determine the proportion of infestation by different types of ectoparasites affecting animals and birds in Bangladesh.

3.1.1. Characteristics of eligible studies

The summary characteristics of eligible studies are presented in [Table 1](#). All included studies were original research articles published in English and were either cross-sectional prevalence studies (76%), hospital registry-based descriptive studies (22%), or case reports (2%). The studies included a wide range of domestic, peri-domestic, and wild animal hosts, with the most frequently reported species being cattle (30%), followed by dogs (18%), and goats (17%); cats accounted for 8%, while buffalo and pigeon accounted for 4% each. The remaining host (Pig, Chicken, Duck, Rabbit, Sheep, Jackal, Bat, Peafowl, Rodent) species were less frequently represented. Among the ectoparasite taxa, both ticks (27%) and lice (26%) were predominantly reported taxa, followed by mites (20%), flies (13%), and fleas (9%). Around 4% of the reported taxa were unspecified or could not be identified to the taxon species.

Considerable variability was observed among studies in terms of ectoparasite diagnostic methods, sampling types, geographical coverage, and sample sizes. Most studies relied on conventional morphological identification based on microscopic observation through standard parasite identification guidelines (79%), while a limited portion also applied naked-eye visual inspection (20%) and molecular confirmation methods (PCR) (1%). The majority of the included studies used non-probability sampling (40%), followed by approximately 28% being hospital-based studies, in which no sampling method was used, as data were collected from registry books of animals visiting the veterinary hospitals. Around 17% of the included studies used probability sampling during data collection, whereas 13% employed mixed-methods sampling procedures. The sample size varied substantially among the 90 included studies, ranging from 5 to 13421 animals, with a

Table 1
Summary characteristics of the included studies (N = 90) in Bangladesh, 1968–2024.

Characteristics	Category	No. of studies (%)
Study design (N = 90)	Cross-sectional	68 (75.6%)
	Hospital registry	20 (22.2%)
	Case report	2 (2.2%)
Host species (N = 123) ^a	Cattle	37 (30.1%)
	Dog	22 (17.9%)
	Goat	21 (17.1%)
	Cat	10 (8.1%)
	Buffalo; Pigeon	5 (4.1%) each
	Pig	4 (3.3%)
	Chicken; Duck; Rabbit; Sheep	3 (2.4%) each
	Jackal	2 (1.6%)
	Bat (<i>Pteropus medius</i>); Peafowl; Rodent (rat/mouse); Cattle-Goat; Dog-Cat	1 (0.8%) each
Ectoparasite taxa (N = 182) ^a	Tick	49 (26.9%)
	Lice	48 (26.4%)
	Mite	37 (20.3%)
	Fly	23 (12.6%)
	Flea	17 (9.3%)
	Unspecified/Combined	8 (4.3%)
Diagnostic method (N = 91) ^a	Microscopy	73 (79.3%)
	Naked eye	18 (19.6%)
	PCR	1 (1.1%)
Sampling type (N = 90)	Non-Probability	36 (40%)
	Hospital-based	25 (27.8%)
	Probability	15 (16.7%)
	Mixed	12 (13.3%)
	NA	2 (2.2%)
Sample size	Range	5–13421
	Median (Q1–Q3)	250 (125–463)
Study area (District) (N = 90)	Mymensingh	23 (25.6%)
	Dhaka	22 (24.4%)
	Chattogram	14 (15.6%)
	Rajshahi	8 (8.9%)
	Cumilla	7 (7.8%)
	Sylhet; Tangail	6 (6.7%) each
	Dinajpur; Jessore	5 (5.6%) each
	Bandarban; Khulna; Rangpur	4 (4.4%) each
	Bhola; Bogra; Chapainawabganj; Faridpur; Gaibandha; Gazipur; Jaypurhat; Khagrachari; Rangamati; Sirajganj	3 (3.3%) each
	Bagerhat; Jamalpur; Manikganj; Moulvibazar; Narshingdi; Natore; Pabna	2 (2.2%) each
	Barisal; Cox's Bazar; Feni; Gopalganj; Kurigram; Kustia; Munshiganj; Naogaon; Narayanganj; Netrakona; Patuakhali; Sherpur	1 (1.1%) each
Publication year (N = 90)	1968–2000 (20th century)	18 (20.0%)
	2001–2024 (21st century)	72 (80.0%)

^a N denotes the denominator. Denominators may exceed the total number of studies (N = 90), and percentages may not sum to 100%, including for districts, where a single study could report on more than one category.

median of 250 animals (Q1–Q3: 125–463). The studies were conducted across 41 districts (64%) of Bangladesh, representing diverse agro-ecological and climatic regions that may influence ectoparasite distribution and infestation patterns. Mymensingh was the most frequently represented district (26%), followed by Dhaka (24%) and Chattogram (16%). Rajshahi (9%) and Cumilla (8%) were also frequently represented, while the remaining districts were represented by fewer studies. Among the 90 included articles, 78 were eligible for estimating the ectoparasite taxa-level pooled infestation proportion, 66 for estimating the species-level pooled infestation for ectoparasite species, and 26 for estimating the seasonal infestation patterns of different types of ectoparasites. The Detailed characteristics of all the included studies are presented in the [Supplementary Table 1](#).

3.1.2. Quality of included studies

The majority of the studies were of moderate methodological quality, with 57% (51/90) rated as moderate, 28% (25/90) as high, and the

remainder 15% (14/90) as low quality, as presented in [Supplementary Table 2](#). High-quality studies generally fulfilled most JBI criteria, particularly regarding outcome measurement and statistical analysis, whereas low-quality studies commonly showed weaknesses in sampling methods, participant selection, and reporting clarity. No study was excluded for lack of merit based on quality assessment. Overall, the included evidence was considered predominantly moderate-to-high quality, supporting the reliability of the review findings.

3.2. Observed proportions of ectoparasitic infestation across host species

The ranges of ectoparasite infestation proportions across different animal species are presented in [Table 2](#). Infestation proportions varied substantially across host species and ectoparasite taxa. Among the major livestock hosts, cattle were the most frequently studied hosts (k = 26), followed by goats (k = 18), dogs (k = 17), and other animal species. Overall infestation proportions ranged from 2.0% to 77.6% in cattle and from 6.0% to 75.6% in goats. In cattle, ticks were the most frequently investigated ectoparasite group (k = 21), with infestation proportions ranging from 5.3% to 87.7%, followed by lice (0.7–23.6%), mites (1.3–12.0%), and flies (1.7–11.0%). At the species level, *Haemaphysalis bispinosa* and *Rhipicephalus microplus* were among the most frequently reported cattle ticks, with infestation proportions ranging from 3.5% to 37.9% and 11.2–71.4%, respectively, while *Rhipicephalus sanguineus* ranged from 0.9% to 43.5%. Among cattle lice, *Haematopinus quadripertusus* showed the highest reported species-level range (8.2–40.8%). In goats, ticks showed particularly wide variation, ranging from 1.8% to 97.0%, while lice, mites, fleas, and flies ranged from 1.1% to 49.7%, 2.9–65.5%, 4.9–61.8%, and 2.1–19.2%, respectively. *Haemaphysalis bispinosa* was the most frequently reported goat tick, with infestation proportions ranging from 3.1% to 55.4%, whereas *Rhipicephalus microplus* ranged from 3.1% to 45.5%. Among goat mites, *Raillietia manfredi* had a reported infestation proportion of 56.4%, while *Ctenocephalides felis* was reported at 50.0–61.8%. Among other ruminants, buffaloes showed tick infestation of 0.2%, whereas lice infestation ranged from 5.8% to 51.3%, with *Haematopinus tuberculatus* ranging from 36.5% to 51.3%. In sheep, lice were more prominent than ticks and mites, with taxon-level infestation proportions of 40.5–62.5%; *Damalinea ovis* ranged from 40.5% to 64.2%. In pigs, tick infestation ranged from 13.2% to 25.0%, while lice infestation was 44.4%, attributable to *Haematopinus suis*.

Companion animals also showed considerable variation among ectoparasite taxa. In dogs, mites had the widest range (1.2–65.0%), followed by ticks (1.2–59.4%), fleas (3.5–25.0%), lice (0.3–10.9%), and flies (2.6–8.7%). *Rhipicephalus sanguineus* was the principal reported dog tick, with infestation proportions of 27.4–59.4%, while *Sarcoptes scabiei* ranged from 18.2% to 60.0%. In cats, fleas showed the highest reported taxon-level infestation range (3.0–86.1%), including an 86.1% infestation proportion for *Ctenocephalides felis*, whereas mites ranged from 3.0% to 46.2%.

Poultry generally exhibited higher infestation proportions than the mammalian hosts. In chickens, lice infestation was 70.3%, while mites were detected at 86.5%; species-level proportions reached 74.0% for *Menacanthus stramineus* and 63.0% for *Menopon gallinae*. All three duck studies reported 100% lice infestation, with several louse species showing proportions exceeding 80%. Pigeons showed a wider range of lice infestation (18.1–100.0%), with *Columbicola columbae* and *Menopon gallinae* each reaching 100%. The single peafowl study also reported 100% lice infestation. Thus, among avian hosts, lice were consistently prominent and frequently occurred at very high infestation proportions.

Less frequently studied hosts showed substantial infestation proportions but were represented by few studies. In rodents, mite infestation was 15.1%, while flea and fly infestation proportions were 9.6% and 1.4%, respectively. Rabbit mite infestation ranged from 12.1% to 100.0%, with mange showing a similar range. The single bat study reported a 72.1% infestation proportion with the bat fly *Cyclopodia sykesii*.

Table 2
Infestation proportions of ectoparasites across different host species.

Host species	Taxon-level infestation proportion range (%)	Species-level infestation Proportion range (%)	Overall infestation proportion range (%)
Cattle (k = 26)	Tick (5.3–87.7); k = 21	<i>Amblyomma testudinarium</i> (4.4–4.4); k = 1	2.0–77.6; k = 30
		<i>Amblyomma variegatum</i> (5.8–5.8); k = 1	
		<i>Dermacentor</i> sp. (0.3–4.5); k = 2	
		<i>Haemaphysalis bispinosa</i> (3.5–37.9); k = 15	
		<i>Haemaphysalis kinneari</i> (10.4–16.4); k = 3	
		<i>Hyalomma anatolicum</i> (2.7–64.6); k = 7	
		<i>Hyalomma</i> sp. (1.9–1.9); k = 1	
		<i>Ixodes</i> sp. (Adult) (6.0–15.8); k = 2	
		<i>Ixodid</i> (larvae) (3.7–5.2); k = 3	
		<i>Rhipicephalus annulatus</i> (4.1–4.1); k = 1	
	Lice (0.7–23.6); k = 12	<i>Rhipicephalus microplus</i> (11.2–71.4); k = 15	
		<i>Rhipicephalus sanguineus</i> (0.9–43.5); k = 12	
		<i>Damalinia bovis</i> (8.3–26.1); k = 4	
		<i>Haematopinus eurytenuis</i> (0.5–23.2); k = 8	
		<i>Haematopinus quadripertusus</i> (8.2–40.8); k = 4	
		<i>Linognathus vituli</i> (5.0–23.3); k = 7	
		<i>Solenopotes capillatus</i> (1.0–1.0); k = 1	
		Mange (2.1–12.0); k = 2	
		<i>Diachlorus</i> sp. (0.2–0.3); k = 3	
		Maggot/ Myiasis (1.7–11.0); k = 5	
	Mite (1.3–12.0); k = 5	<i>Musca domestica</i> (43.1–58.3); k = 3	
		<i>Stomoxys calcitrans</i> (0.3–5.7); k = 3	
		<i>Tabanus striatus</i> (2.7–7.8); k = 3	
		<i>Dermacentor</i> sp. (2.5–5.8); k = 2	
		<i>Haemaphysalis bispinosa</i> (3.1–55.4); k = 10	
		<i>Haemaphysalis kinneari</i> (3.6–21.8); k = 3	
		<i>Hyalomma anatolicum</i> (1.8–4.6); k = 2	
		<i>Ixodes</i> sp. (Adult) (1.1–3.1); k = 2	
		<i>Ixodid</i> (larvae) (0.5–5.8); k = 2	
		<i>Rhipicephalus microplus</i> (3.1–45.5); k = 9	
	Lice (1.1–49.7); k = 7	<i>Rhipicephalus sanguineus</i> (1.0–31.5); k = 6	6.0–75.6; k = 17
		<i>Damalinia bovis</i> (29.1–52.4); k = 3	
		<i>Damalinia caprae</i> (8.5–48.0); k = 6	
		<i>Haematopinus eurytenuis</i> (15.8–15.8); k = 1	
		<i>Linognathus africanus</i> (22.5–22.5); k = 1	
		<i>Linognathus stenopsis</i> (18.4–24.3); k = 3	
		<i>Linognathus vituli</i> (4.2–28.3); k = 5	
		<i>Demodex</i> sp. (2.9–2.9); k = 1	
		Mange (3.6–9.1); k = 3	
		<i>Psoroptes cuniculi</i> (5.6–9.1); k = 3	
	Flea (4.9–61.8); k = 5	<i>Raillietia manfredi</i> (56.4–56.4); k = 1	19.7–19.7; k = 1
		<i>Ctenocephalides canis</i> (4.8–9.2); k = 2	
		<i>Ctenocephalides felis</i> (50.0–61.8); k = 3	
		Maggot/ Myiasis (2.1–11.1); k = 3	
		<i>Oestrus ovis</i> (19.2–19.2); k = 1	
		Not reported	
	Fly (2.1–19.2); k = 4	<i>Haemaphysalis bispinosa</i> (10.8–11.4); k = 2	5.8–61.9; k = 3
		<i>Rhipicephalus microplus</i> (12.5–14.0); k = 2	
		<i>Haematopinus tuberculatus</i> (36.5–51.3); k = 2	
		<i>Haemaphysalis bispinosa</i> (16.7–16.7); k = 1	
		<i>Rhipicephalus microplus</i> (12.5–12.5); k = 1	
		<i>Damalinia ovis</i> (40.5–64.2); k = 2	
		<i>Linognathus pedalis</i> (15.8–15.8); k = 1	
		<i>Psoroptes ovis</i> (5.8–5.8); k = 1	
		<i>Amblyomma testudinarium</i> (2.4–2.4); k = 1	
		<i>Haemaphysalis bispinosa</i> (13.2–13.2); k = 1	
	Tick (13.2–25.0); k = 2	<i>Rhipicephalus microplus</i> (8.2–25.0); k = 2	13.2–57.3; k = 2
		<i>Haematopinus suis</i> (44.4–44.4); k = 1	
		<i>Rhipicephalus sanguineus</i> (27.4–59.4); k = 4	
		<i>Trichodectes canis</i> (10.9–10.9); k = 1	
		<i>Demodex canis</i> (35.4–35.4); k = 1	
		<i>Demodex</i> sp. (27.0–27.0); k = 1	
		Mange (1.2–65.0); k = 7	
		<i>Otodectes cynotis</i> (8.4–19.8); k = 2	
		<i>Sarcoptes scabiei</i> (18.2–60.0); k = 3	
		<i>Ctenocephalides canis</i> (13.8–13.8); k = 1	
	Lice (44.4–44.4); k = 1	Maggot/ Myiasis (3.5–8.7); k = 4	6.1–75.0; k = 20
		<i>Rhipicephalus</i> sp. (Not reported); k = 1	
		Not reported	
		<i>Demodex cati</i> (11.1–11.1); k = 1	
		Mange (3.0–23.7); k = 2	
		<i>Otodectes cynotis</i> (46.2–46.2); k = 1	
	Tick (1.2–59.4); k = 9		2.7–88.9; k = 9
	Lice (0.3–10.9); k = 8		
	Mite (1.2–65.0); k = 14		
	Flea (3.5–25.0); k = 6		
	Fly (2.6–8.7); k = 5		
	Tick (1.5–1.5); k = 1		
	Lice (1.4–1.5); k = 2		
	Mite (3.0–46.2); k = 4		

(continued on next page)

Table 2 (continued)

Host species	Taxon-level infestation proportion range (%)	Species-level infestation Proportion range (%)	Overall infestation proportion range (%)
Dog-Cat (k = 1)	Flea (3.0–86.1); k = 3 Fly (1.3–7.9); k = 3 Tick (1.2–1.2); k = 1 Mite (20.1–20.1); k = 1 Flea (2.9–2.9); k = 1	<i>Ctenocephalides felis</i> (86.1–86.1); k = 1 Maggot/ Myiasis (1.3–7.9); k = 3 Not reported	60.3–60.3; k = 1
Chicken (k = 3)	Lice (70.3–70.3); k = 1	<i>Cuclotogaster heterographus</i> (25.0–25.0); k = 1 <i>Goniocotes gallinae</i> (14.0–18.4); k = 2 <i>Goniodes gigas</i> (18.0–18.0); k = 1 <i>Goniodes dissimilis</i> (25.1–25.1); k = 1 <i>Lipeurus caponis</i> (44.9–48.0); k = 2 <i>Lipeurus lawrensis tropicalis</i> (8.8–8.8); k = 1 <i>Menacanthus pallidulus</i> (6.7–6.7); k = 1 <i>Menacanthus stramineus</i> (0.3–74.0); k = 2 <i>Menopon gallinae</i> (56.7–63.0); k = 2 <i>Dermanyssus gallinae</i> (56.5–57.0); k = 2 <i>Knemidocoptes mutans</i> (5.5–43.0); k = 2 <i>Ornithonyssus bursa</i> (9.0–9.0); k = 1 <i>Ornithonyssus sylviae</i> (15.5–15.5); k = 1	70.3–86.7; k = 3
Duck (k = 3)	Mite (86.5–86.5); k = 1 Fly (3.7–3.7); k = 1 Lice (100.0–100.0); k = 3	<i>Simulium</i> sp. (3.7–3.7); k = 1 <i>Anaticola crassicornis</i> (83.3–100.0); k = 2 <i>Colpocephalum turbinatum</i> (36.7–36.7); k = 1 <i>Goniocotes hologaster</i> (72.2–100.0); k = 3 <i>Goniodes gigas</i> (36.7–36.7); k = 1 <i>Holomenopon leucoxanthum</i> (60.0–80.6); k = 3 <i>Lipeurus caponis</i> (100.0–100.0); k = 2 <i>Lipeurus squalidus</i> (100.0–100.0); k = 1 <i>Menacanthus stramineus</i> (55.6–66.7); k = 3 <i>Menopon gallinae</i> (88.9–96.7); k = 2 <i>Dermanyssus gallinae</i> (50.0–50.0); k = 1 <i>Chelopistes meleagridis</i> (46.7–46.7); k = 1 <i>Colpocephalum turbinatum</i> (33.3–71.7); k = 2 <i>Columbicola columbae</i> (18.1–100.0); k = 5 <i>Goniocotes gallinae</i> (31.7–31.7); k = 1 <i>Lipeurus caponis</i> (25.0–51.7); k = 3 <i>Lipeurus</i> sp. (61.5–61.5); k = 1 <i>Menacanthus stramineus</i> (15.4–46.7); k = 3 <i>Menopon gallinae</i> (16.7–100.0); k = 3 <i>Menopon</i> sp. (45.1–45.1); k = 1 <i>Dermanyssus gallinae</i> (13.3–13.3); k = 1 <i>Echidnophaga gallinacea</i> (8.3–8.3); k = 1 <i>Pseudolynchia canariensis</i> (1.6–63.3); k = 2 <i>Amyrsidea minuta</i> (100.0–100.0); k = 1 <i>Laelaps echidninus</i> (4.1–4.1); k = 1 <i>Laelaps nuttalli</i> (5.5–5.5); k = 1 <i>Laelaps</i> sp. (4.1–4.1); k = 1 <i>Liponyssoides</i> sp. (2.7–2.7); k = 1 <i>Ornithonyssus bacoti</i> (1.4–1.4); k = 1 <i>Xenopsylla cheopis</i> (9.6–9.6); k = 1 Botfly larvae (1.4–1.4); k = 1	100.0–100.0; k = 3
Pigeon (k = 4)	Mite (50.0–50.0); k = 1 Lice (18.1–100.0); k = 4	<i>Mange</i> (12.0–100.0); k = 3 <i>Cyclopodia sykesii</i> (72.1–72.1); k = 1	19.6–100.0; k = 4
Peafowl (k = 1)	Mite (13.3–13.3); k = 1 Flea (8.3–8.3); k = 1 Fly (1.6–63.3); k = 2 Lice (100.0–100.0); k = 1		100.0–100.0; k = 1
Rodent (Rat, Mouse) (k = 1)	Mite (15.1–15.1); k = 1		26.0–26.0; k = 1
Rabbit (k = 3)	Flea (9.6–9.6); k = 1 Fly (1.4–1.4); k = 1 Mite (12.1–100.0); k = 3		12.1–100.0; k = 3
Bat (k = 1)	Fly (72.1–72.1); k = 1		72.1–72.1; k = 1

k = number of studies

3.3. Estimated pooled infestation proportions in ectoparasite taxa- and genus/species-level

Forest plots showing the pooled infestation proportions of the major ectoparasite taxa- ticks, lice, mites, fleas, and flies- are presented in Fig. 2, while genus- and species-level pooled infestation proportions are presented in Table 3. A total of 167 and 304 data points from 90 articles on Bangladesh were used to estimate the infestation proportions at the taxon and genus/species levels, respectively. Across the included studies, ticks were evaluated in 44 studies, followed by lice in 45, mites in 39, flies in 22, and fleas in 17. There were 17 articles where the genus or species of ectoparasites was not mentioned. Among the ectoparasite taxa, tick infestation had the highest pooled infestation proportion at 22.2% (95% CI: 16.6–29.0), with substantial heterogeneity ($I^2 = 99.5\%$). Conversely, flies showed the lowest infestation proportion at 6.2% (95% CI: 3.8–9.8) with high heterogeneity ($I^2 = 98.2\%$). Among different types of ectoparasites, ticks and lice were reported most frequently, while fleas (k = 17) were reported to a lesser extent. This

study identified 11 tick species, 30 lice species, 15 mite species, 4 flea species, and 12 fly species across the included studies from Bangladesh.

Among tick genera, pooled infestation proportion was highest in *Rhipicephalus* and *Haemaphysalis* (16.2% each) and lowest in *Dermacentor* (3.1%). *Rhipicephalus microplus* (k = 29), *Haemaphysalis bispinosa* (k = 29), and *Rhipicephalus sanguineus* (k = 23) were the species reported most frequently in the literature. Under the genus *Rhipicephalus*, *R. microplus* had the highest pooled proportion (19.5%), followed by *R. sanguineus* (13.1%). Among *Haemaphysalis*, pooled infestation proportions were 16.5% for *H. bispinosa* and 15.5% for *H. kinneari*. *Hyalomma* had a pooled infestation proportion of 6.8%, while *Amblyomma* had 5.3%. Lower pooled proportions were observed for *Ixodes* sp. (adult) (4.7%), *Ixodid* larvae (4.6%), and *Dermacentor* sp. (3.1%). Amongst all tick species, *Rhipicephalus microplus* exhibited the highest pooled proportion at 19.5% with a high degree of heterogeneity ($I^2 = 98.5\%$) (Table 3).

Pertaining to lice, the pooled infestation proportion was 16.6% (95% CI: 11.2–24.0), marked by a high heterogeneity ($I^2 = 99.6\%$) (Fig. 2).

Lice infestation proportions varied considerably among species, ranging from 1.0% in *Solenopotes capillatus* to 99.0% in *Amyrsidea minuta* (Table 3). The most frequently reported genera were *Linognathus* (17 studies), *Haematopinus* (16), *Damalinia* (15), *Lipeurus* (10), and *Menacanthus* (9). At the species level, *Linognathus vituli* (12), *Haematopinus eurysternus* (9 studies), and *Damalinia bovis* (7) were among the most frequently reported species. Among louse taxa reported in at least two studies ($k \geq 2$), at the genus level, *Anaticola* had the highest pooled infestation proportion (94.9%), followed by *Menopon* (69.0%) and *Lipeurus* (63.3%), whereas *Linognathus* (14.9%) and *Haematopinus* (15.4%) had the lowest pooled proportion. At the species level, *Anaticola crassicornis* showed the highest pooled infestation proportion (94.9%), followed by *Goniocotes hologaster* (84.0%), *Menopon gallinae* (72.8%), and *Holomenopon leucoanthum* (72.6%), whereas *Haematopinus eurysternus* (7.6%) and *Linognathus vituli* (13.0%) had the lowest pooled proportion.

The estimated pooled infestation proportion of mites was 13% (95% CI: 9.4–17.6) with a high degree of heterogeneity ($I^2 = 98.0\%$) (Fig. 2). *Demodex*, *Dermanyssus*, and *Psoroptes* were the most frequently reported genera ($k = 4$ each), and *Dermanyssus gallinae* was the most frequently reported species ($k = 4$). In consideration of mite taxa reported in at least two studies ($k \geq 2$), *Dermanyssus* had the highest pooled infestation proportion (42.8%), followed by *Sarcoptes* (37.3%), *Otodectes* (21.2%), and *Knemidocoptes* (17.6%), whereas *Laelaps* had the lowest proportion (4.6%). At the species level, *Dermanyssus gallinae* had the highest pooled infestation proportion (42.8%), followed by *Sarcoptes scabiei* (37.3%), *Otodectes cynotis* (21.2%), and *Knemidocoptes mutans* (17.6%), while *Demodex* sp. had the lowest proportion (9.5%). Mange, a skin disease in animals caused by mites (*Demodex* and *Sarcoptes* spp.), was documented in 17 studies, with a pooled infestation proportion of 9.2% (Table 3).

The pooled proportion of fleas infested was 16.2% (95% CI: 10.2–24.9), with high heterogeneity ($I^2 = 98.5\%$) (Fig. 2). The pooled infestation proportions for the most commonly reported genus, *Ctenocephalides* ($k = 7$), and species, *Ctenocephalides felis* ($k = 4$), were 34.1% and 62.7%, respectively, which were markedly higher than the other species (Table 3). Regarding flies, myiasis infestation caused by maggots was estimated at 4.7% across 15 studies. Considering the reporting of at least 2 studies ($k \geq 2$), the pooled infestation was highest in *Musca domestica* (51.6%), followed by *Pseudolynchia canariensis* (14.1%) (Table 3).

3.4. Subgroup analyses by ectoparasite taxa

Subgroup analyses of pooled infestation proportions across all moderator categories are presented in Table 4; however, moderator categories represented by at least two studies ($k \geq 2$) were considered in the narrative interpretation below. For ticks, infestation proportions were higher in population-based cross-sectional studies (26.7%) than in hospital-based studies (8.3%). By sampling type, proportion estimates ranged from 5.6% for hospital-based sampling to 37.8% for non-probability sampling; mixed sampling also yielded a high pooled proportion estimate of 42.5%. Microscopy-based diagnosis was associated with a higher pooled infestation proportion (28.1%) than naked-eye examination (4.7%). Among host species, cattle had the highest pooled infestation proportion (39.1%), followed by goats (26.6%), pigs (19.2%), and dogs (12.9%). At the host-order level, Artiodactyla showed a higher pooled infestation proportion (28.0%) than Carnivora (10.0%). Correspondingly, livestock had a higher pooled proportion (28.0%) than pets (10.0%). By study quality, pooled infestation proportion were 29.7% for moderate-quality studies, 21.2% for high-quality studies, and 11.6% for low-quality studies.

For lice, population-based cross-sectional studies showed a markedly higher pooled infestation proportion (30.7%) than hospital-based studies (1.7%). Pooled infestation proportions by sampling type ranged from 1.7% for hospital-based sampling to 50.4% for non-probability sampling, with probability sampling yielding 27.2%.

Microscopy-based diagnosis produced a substantially higher pooled proportion (31.8%) than naked-eye examination (1.5%). Among host species, pooled infestation proportions were highest in ducks (98.6%), followed by pigeons (73.8%), sheep (52.2%), and cattle (11.1%); dogs and cats had substantially lower proportion estimates of 1.7% and 1.4%, respectively. At the host-order level, Anseriformes had the highest pooled proportion (98.6%), followed by Columbiformes (73.8%) and Artiodactyla (16.1%), whereas Carnivora had a substantially lower proportion (1.7%). Galliformes was represented by only two studies and had a pooled proportion of 92.2%. Accordingly, poultry showed the highest pooled infestation proportion among host categories (89.4%), followed by livestock (16.1%) and pets (1.7%). Study-quality proportion estimates were 28.2% for moderate-quality studies, 22.5% for high-quality studies, and 1.8% for low-quality studies.

For mites, population-based cross-sectional studies had a higher pooled infestation proportion (16.5%) than hospital-based studies (9.1%). By sampling type, non-probability sampling produced a pooled proportion of 25.7%, compared with 9.1% for hospital-based sampling and 6.7% for mixed sampling. Probability sampling, based on three studies, yielded a proportion estimate of 43.1%. Microscopy yielded a higher pooled estimate (16.3%) than naked-eye examination (7.8%). Among host species, rabbits had the highest pooled infestation proportion (43.2%), followed by cats (15.8%), dogs (12.8%), and goats (8.3%), while cattle had the lowest estimate (4.1%). At the host-order level, Carnivora had a pooled infestation proportion of 13.8%, Artiodactyla 6.1%, and Lagomorpha 43.2%. Host-category estimates were 15.8% for pets and 6.1% for livestock. Study-quality estimates were similar across categories: 12.8% for moderate-quality, 13.5% for low-quality, and 12.3% for high-quality studies.

For fleas, population-based cross-sectional studies had a higher pooled infestation proportion (19.7%) than hospital-based studies (11.9%). Non-probability sampling yielded a pooled estimate of 35.6%, compared with 15.9% for probability sampling and 9.5% for hospital-based sampling. Microscopy-based diagnosis resulted in a higher pooled estimate (21.2%) than naked-eye examination (8.3%). Among host species, goats had a pooled infestation proportion of 29.7%, cats 34.3%, and dogs 10.1%. At the host-order level, Artiodactyla had a pooled infestation proportion of 29.7%, whereas Carnivora had 12.6%. Host-category estimates were 29.7% for livestock and 12.6% for pets. Study-quality estimates were 41.0% for high-quality studies, 14.7% for moderate-quality studies, and 8.3% for low-quality studies.

For flies, population-based cross-sectional studies showed a higher pooled infestation proportion (9.5%) than hospital-based studies (4.4%). Among sampling methods, hospital-based sampling accounted for 4.5%, whereas non-probability sampling accounted for 8.5%. The mixed-sampling estimate of 63.3% and the probability-sampling estimate of 2.1% were each based on a single study and were therefore not considered subgroup-pooled findings. Microscopy-based diagnosis yielded a pooled estimate of 7.7%, compared with 4.4% for naked-eye examination. Among host species represented by at least two studies, dogs had a pooled infestation proportion of 4.5%, cats 2.7%, cattle 5.1%, goats 7.0%, and pigeons 14.1%. At the host-order level, Artiodactyla had a pooled infestation proportion of 6.0%, Carnivora 3.9%, and Columbiformes 14.1%. Study-quality estimates were highest among high-quality studies (18.7%), followed by 5.8% for moderate-quality studies and 2.9% for low-quality studies.

3.5. Meta-regression analyses for the source of heterogeneity

Univariable and multivariable random-effects meta-regression analyses were conducted separately for each ectoparasite taxon to investigate potential study-level sources of between-study heterogeneity (Table 5).

For ticks, univariable meta-regression identified several potential sources of between-study heterogeneity. Sampling type showed the strongest evidence of association, accounting for 23.9% of the between-

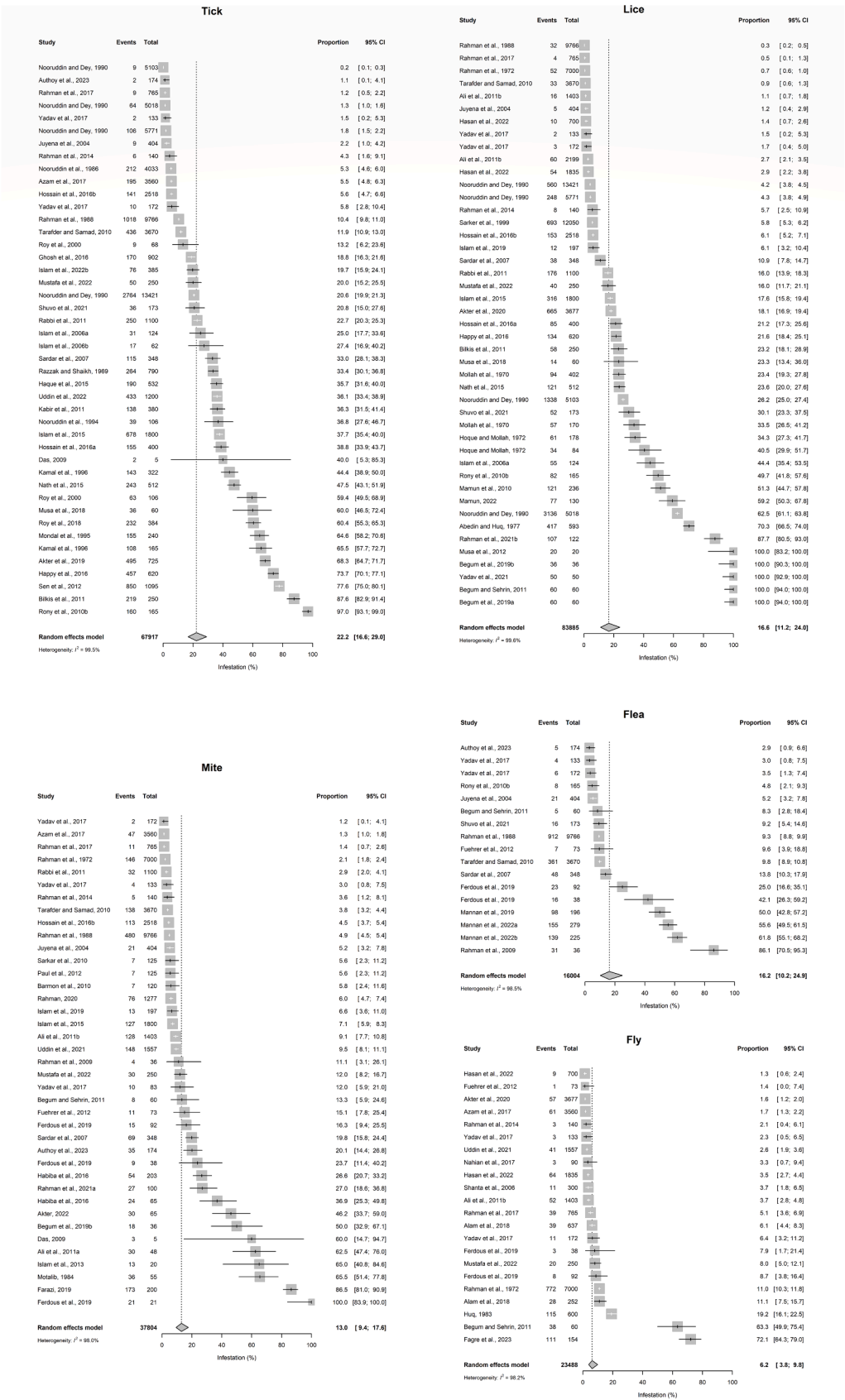


Fig. 2. Forest plots of meta-analysis showing pooled infestation proportion estimates for five major ectoparasite taxa in Bangladesh: Tick, Lice, Mite, Flea, and Fly. Study-specific estimates are represented by squares with horizontal lines indicating 95% CIs; square size reflects study weight. Diamonds represent the pooled infestation proportion estimates, with their centers indicating the pooled estimates and widths representing the 95% CIs.

Table 3

Genus- and species-specific observed infestation range and pooled infestation proportion estimates of ectoparasite taxa in Bangladesh, 1968–2024.

Genus/species	k	Observed infestation proportion range (%)	Pooled infestation Proportion % (95% CI)	Cochran's Q	p-value	I ² (%)
Taxon: Tick	44	0.2–97.0	22.2 (16.6–29.0)	8552.3	< 0.001	99.5
<i>Amblyomma</i>	3	2.4–5.8	5.3 (4.1–6.8)	2.2	0.329	10.1
<i>A. variegatum</i>	1	5.8–5.8	5.7 (4.6–7.2)	0.0	-	-
<i>A. testudinarium</i>	2	2.4–4.4	4.0 (2.3–6.8)	0.7	0.406	0.0
<i>Hyalomma</i>	10	1.8–64.6	6.8 (3.0–14.8)	582.4	< 0.001	98.5
<i>H. anatolicum</i>	9	1.8–64.6	7.8 (3.3–17.4)	521.8	< 0.001	98.5
<i>Hyalomma</i> sp.	1	1.9–1.9	1.9 (1.1–3.1)	0.0	-	-
<i>Rhipicephalus</i>	53	0.9–71.4	16.2 (12.2–21.1)	2752.7	< 0.001	98.1
<i>R. annulatus</i>	1	4.1–4.1	4.1 (2.6–6.3)	0.0	-	-
<i>R. microplus</i>	29	3.1–71.4	19.5 (14.3–25.9)	1821.8	< 0.001	98.5
<i>R. sanguineus</i>	23	0.9–59.4	13.1 (7.8–21.4)	811.2	< 0.001	97.3
<i>Haemaphysalis</i>	36	3.1–66.7	16.2 (12.7–20.4)	1114.3	< 0.001	96.9
<i>H. bispinosa</i>	29	3.1–55.4	16.5 (12.7–21.0)	1008.5	< 0.001	97.2
<i>H. kinneari</i>	7	3.6–66.7	15.5 (7.3–29.7)	69.1	< 0.001	91.3
<i>Dermacentor</i> sp.	4	0.3–5.8	3.1 (1.4–6.7)	10.0	0.018	70.1
<i>Ixodes</i> sp. (Adult)	4	1.1–15.8	4.7 (1.5–13.4)	47.3	< 0.001	93.7
<i>Ixodid</i> (larvae)	5	0.5–5.8	4.6 (3.6–5.8)	6.8	0.148	40.9
<i>Haemaphysalis intermedia</i>	1	Not reported	-	-	-	-
<i>Haemaphysalis leachi</i>	1	Not reported	-	-	-	-
<i>Rhipicephalus decoloratus</i>	1	Not reported	-	-	-	-
Taxon: Lice	45	0.3–100.0	16.6 (11.2–24.0)	12085	< 0.001	99.6
<i>Damalinia</i>	15	8.3–64.2	25.6 (17.5–35.7)	463.7	< 0.001	97.0
<i>D. bovis</i>	7	8.3–52.4	24.2 (13.4–39.9)	219.3	< 0.001	97.3
<i>D. caprae</i>	6	8.5–48.0	20.3 (11.9–32.4)	117.0	< 0.001	95.7
<i>D. ovis</i>	2	40.5–64.2	52.6 (30.1–74.2)	11.0	< 0.001	90.9
<i>Goniocotes</i>	6	14.0–100.0	54.5 (20.4–84.9)	134.3	< 0.001	96.3
<i>G. gallinae</i>	3	14.0–31.7	19.8 (12.4–30.2)	10.5	0.005	81.0
<i>G. hologaster</i>	3	72.2–100.0	84.0 (65.7–93.5)	5.5	0.064	63.5
<i>Goniodes</i>	3	18.0–36.7	25.2 (16.8–35.9)	11.4	0.003	82.4
<i>G. gigas</i>	2	18.0–36.7	25.8 (11.9–47.3)	10.0	0.002	90.0
<i>G. dissimilis</i>	1	25.1–25.1	25.1 (21.8–28.8)	0.0	-	-
<i>Haematopinus</i>	16	0.5–51.3	15.4 (8.5–26.2)	543.1	< 0.001	97.2
<i>H. eurysternus</i>	9	0.5–23.2	7.6 (3.6–15.3)	117.9	< 0.001	93.2
<i>H. quadripertusus</i>	4	8.2–40.8	26.3 (12.5–47.1)	106.8	< 0.001	97.2
<i>H. suis</i>	1	44.4–44.4	44.4 (35.9–53.2)	0.0	-	-
<i>H. tuberculatus</i>	2	36.5–51.3	43.9 (30.2–58.6)	8.7	0.003	88.5
<i>Linognathus</i>	17	4.2–28.3	14.9 (11.2–19.5)	231.6	< 0.001	93.1
<i>L. africanus</i>	1	22.5–22.5	22.5 (16.9–29.2)	0.0	-	-
<i>L. pedalis</i>	1	15.8–15.8	15.8 (10.3–23.5)	0.0	-	-
<i>L. stenopsis</i>	3	18.4–24.3	21.6 (17.9–25.8)	1.5	0.465	0.0
<i>L. vituli</i>	12	4.2–28.3	13.0 (8.9–18.7)	206.5	< 0.001	94.7
<i>Lipeurus</i>	10	8.8–100.0	63.3 (31.9–86.4)	251.8	< 0.001	96.4
<i>L. caponis</i>	7	25.0–100.0	65.4 (31.1–88.7)	30.3	< 0.001	80.2
<i>L. lawrensis tropicalis</i>	1	8.8–8.8	8.8 (6.7–11.3)	0.0	-	-
<i>L. sp.</i>	1	61.5–61.5	61.5 (52.6–69.7)	0.0	-	-
<i>L. squalidus</i>	1	100.0–100.0	97.6 (71.3–99.9)	0.0	-	-
<i>Menacanthus</i>	9	0.3–74.0	29.0 (9.7–60.8)	414.0	< 0.001	98.1
<i>M. pallidulus</i>	1	6.7–6.7	6.7 (5.0–9.1)	0.0	-	-
<i>M. stramineus</i>	8	0.3–74.0	33.7 (10.8–68.1)	181.1	< 0.001	96.1
<i>Menopon</i>	8	16.7–100.0	69.0 (36.0–89.8)	112.0	< 0.001	93.7
<i>M. gallinae</i>	7	16.7–100.0	72.8 (35.0–93.0)	106.8	< 0.001	94.4
<i>Menopon</i> sp.	1	45.1–45.1	45.1 (36.5–54.0)	0.0	-	-
<i>Amyrsidea minuta</i>	1	100.0–100.0	99.0 (86.2–99.9)	0.0	-	-
<i>Anaticola crassicornis</i>	2	83.3–100.0	94.9 (46.1–99.8)	4.6	0.032	78.2
<i>Chelopistes meleagridis</i>	1	46.7–46.7	46.7 (34.5–59.2)	0.0	-	-
<i>Colpocephalum turbinatum</i>	3	33.3–71.7	47.9 (24.8–72.0)	17.2	< 0.001	88.4
<i>Columbicola columbae</i>	5	18.1–100.0	61.7 (20.7–90.9)	197.3	< 0.001	98.0
<i>Cuclotogaster heterographus</i>	1	25.0–25.0	25.0 (20.4–30.2)	0.0	-	-
<i>Holomenopon leucoxanthum</i>	3	60.0–80.6	72.6 (56.0–84.7)	5.5	0.063	63.7
<i>Solenopotes capillatus</i>	1	1.0–1.0	1.0 (0.4–2.6)	0.0	-	-
<i>Trichodectes canis</i>	1	10.9–10.9	10.9 (8.0–14.7)	0.0	-	-
Taxon: Mite	39	1.2–100.0	13.0 (9.4–17.6)	1920.0	< 0.001	98.0
<i>Demodex</i>	4	2.9–35.4	14.2 (4.3–38.2)	109.9	< 0.001	97.3
<i>D. canis</i>	1	35.4–35.4	35.4 (23.3–49.8)	0.0	-	-
<i>D. cati</i>	1	11.1–11.1	11.1 (4.2–26.1)	0.0	-	-
<i>Demodex</i> sp.	2	2.9–27.0	9.5 (0.9–55.2)	76.2	< 0.001	98.7
<i>Laelaps</i>	3	4.1–5.5	4.6 (2.5–8.4)	0.2	0.901	0.0
<i>L. echidninus</i>	1	4.1–4.1	4.1 (1.3–12.0)	0.0	-	-
<i>L. nuttalli</i>	1	5.5–5.5	5.5 (2.1–13.7)	0.0	-	-
<i>Laelaps</i> sp.	1	4.1–4.1	4.1 (1.3–12.0)	0.0	-	-
<i>Ornithonyssus</i>	3	1.4–15.5	8.1 (2.8–21.6)	9.1	0.01	78.1
<i>O. bacoti</i>	1	1.4–1.4	1.4 (0.2–9.1)	0.0	-	-
<i>O. bursa</i>	1	9.0–9.0	9.0 (5.7–13.8)	0.0	-	-

(continued on next page)

Table 3 (continued)

Genus/species	k	Observed infestation proportion range (%)	Pooled infestation Proportion % (95% CI)	Cochran's Q	p-value	I ² (%)
<i>O. sylviarum</i>	1	15.5–15.5	15.5 (11.1–21.2)	0.0	-	-
<i>Psoroptes</i>	4	5.6–9.1	6.2 (4.3–9.0)	1.0	0.811	0.0
<i>P. cuniculi</i>	3	5.6–9.1	6.3 (4.1–9.7)	0.9	0.631	0.0
<i>P. ovis</i>	1	5.8–5.8	5.8 (2.8–11.7)	0.0	-	-
<i>Dermanyssus gallinae</i>	4	13.3–57.0	42.8 (22.1–66.4)	30.4	< 0.001	90.1
<i>Knemidocoptes mutans</i>	2	5.5–43.0	17.6 (1.7–72.4)	59.8	< 0.001	98.3
<i>Liponyssoides</i> sp.	1	2.7–2.7	2.7 (0.7–10.3)	0.0	-	-
Mange	17	1.2–100.0	9.2 (4.5–17.7)	446.5	< 0.001	96.4
<i>Otodectes cynotis</i>	3	8.4–46.2	21.2 (7.1–48.5)	40.2	< 0.001	95.0
<i>Raillietia manfredi</i>	1	56.4–56.4	56.4 (43.1–68.8)	0.0	-	-
<i>Sarcoptes scabiei</i>	3	18.2–60.0	37.3 (15.4–66.1)	21.9	< 0.001	90.9
<i>Notoedres cati</i>	1	Not reported	-	-	-	-
Taxon: Flea	17	2.9–86.1	16.2 (10.2–24.9)	1094.6	< 0.001	98.5
<i>Ctenocephalides</i>	7	4.8–86.1	34.1 (12.8–64.6)	283.4	< 0.001	97.9
<i>C. canis</i>	3	4.8–13.8	9.1 (5.1–15.8)	9.3	0.01	78.4
<i>C. felis</i>	4	50.0–86.1	62.7 (46.8–76.2)	16.5	< 0.001	81.8
<i>Echidnophaga gallinacea</i>	1	8.3–8.3	8.3 (3.5–18.5)	0.0	-	-
<i>Xenopsylla cheopis</i>	1	9.6–9.6	9.6 (4.6–18.8)	0.0	-	-
Taxon: Fly	22	1.3–72.1	6.2 (3.8–9.8)	1179.6	< 0.001	98.2
<i>Botfly larvae</i>	1	1.4–1.4	1.4 (0.2–9.1)	0.0	-	-
<i>Cyclopodia sykesii</i>	1	72.1–72.1	72.1 (64.5–78.6)	0.0	-	-
<i>Diachlorus</i> sp.	3	0.2–0.3	0.3 (0.1–0.9)	0.1	0.95	0.0
Maggot/Myiasis	15	1.3–11.1	4.7 (3.3–6.7)	382.8	< 0.001	96.3
<i>Musca domestica</i>	3	43.1–58.3	51.6 (42.9–60.2)	16.6	< 0.001	88.0
<i>Oestrus ovis</i>	1	19.2–19.2	19.2 (16.2–22.5)	0.0	-	-
<i>Pseudolynchia canariensis</i>	2	1.6–63.3	14.1 (0.2–94.2)	246.3	< 0.001	99.6
<i>Simulium</i> sp.	1	3.7–3.7	3.7 (2.0–6.5)	0.0	-	-
<i>Stomoxys calcitrans</i>	3	0.3–5.7	2.0 (0.5–7.9)	13.4	0.001	85.1
<i>Tabanus striatus</i>	3	2.7–7.8	5.5 (3.0–9.8)	7.9	0.019	74.8
<i>Chrysops dispar</i>	1	Not reported	-	-	-	-
<i>Haematobia exigua</i>	1	Not reported	-	-	-	-
<i>Haematopota pluvialis</i>	1	Not reported	-	-	-	-
<i>Hypoderma bovis</i>	1	Not reported	-	-	-	-
<i>Stomoxys bengalensis</i>	1	Not reported	-	-	-	-
<i>Stomoxys indica</i>	1	Not reported	-	-	-	-
Unspecified	4	2.0–5.6	4.1 (3.0–5.6)	6.6	0.086	54.5

k = number of studies;

Observed infestation proportion range (%): range of infestation proportions/prevalences actually reported among the included studies

CI: confidence interval

Cochran's Q: test for heterogeneity;

I²(%): percentage of variability due to between-study heterogeneity.

study heterogeneity ($p = 0.003$), followed by diagnostic method, which explained 17.5% ($p = 0.003$). Host category and host order each accounted for 7.0% of the heterogeneity ($p = 0.046$), while study design explained 6.8% and showed borderline evidence of association ($p = 0.051$). Sample size was inversely associated with infestation proportion ($p = 0.024$), although its R^2 was 0%. Host ($p = 0.296$), study quality ($p = 0.349$), and publication year ($p = 0.357$, $R^2 = 0\%$) showed no statistically significant associations. The multivariable meta-regression model for tick infestation explained 28.4% of the between-study variance ($R^2 = 28.4\%$, $p = 0.009$), with substantial residual heterogeneity ($\tau^2 = 2.614$; residual $I^2 = 99.57\%$). Although the final model was significant, none of the moderators showed a significant association with tick infestation in the fully adjusted model.

In the univariable meta-regression for lice, study design, diagnostic method, host category, sampling type, host, host order, study quality, and sample size were significantly associated with variation in lice infestation proportion. Sampling type showed the strongest association, explaining 64.2% of the between-study variance ($p < 0.001$), followed by host ($R^2 = 64.4\%$; $p < 0.001$), host order ($R^2 = 63.5\%$; $p < 0.001$), host category ($R^2 = 62.9\%$; $p < 0.001$), and diagnostic method ($R^2 = 51.2\%$; $p < 0.001$). Study design explained 44.4% of the between-study variance ($p < 0.001$), while study quality explained 30.7% ($p = 0.001$). Sample size was inversely associated with infestation proportion ($p = 0.012$), explaining 14.3% of the between-study variance. Publication year was not significantly associated with infestation proportion ($p = 0.612$; $R^2 = 0\%$). The multivariable meta-regression explained

82.9% of the between-study variance ($R^2 = 82.9\%$; $p < 0.001$), with substantial residual heterogeneity ($\tau^2 = 0.963$; residual $I^2 = 99.03\%$). In the fully adjusted model, diagnostic method ($p = 0.010$), host category ($p < 0.001$), and sample size ($p = 0.002$) remained significantly associated with infestation proportion, whereas study design was no longer significant ($p = 0.129$).

In the mite univariable meta-regression, host category, sample size, and host order were significantly associated with variation in mite infestation proportion. Host category explained 21.2% of the between-study variance ($p = 0.016$), while sample size explained 16.1% and was inversely associated with infestation proportion ($p = 0.014$). Host order explained 11.9% of the variance ($p = 0.039$). Sampling type showed borderline evidence of association, explaining 17.7% of the between-study variance ($p = 0.053$). Diagnostic method ($p = 0.147$), study quality ($p = 0.993$), study design ($p = 0.271$), host ($p = 0.163$), and publication year ($p = 0.431$, $R^2 = 0\%$) were not significantly associated with infestation proportion. The multivariable meta-regression included 38 studies and explained 39.9% of the between-study variance ($R^2 = 39.9\%$; $p = 0.019$), with substantial residual heterogeneity ($\tau^2 = 1.518$; residual $I^2 = 97.56\%$), however none of the moderators showed a significant overall association with mite infestation proportion in the fully adjusted model, including sampling type ($p = 0.122$), diagnostic method ($p = 0.345$), host category ($p = 0.099$), study quality ($p = 0.324$), and sample size ($p = 0.141$).

In the univariable analyses for flea, among the examined moderators, sampling type, diagnostic method, host, host order, host category, and

Table 4

Subgroup analysis on pooled infestation proportions of ectoparasite taxa in animal species.

Moderator	k	Pooled infestation proportion % (95% CI)	Cochran's Q	p-value	I ² (%)
Taxon: Tick					
Study design			25.6	< 0.001	
Hospital-based studies	7	8.3 (5.9–11.4)	232.8	< 0.001	97.4
Cross-sectional	37	26.7 (19.5–35.3)	6303.3	< 0.001	99.4
Sampling type			71.9	< 0.001	
Hospital-based	10	5.6 (4.0–7.9)	308.8	< 0.001	97.1
Probability	11	20.0 (8.8–39.3)	2500.8	< 0.001	99.6
Non-Probability	18	37.8 (25.2–52.3)	2340.5	< 0.001	99.3
Mixed	5	42.5 (28.0–58.4)	252.0	< 0.001	98.4
Diagnostic method			228.9	< 0.001	
Naked eye	7	4.7 (3.2–6.9)	191.6	< 0.001	96.9
Microscopy	36	28.1 (20.7–36.9)	6336.1	< 0.001	99.4
PCR	1	60.4 (55.4–65.2)	-	-	-
Host			510.0	< 0.001	
Dog	9	12.9 (8.2–19.8)	397.0	< 0.001	98.0
Goat	7	26.6 (9.1–56.7)	932.9	< 0.001	99.4
Cattle	21	39.1 (28.1–51.3)	5065.9	< 0.001	99.6
Buffalo	1	0.2 (0.1–0.3)	-	-	-
Pig	2	19.2 (10.0–33.7)	3.6	0.0588	72.0
Cat	1	1.5 (0.4–5.8)	-	-	-
Sheep	1	1.3 (1.0–1.6)	-	-	-
Cattle-Goat	1	19.7 (16.1–24.0)	-	-	-
Dog-Cat	1	1.1 (0.3–4.5)	-	-	-
Host order			14.1	0.0002	
Carnivora	11	10.0 (6.4–15.4)	418.1	< 0.001	97.6
Artiodactyla	33	28.0 (20.1–37.5)	7131.5	< 0.001	99.6
Host category			14.1	0.0002	
Pet	11	10.0 (6.4–15.4)	418.1	< 0.001	97.6
Livestock	33	28.0 (20.1–37.5)	7131.5	< 0.001	99.6
Study quality			7.1	0.0294	
MQ	17	29.7 (18.2–44.4)	407.5	< 0.001	99.2
HQ	21	21.2 (12.9–32.7)	5389.2	< 0.001	99.6
LQ	6	11.6 (6.8–19.3)	1918.5	< 0.001	98.8
Taxon: Lice					
Study design			60.2	< 0.001	
Hospital-based studies	11	1.7 (0.9–3.2)	395.5	< 0.001	97.5
Cross-sectional	34	30.7 (21.3–42.0)	9313.2	< 0.001	99.6
Sampling type			101.6	< 0.001	
Hospital-based	14	1.7 (1.0–2.9)	638.7	< 0.001	98.0
Mixed	4	37.2 (20.2–58.1)	141	< 0.001	97.9
Non-Probability	12	50.4 (32.6–68.2)	915.8	< 0.001	98.8
Probability	15	27.2 (14.3–45.5)	6287.1	< 0.001	99.8
Diagnostic method			83.5	< 0.001	
Microscopy	34	31.8 (22.3–43.3)	9539.5	< 0.001	99.7
Naked eye	11	1.5 (0.9–2.5)	199.7	< 0.001	95.0
Host			467.2	< 0.001	
Dog	8	1.7 (0.7–4.5)	268.4	< 0.001	97.4
Cattle	12	11.1 (6.3–18.9)	1447.2	< 0.001	99.2
Buffalo	4	24.6 (8.8–52.6)	1438.4	< 0.001	99.8
Duck	3	98.6 (93.4–99.7)	0.3	0.866	0
Goat	7	12.8 (5.1–28.7)	679.8	< 0.001	99.1
Pigeon	4	73.8 (30.9–94.7)	270.3	< 0.001	98.9
Sheep	2	52.2 (31.3–72.4)	16	0.0001	93.7
Cat	2	1.4 (0.8–2.5)	0	0.947	0
Chicken	1	70.3 (66.5–73.9)	-	-	-
Peafowl	1	99.0 (86.2–99.9)	-	-	-
Pig	1	44.4 (35.9–53.2)	-	-	-
Host order			96.3	< 0.001	
Carnivora	10	1.7 (0.7–3.8)	269.7	< 0.001	96.7
Anseriformes	3	98.6 (93.4–99.7)	0.3	0.8657	0
Artiodactyla	26	16.1 (9.7–25.5)	9676.8	< 0.001	99.7
Columbiformes	4	73.8 (30.9–94.7)	270.3	< 0.001	98.9
Galliformes	2	92.2 (23.7–99.8)	6.9	0.0084	85.6
Host category			64.5	< 0.001	
Pet	10	1.7 (0.7–3.8)	269.7	< 0.001	96.7
Livestock	26	16.1 (9.7–25.5)	9676.8	< 0.001	99.7
Poultry	9	89.4 (70.3–96.8)	816.6	< 0.001	99.0
Study quality			49.3	< 0.001	
LQ	9	1.8 (0.9–3.6)	435.1	< 0.001	98.2

Table 4 (continued)

Moderator	k	Pooled infestation proportion % (95% CI)	Cochran's Q	p-value	I ² (%)
HQ	13	22.5 (10.7–41.1)	6782	< 0.001	99.8
MQ	23	28.2 (19.3–39.2)	1565.2	< 0.001	98.6
Taxon: Mite					
Study design			3.2	0.073	
Hospital-based studies	17	9.1 (6.1–13.4)	760.7	< 0.001	97.9
Cross-sectional	22	16.5 (9.8–26.6)	872.2	< 0.001	97.6
Sampling type			15.2	0.002	
Mixed	6	6.7 (5.7–7.8)	6.2	0.291	18.8
Hospital-based	21	9.1 (6.2–13.0)	907.5	< 0.001	97.8
Non-Probability	9	25.7 (11.9–46.8)	232.7	< 0.001	96.6
Probability	3	43.1 (5.7–90.4)	107.9	< 0.001	98.1
Diagnostic method			4.8	0.03	
Naked eye	11	7.8 (4.8–12.4)	521.5	< 0.001	98.1
Microscopy	28	16.3 (10.2–24.9)	1339	< 0.001	98.0
Host			299.5	< 0.001	
Cattle	5	4.1 (2.1–7.8)	202.8	< 0.001	98
Cat	4	15.8 (4.4–43.4)	39.6	< 0.001	92.4
Dog	14	12.8 (8.0–19.8)	577.1	< 0.001	97.7
Goat	7	8.3 (4.1–16.2)	168	< 0.001	96.4
Rabbit	3	43.2 (12.3–80.5)	22.9	< 0.001	91.3
Chicken	1	86.5 (81.0–90.6)	-	-	-
Dog, Cat	1	20.1 (14.8–26.7)	-	-	-
Duck	1	50.0 (34.2–65.8)	-	-	-
Pigeon	1	13.3 (6.8–24.5)	-	-	-
Rodent	1	15.1 (8.5–25.2)	-	-	-
Sheep	1	5.8 (2.8–11.7)	-	-	-
Host order			264.1	< 0.001	
Artiodactyla	13	6.1 (3.8–9.6)	466	< 0.001	97.4
Carnivora	19	13.8 (9.1–20.5)	727.4	< 0.001	97.5
Lagomorpha	3	43.2 (12.3–80.5)	22.9	< 0.001	91.3
Anseriformes	1	50.0 (34.2–65.8)	-	-	-
Columbiformes	1	13.3 (6.8–24.5)	-	-	-
Galliformes	1	86.5 (81.0–90.6)	-	-	-
Rodentia	1	15.1 (8.5–25.2)	-	-	-
Host category			14.4	0.002	
Livestock	13	6.1 (3.8–9.6)	466	< 0.001	97.4
Poultry	3	50.3 (10.3–89.9)	81.3	< 0.001	97.5
Pet	22	15.8 (10.6–22.9)	807.5	< 0.001	97.4
Wild	1	15.1 (8.5–25.2)	-	-	-
Study quality			0	0.987	
HQ	4	12.3 (1.0–65.5)	467.9	< 0.001	99.4
MQ	26	12.8 (8.5–18.9)	949.6	< 0.001	97.4
LQ	9	13.5 (7.9–22.1)	437.6	< 0.001	98.2
Taxon: Flea					
Study design			1.5	0.214	
Hospital-based studies	6	11.9 (8.7–16.1)	70.4	< 0.001	92.9
Cross-sectional	11	19.7 (9.3–36.7)	476.4	< 0.001	97.9
Sampling type			6	0.110	
Hospital-based	8	9.5 (7.1–12.7)	87	< 0.001	92.0
Non-Probability	4	35.6 (12.0–69.1)	118.3	< 0.001	97.5
Probability	3	15.9 (2.2–61.9)	128.6	< 0.001	98.4
Mixed	2	28.4 (2.3–86.9)	34.9	< 0.001	97.1
Diagnostic method			8.2	0.004	
Naked eye	4	8.3 (6.8–10.0)	16.5	< 0.001	81.9
Microscopy	13	21.2 (11.6–35.6)	410.2	< 0.001	97.1
Host			17.8	0.003	
Dog	6	10.1 (8.0–12.7)	46	< 0.001	89.1
Cat	3	34.3 (3.6–88.0)	57.9	< 0.001	96.5
Goat	5	29.7 (14.2–52.0)	157.7	< 0.001	97.5
Dog, Cat	1	2.9 (1.2–6.7)	-	-	-
Pigeon	1	8.3 (3.5–18.5)	-	-	-
Rodent	1	9.6 (4.6–18.8)	-	-	-
Host order			6.6	0.085	
Carnivora	10	12.6 (9.1–17.1)	164.8	< 0.001	94.5
Artiodactyla	5	29.7 (14.2–52.0)	157.7	< 0.001	97.5
Columbiformes	1	8.3 (3.5–18.5)	-	-	-
Rodentia	1	9.6 (4.6–18.8)	-	-	-
Host category			6.6	0.085	
Pet	10	12.6 (9.1–17.1)	164.8	< 0.001	94.5
Livestock	5	29.7 (14.2–52.0)	157.7	< 0.001	97.5
Poultry	1	8.3 (3.5–18.5)	-	-	-
Wild	1	9.6 (4.6–18.8)	-	-	-

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Table 4 (continued)

Moderator	k	Pooled infestation proportion % (95% CI)	Cochran's Q	p-value	I ² (%)
Study quality			23.8	< 0.001	
LQ	4	8.3 (6.8–10.0)	16.5	< 0.001	81.9
HQ	4	41.0 (23.4–61.3)	91.1	0	96.7
MQ	9	14.7 (7.0–28.4)	122	0	93.4
Taxon: Fly					
Study design			1.5	0.226	
Hospital-based studies	13	4.4 (2.7–7.2)	422.7	< 0.001	97.2
Cross-sectional	9	9.5 (3.0–26.5)	715.7	< 0.001	98.9
Sampling type			115.2	< 0.001	
Hospital-based	14	4.5 (2.8–7.0)	430.2	< 0.001	97
Non-Probability	6	8.5 (1.8–32.1)	584.1	< 0.001	99.1
Mixed	1	63.3 (50.5–74.5)	-	-	-
Probability	1	2.1 (0.7–6.4)	-	-	-
Diagnostic method			1	0.324	
Naked eye	9	4.4 (2.6–7.6)	339.9	< 0.001	97.6
Microscopy	13	7.7 (2.9–18.8)	807.6	< 0.001	98.5
Host			321.7	< 0.001	
Cat	3	2.7 (0.9–7.6)	7.5	0.023	73.4
Dog	5	4.5 (3.1–6.3)	18.4	0.001	78.3
Cattle	5	5.1 (2.1–12.0)	224.4	< 0.001	98.2
Goat	4	7.0 (2.5–18.1)	116.4	< 0.001	97.4
Bat	1	72.1 (64.5–78.6)	-	-	-
Chicken	1	3.7 (2.0–6.5)	-	-	-
Pigeon	2	14.1 (0.2–94.2)	246.3	< 0.001	99.6
Rodent	1	1.4 (0.2–9.1)	-	-	-
Host order			324.8	< 0.001	
Carnivora	8	3.9 (2.7–5.5)	31.7	< 0.001	77.9
Artiodactyla	9	6.0 (3.5–10.2)	344.8	< 0.001	97.7
Chiroptera	1	72.1 (64.5–78.6)	-	-	-
Columbiformes	2	14.1 (0.2–94.2)	246.3	< 0.001	99.6
Galliformes	1	3.7 (2.0–6.5)	-	-	-
Rodentia	1	1.4 (0.2–9.1)	-	-	-
Host category			2.3	0.509	
Pet	8	3.9 (2.7–5.5)	31.7	< 0.001	77.9
Livestock	9	6.0 (3.5–10.2)	344.8	< 0.001	97.7
Poultry	3	9.2 (0.6–64.5)	246.4	< 0.001	99.2
Wild	2	17.2 (0.1–97.2)	26.1	< 0.001	96.2
Study quality			6	0.049	
LQ	3	2.9 (1.9–4.3)	9.2	0.010	78.2
HQ	3	18.7 (1.8–74.2)	276.8	< 0.001	99.3
MQ	16	5.8 (3.4–9.8)	695.7	< 0.001	97.8

k = number of studies; CI: confidence interval; Cochran's Q: test for heterogeneity; I²(%): percentage of between-study heterogeneity.

study quality explained 3.3–21.6% of the between-study variance in the proportion of flea infestation, whereas study design, sample size, and publication year were not accounted for heterogeneity. However, none showed a statistically significant overall association.

Similarly, in fly infestation, the examined moderators, including study design, sampling type, diagnostic method, host, host order, and study quality, accounted for 1–10.2% of the between-study variance in the proportion of fly infestation, whilst host category, sample size, and publication year explained none of the between-study heterogeneity. Nevertheless, none of the moderators showed a statistically significant overall association. For flea and fly, multivariable meta-regression was not performed because the candidate moderators that met the pre-defined screening criterion ($p < 0.20$) were highly correlated.

3.6. Sensitivity analyses based on study quality and leave-one-out

Sequential exclusion of low- and moderate-quality studies generally resulted in modest changes to the pooled infestation estimates, with the extent of changes varying across ectoparasite taxa (Table 6). For ticks, the pooled estimate increased from 22.2% in the primary analysis to 24.7% after excluding low-quality studies and remained similar in the high-quality-only analysis (21.2%). For lice, the estimate increased from 16.6% to 26.9% after excluding low-quality studies, and was 22.5% in

high-quality studies. Mite estimates were highly stable, remaining at approximately 13% after exclusion of low-quality studies and in the high-quality-only analysis (12.3%), although the latter was based on only four studies. In contrast, flea and fly estimates increased progressively with increasing study quality, from 16.2% to 21.2% and 41.0% for fleas, and from 6.2% to 7.1% and 18.7% for flies, respectively. Overall, the sensitivity analyses did not show a consistent pattern of change in pooled infestation estimates across study quality levels.

The Leave-one-out sensitivity analysis demonstrated that omitting any individual study did not materially alter the pooled proportion estimate or heterogeneity statistics, indicating that the overall results were robust and not disproportionately influenced by any single study, while heterogeneity remained consistently high ($I^2 = 98.0$ – 99.6%) (Supplementary Figure 1–5).

3.7. Funnel-plot symmetry and Egger's test

Visual inspection of the funnel plots revealed notable dispersion of effect estimates and apparent asymmetry across all ectoparasite taxa, with several studies falling outside the pseudo-95% confidence limits (Fig. 3). To quantify funnel-plot asymmetry, Egger's linear regression test was performed and detected statistically significant asymmetry only for mites ($p = 0.005$), indicating potential small-study effects. In contrast, no statistically significant asymmetry or evidence of small-study effects was detected for ticks ($p = 0.454$), lice ($p = 0.283$), fleas ($p = 0.218$), or flies ($p = 0.304$) (Table 7).

3.8. Spatial distribution of study areas and institutes

The selected articles covered a total of 41 districts as study areas out of 64 total districts in Bangladesh. A total of 12 institutes led those studies throughout the districts (Fig. 4). The majority of the studies had been conducted by Bangladesh Agricultural University (BAU) (64.3%), followed by Chattogram Veterinary and Animal Sciences University (CVASU) (9.9%) and Sylhet Agricultural University (SylAU) (7%) (Supplementary Table 3, Supplementary Figure 6). Among the reported studies, the highest number was conducted in the Mymensingh District (25.6%), followed by Dhaka (24.4%) and Chattogram (15.6%). However, no ectoparasite research was conducted in 23 districts, and the majority of them were in the southwestern part of the country (Table 1, Fig. 4). The Poisson regression analysis revealed that the tendency to select research studies by the lead research institutes was in their respective base region. BAU carried out 20 of its 110 studies (18.2%) in Mymensingh, even though it operated across 34 different locations. Poisson regression showed that BAU was approximately 7 times more likely to conduct research in its base region Mymensingh than elsewhere (Rate Ratio = 7.03, $p < 0.001$), while both a binomial test ($p < 0.001$) and a chi-squared test ($p < 0.001$) confirmed that the selection of the study areas was mostly purposive rather than random allocation. Similarly, CVASU conducted 8 out of 17 studies (47.1%) in Chattogram, its base. The likelihood of conducting research in Chattogram was found to be 5.33 times higher than in other regions ($p = 0.001$), with the binomial test again confirming statistical significance ($p = 0.001$). SylAU conducted 4 out of 12 studies (33.3%) in Sylhet, its base, out of six total locations. Although the estimated rate ratio was 2.5, the Poisson regression did not reach statistical significance ($p = 0.135$), and the binomial test ($p = 0.125$) also failed to reject the null hypothesis of random allocation (Supplementary Table 3).

3.9. Seasonal pattern

Season-specific pooled infestation estimates varied across ectoparasite taxa, although none of the seasonal differences were statistically significant ($p > 0.05$) (Table 8). Tick infestation showed a gradual increase from summer (16.8%) to the rainy season (17.7%) and winter (18.5%). In contrast, lice infestation declined across seasons, from

Table 5

Univariable and multivariable meta-regression of pooled infestation proportion estimates of ectoparasite taxa.

Moderator	k	Univariable Meta-regression			Multivariable Meta-regression		
		OR (95% CI)	R ² (%)	p-value	aOR (95% CI)	R ² (%)	p-value
Taxa: Tick	44					28.4	0.009
Study design			6.8	0.051			0.219
Hospital registry-based	7	Ref			Ref		
Cross-sectional	37	4.72 (0.99–22.43)			0.17 (0.01–3.01)		
Sampling type			23.9	0.003			0.129
Hospital-based	10	Ref			Ref		
Probability	11	5.26 (1.18–23.52)		0.031	14.74 (0.59–369.58)		0.099
Non-Probability	18	12.78 (3.30–49.52)		< 0.001	27.26 (1.40–529.37)		0.030
Mixed	5	15.34 (2.37–99.13)		0.005	32.24 (1.23–842.82)		0.038
Diagnostic method			17.5	0.003			0.648
Naked eye	7	Ref			Ref		
Microscopy	36	9.80 (2.22–43.18)			1.56 (0.22–11.06)		
Host category			7	0.046			0.976
Pet	11	Ref			Ref		
Livestock	33	3.87 (1.03–14.59)			1.02 (0.22–4.78)		
Sample size (per 100 animals)	44	0.98 (0.96–1.00)	0	0.024	0.98 (0.96–1.00)		0.107
Host			8.4	0.095			
Dog	9	Ref					
Goat	7	2.40 (0.45–12.85)		0.296			
Cattle	21	4.29 (1.14–16.17)		0.032			
Host order			7	0.046			
Carnivora	11	Ref					
Artiodactyla	33	3.87 (1.03–14.59)					
Study quality			0.2	0.349			
LQ	6	Ref					
HQ	21	2.45 (0.40–15.00)		0.323			
MQ	17	3.85 (0.60–24.80)		0.152			
Publication year (per 1-year increase)	44	1.02 (0.97–1.07)	0	0.357			
Tick multivariable model statistics: k (number of studies) = 43; $\tau^2 = 2.614$; residual $I^2 = 99.57\%$							
Moderator	k	Univariable Meta-regression			Multivariable Meta-regression		
		OR (95% CI)	R ² (%)	p-value	aOR (95% CI)	R ² (%)	p-value
Taxa: Lice	45					82.9	< 0.001
Study design			44.4	< 0.001			0.129
Hospital registry-based	11				Ref		
Cross-sectional	34	28.30 (7.09–112.88)			2.32 (0.77–6.98)		
Diagnostic method			51.2	< 0.001			0.01
Naked eye	11	Ref			Ref		
Microscopy	34	33.32 (8.92–124.37)			4.49 (1.47–13.68)		
Host category			62.9	< 0.001			< 0.001
Pet	10	Ref			Ref		
Livestock	26	11.23 (3.64–34.67)		< 0.001	3.16 (1.11–8.97)		0.032
Poultry	9	427.70 (94.69–1931.87)		< 0.001	42.68 (10.60–171.77)		< 0.001
Sample size (per 100 animals)	45	0.97 (0.95–0.99)	14.3	0.012	0.98 (0.97–0.99)		0.002
Sampling type			64.2	< 0.001			
Hospital-based	14	Ref					
Mixed	4	52.72 (7.61–364.97)		< 0.001			
Non-Probability	12	65.87 (17.36–249.87)		< 0.001			
Probability	15	21.58 (6.34–73.43)		< 0.001			
Host			64.4	< 0.001			
Dog	8	Ref					
Cattle	12	7.09 (1.92–26.15)		0.004			
Buffalo	4	18.47 (3.25–104.85)		0.002			
Duck	3	4040.96 (315.61–51738.59)		< 0.001			
Goat	7	8.29 (1.89–36.36)		0.006			
Pigeon	4	138.01 (22.24–856.57)		< 0.001			
Host order			63.5	< 0.001			
Carnivora	10	Ref					
Anseriformes	3	4174.70 (350.40–49737.45)		< 0.001			
Artiodactyla	26	11.22 (3.90–32.29)		< 0.001			
Columbiformes	4	142.21 (24.84–814.17)		< 0.001			
Study quality			30.7	0.001			
LQ	9	Ref					
HQ	13	16.60 (2.53–109.11)		0.004			
MQ	23	27.20 (4.89–151.29)		< 0.001			
Publication year (per 1-year increase)	45	1.01 (0.97–1.06)	0	0.612			
Lice multivariable model statistics: k (number of studies) = 45; $\tau^2 = 0.963$; residual $I^2 = 99.03\%$							
Moderator	k	Univariable Meta-regression			Multivariable Meta-regression		
		OR (95% CI)	R ² (%)	p-value	aOR (95% CI)	R ² (%)	p-value
Taxa: Mite	39					39.9	0.019

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Table 5 (continued)

Moderator	k	Univariable Meta-regression		Multivariable Meta-regression	
Sampling type			17.7	0.053	0.122
Mixed	6	Ref		Ref	
Hospital-based	21	1.42 (0.33–6.04)		1.49 (0.24–9.07)	0.657
Non-Probability	9	4.70 (0.90–24.62)		4.59 (0.81–26.17)	0.083
Probability	3	10.68 (1.17–97.43)		7.41 (0.80–68.82)	0.076
Diagnostic method			3.1	0.147	0.345
Naked eye	11	Ref		Ref	
Microscopy	28	2.35 (0.73–7.59)		1.91 (0.48–7.63)	0.345
Host category			21.2	0.016	0.099
Livestock	13	Ref		Ref	
Poultry	3	15.73 (2.19–113.06)		7.32 (1.08–49.37)	0.042
Pet	22	2.99 (1.01–8.82)		2.08 (0.54–7.93)	0.272
Study quality			0	0.993	0.324
HQ	4	Ref		Ref	
MQ	26	1.09 (0.17–6.93)		2.51 (0.47–13.45)	0.272
LQ	9	1.13 (0.14–8.85)		4.57 (0.60–34.89)	0.137
Sample size (per 100 animals)	39	0.97 (0.95–0.99)	16.1	0.014	0.141
Study design			2.0	0.271	
Hospital registry-based	17	Ref			
Cross-sectional	22	1.82 (0.61–5.41)			
Host			6.6	0.163	
Cattle	5	Ref			
Cat	4	4.40 (0.53–36.71)		0.163	
Dog	14	3.53 (0.70–17.91)		0.122	
Goat	7	2.13 (0.34–13.21)		0.403	
Rabbit	3	19.19 (1.71–214.68)		0.018	
Host order			11.9	0.039	
Artiodactyla	13	Ref			
Carnivora	19	2.47 (0.85–7.17)		0.093	
Lagomorpha	3	11.94 (1.55–91.90)		0.019	
Publication year (per 1-year increase)	39	1.02 (0.97–1.08)	0	0.431	
Mite multivariable model statistics: k (Number of studies) = 38; $\tau^2 = 1.518$; residual $I^2 = 97.56\%$					
Moderator	k	Univariable Meta-regression OR (95% CI)		R ² (%)	p-value
Taxa: Flea	17				
Study design			0	0.405	
Hospital registry-based	6	Ref			
Cross-sectional	11	1.99 (0.36–10.97)			
Sampling type			12.4	0.179	
Hospital-based	8	Ref			
Non-Probability	4	5.89 (0.85–41.05)		0.07	
Probability	3	2.05 (0.24–17.31)		0.477	
Diagnostic method			10.9	0.121	
Naked eye	4	Ref			
Microscopy	13	4.02 (0.66–24.35)			
Host			9.7	0.254	
Dog	6	Ref			
Cat	3	5.07 (0.44–58.97)		0.173	
Goat	5	3.97 (0.51–31.07)		0.168	
Host order			3.3	0.269	
Carnivora	10	Ref			
Artiodactyla	5	2.79 (0.41–19.12)		0.269	
Host category			3.3	0.269	
Pet	10	Ref			
Livestock	5	2.79 (0.41–19.12)			
Study quality			21.6	0.091	
LQ	4	Ref			
HQ	4	10.22 (1.24–83.92)		0.033	
MQ	9	2.59 (0.42–15.80)		0.279	
Sample size (per 100 animals)	17	0.99 (0.96–1.03)	0	0.593	
Publication year (per 1-year increase)	17	1.04 (0.94–1.14)	0	0.43	
Moderator	k	Univariable Meta-regression OR (95% CI)		R ² (%)	p-value
Taxa: Fly	22				
Study design			7.3	0.153	
Hospital registry-based	13	Ref			
Cross-sectional	9	2.39 (0.70–8.17)			
Sampling type			5.8	0.204	
Hospital-based	14	Ref			
Non-Probability	6	2.17 (0.63–7.46)			
Diagnostic method			1	0.297	
Naked eye	9	Ref			

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Table 5 (continued)

Moderator	k	Univariable Meta-regression	Multivariable Meta-regression	
Microscopy	13	1.90 (0.54–6.64)	2.5	0.466
Host				
Cat	3	Ref		
Dog	5	1.83 (0.47–7.17)		
Cattle	5	2.03 (0.52–7.98)	4.8	0.283
Goat	4	2.94 (0.71–12.21)		
Host order				
Carnivora	8	Ref		
Artiodactyla	9	1.58 (0.69–3.61)	0	0.509
Host category				
Pet	8	Ref		
Livestock	9	1.52 (0.47–4.94)		
Poultry	3	2.41 (0.47–12.23)	10.2	0.140
Study quality				
LQ	3	Ref		
HQ	3	8.64 (0.95–78.31)		
MQ	16	2.29 (0.41–12.63)	0	0.428
Sample size	22	0.99 (0.95–1.02)		
(per 100 animals)				
Publication year	22	0.98 (0.93–1.03)		
(per 1-year increase)				0.387

R^2 (%): percentage of between-study heterogeneity explained by the moderator(s);

CI: confidence interval; OR: odds ratio; aOR: adjusted odds ratio.

Table 6

Sequential study quality sensitivity analysis of pooled ectoparasite-taxa infestation estimates.

Taxa	Analysis (Studies included)	k	Pooled infestation % (95% CI)	I^2 (%)	Q p-value
Tick	Primary (LQ + MQ + HQ)	44	22.2 (16.6–29.0)	99.5	< 0.001
	Excluding LQ (MQ + HQ)	38	24.7 (17.8–33.2)	99.5	
	HQ only	21	21.2 (13.0–32.7)	99.6	
Lice	Primary (LQ + MQ + HQ)	45	16.6 (11.2–24.0)	99.6	< 0.001
	Excluding LQ (MQ + HQ)	36	26.9 (18.5–37.3)	99.6	
	HQ only	13	22.5 (10.7–41.1)	99.8	
Mite	Primary (LQ + MQ + HQ)	39	13.0 (9.4–17.6)	98.0	< 0.001
	Excluding LQ (MQ + HQ)	30	13.0 (8.3–19.6)	98.0	
	HQ only	4	12.3 (1.0–65.5)	99.4	
Flea	Primary (LQ + MQ + HQ)	17	16.2 (10.2–24.9)	98.5	< 0.001
	Excluding LQ (MQ + HQ)	13	21.2 (11.6–35.6)	97.1	
	HQ only	4	41.0 (23.4–61.3)	96.7	
Fly	Primary (LQ + MQ + HQ)	22	6.2 (3.8–9.8)	98.2	< 0.001
	Excluding LQ (MQ + HQ)	19	7.1 (4.2–11.9)	98.3	
	HQ only	3	18.7 (1.8–74.2)	99.3	

LQ= Low quality; MQ= Moderate quality; HQ= High quality.

CI: confidence interval; I^2 (%): percentage of variability due to between-study heterogeneity;

Q p-value: p-value from Cochran's Q test for between-study heterogeneity.

23.2% in summer to 21.5% in the rainy season and 19.3% in winter. Mite infestation showed an increasing pattern, rising from 4.5% in summer to 6.8% in the rainy season and 6.9% in winter. Flea infestation decreased slightly from summer to the rainy season but increased markedly in winter, with estimates of 22.0%, 19.8%, and 29.2%, respectively. Fly infestation demonstrated a consistent downward trend, decreasing from 3.2% in summer to 2.4% in the rainy season and 2.0% in winter. For unspecified ectoparasites, pooled estimates decreased from summer to the rainy season and then increased slightly in winter, from 8.9% to 7.7% and 8.0%, respectively. Thus, tick and mite infestations tended to increase toward winter, whereas lice and fly infestations showed decreasing trends; flea infestations peaked in winter (Table 8).

3.10. Temporal trend in yearly infestation proportion and publications

The temporal trend of publication showed a clear increase in research output over time. Research activity was very limited between 1968 and 2005, with most years contributing no more than 1.1% of the total publications. Small peaks were observed in 1972 and 1999, when each year contributed 2.2%. Publication output began to increase in

2006 (3.3%) and rose sharply after 2010. The highest level of activity in the early growth period was observed in 2010 and 2011, with each year accounting for 7.8% of total publications. Although output shortly declined in 2013 (1.1%), publication rates remained relatively high from 2014 to 2023, ranging from 3.3% to 7.8%, with another notable peak in 2019. The highest annual contribution was observed in 2022 (10%), followed by a decline to 4.4% in 2023, with no publications identified for 2024 (Supplementary Figure 7).

4. Discussion

The geo-climatic conditions of Bangladesh support the survival and growth of various ectoparasites, which cause economic loss directly by affecting production or indirectly by transmitting pathogens, including zoonotic ones [44–47]. This is the first systematic review and meta-analysis of ectoparasitic infestations in various vertebrate hosts in Bangladesh. Among the included studies, about three-quarters were cross-sectional, with research concentrated on cattle, dogs, and goats, indicating uneven representation across host species, likely due to limited resources and the priority of major domesticated animals. Ticks and lice were the most frequently investigated ectoparasite taxa, while

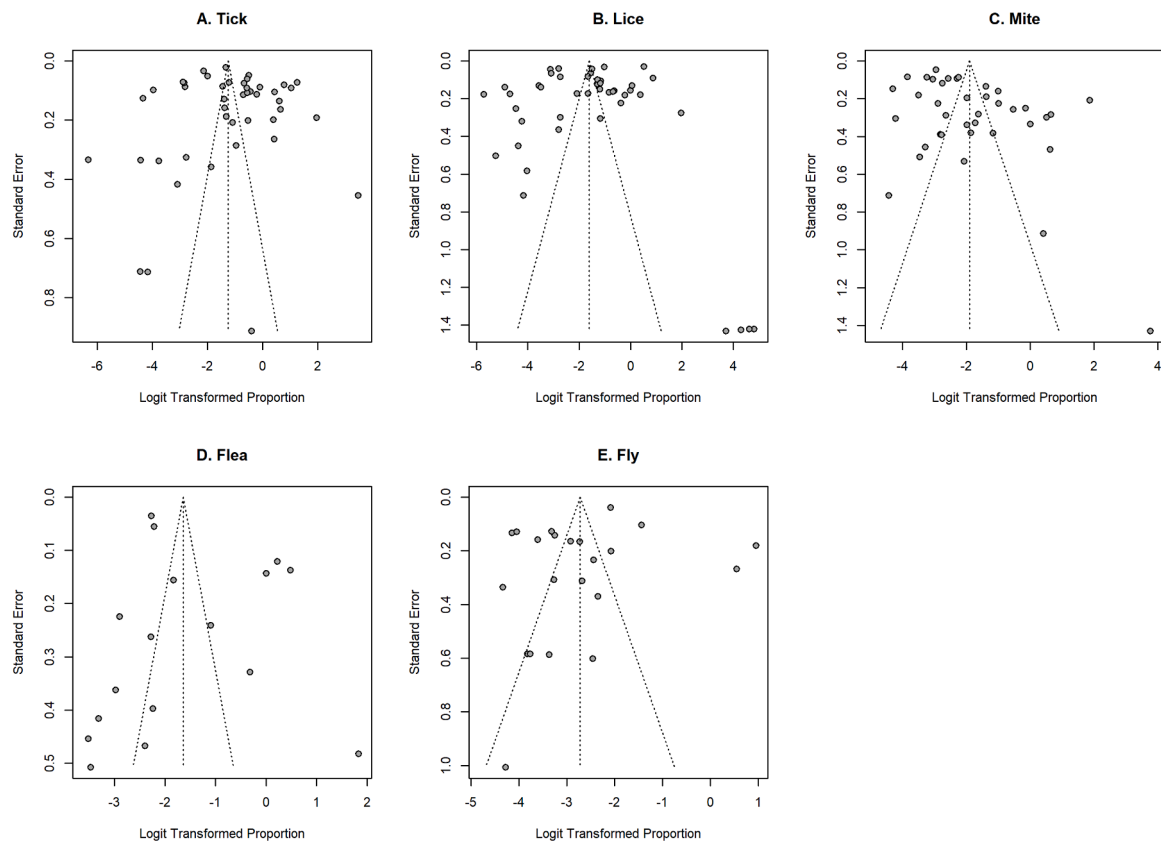


Fig. 3. Funnel plots of meta-analysis assessing small-study effects for five major ectoparasite taxa: Tick, Lice, Mite, Flea, and Fly. Each open circle represents an individual study. The x-axis represents the logit-transformed infestation proportion, and the y-axis represents the standard error, with more precise estimates appearing toward the top of the plots. The vertical dotted line indicates the pooled effect estimate on the logit scale, while the diagonal dotted lines represent the pseudo-95% confidence limits around the pooled estimate.

Table 7
Egger's test for funnel-plot asymmetry for potentially missing studies.

Taxa	k	Egger's Test		
		Bias estimate (SE)	Egger's t	p-value
Tick	44	2.5 (3.3)	0.8	0.454
Lice	45	-3.9 (3.6)	-1.1	0.283
Mite	39	5.1 (1.7)	3.0	0.005
Flea	17	3.5 (2.7)	1.3	0.218
Fly	22	-2.5 (2.4)	-1.1	0.304

k = number of studies; SE: standard error

approximately 80% of studies used microscopy as the diagnostic method, with molecular detection being rarely used, indicating limited resources for conducting research. Studies were disproportionately distributed geographically, with nearly half originating from just two districts, Mymensingh and Dhaka. Temporally, 80% of the included studies were published after 2000, with a dense distribution of data points from 2008 to 2024 (Supplementary Figure 7), reflecting increased research interest and activities in ectoparasite infestation in animals over the last 15 years, rather than an increase in infestation. However, the number of publications was rising from the beginning of the 21st century as new agricultural educational and research institutes developed over the years.

Among the ectoparasite taxa, ticks (22.2%) showed the highest taxon-specific pooled infestation proportion, followed by lice (16.6%), fleas (16.2%), mites (13.0%), and flies (6.2%) across different animal hosts. These estimates provide a quantitative summary of the available evidence and should not be generalized to precise national infestation proportions or prevalence estimates, given the substantial between-

study heterogeneity. The finding is consistent with previous syntheses that report ticks as the dominant ectoparasites of livestock and other animals [29], attributable to their wide host range, efficient off-host survival strategies, persistence across diverse agro-ecological zones, and greater visibility during inspection due to their larger size. At the genus level, *Rhipicephalus* and *Haemaphysalis* were the most frequently represented tick taxa, and each showed a pooled infestation proportion of 16.2%. *R. microplus*, known as the ‘tropical cattle tick’, had the highest pooled infestation proportion, followed by *H. bispinosa* and *R. sanguineus*, which aligns with a previous study from India [48], suggesting their established role as the dominant tick species in South Asia. Although *R. microplus* preferably infests ruminants throughout the country, *Haemaphysalis* spp. are prevalent mainly in the northwest part of the country [49]. Among hosts, tick infestation was highest in livestock (28%), especially cattle, which had the highest pooled infestation proportion (39.1%), consistent with previous reports from several Ethiopian studies [50,51]. This may be related to the fact that livestock are often grazed outdoors or in semi-intensive environments may encounter more frequent exposure to tick habitats in pasture vegetation and pasture-associated wooded or humid areas [52–54]. Lice infestation remains common because they are permanently associated with their hosts, maintain large colonies on the same animals, and spread rapidly through close contact [18]. Several avian genera of lice, particularly *Anaticola* (94.9%), *Menopon* (69%), and *Lipeurus* (63.3%), showed higher pooled infestation proportions, despite being reported in only a few studies. In contrast, the more frequently documented genera *Linognathus* (k = 17) and *Haematopinus* (k = 16) showed comparatively lower pooled infestation proportions. This suggests that the estimates derived from a few studies should be considered as preliminary indications rather than conclusive. Lice infestation was highest in poultry

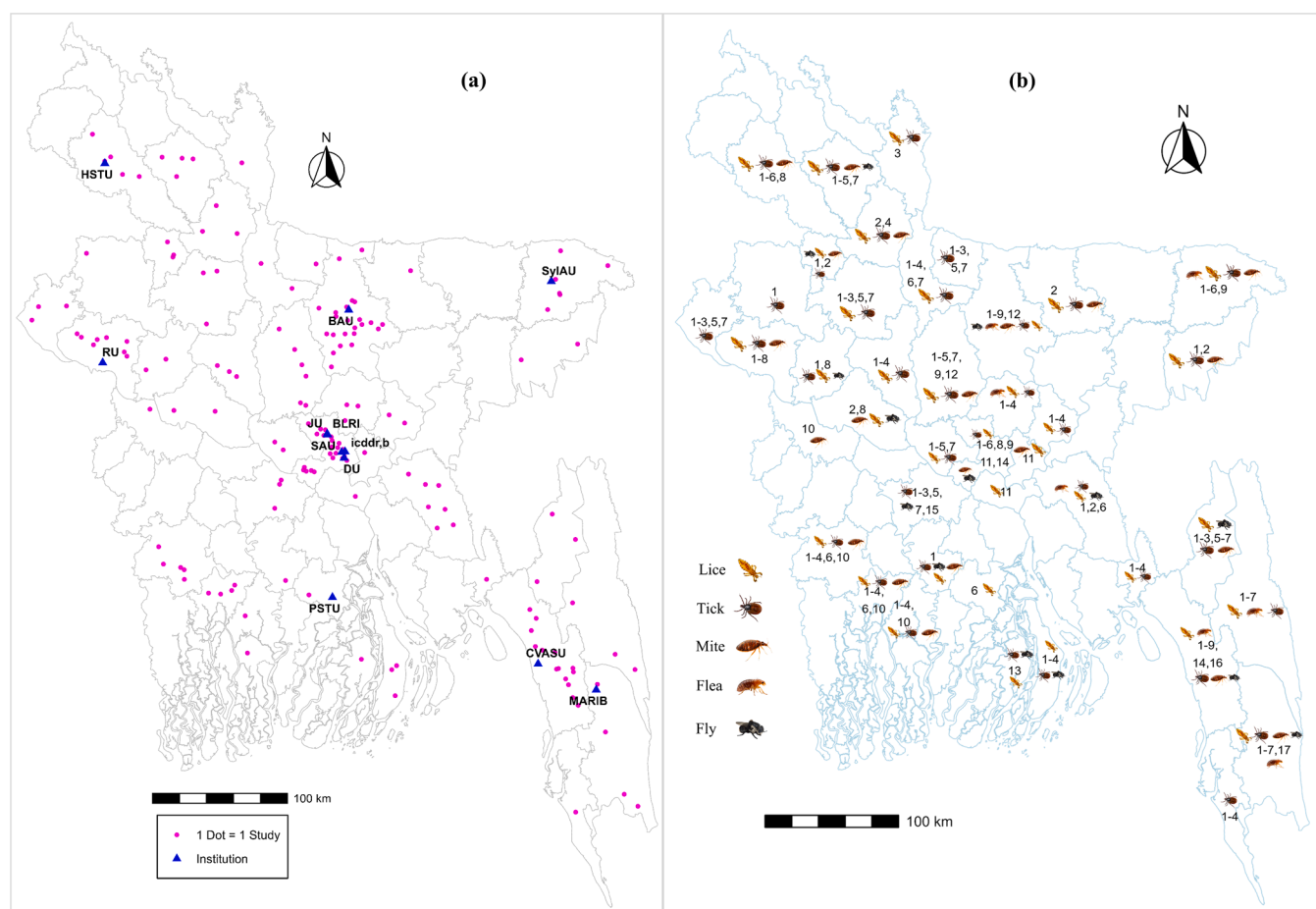


Fig. 4. (a) Geographic distribution of the study areas and lead institutes across the country. (b) Geographical distribution of different ectoparasites in various host species. 1. Cattle 2. Goat 3. Buffalo 4. Sheep 5. Dog 6. Fowl 7. Pig 8. Pigeon 9. Cat 10. Chicken 11. Duck 12. Jackal 13. Poultry 14. Rabbit 15. Bat 16. Peafowl 17. Rat.

Table 8

Seasonal patterns of the estimates of ectoparasitic infestations.

Taxa	Season	k	Infestation range (%)	Pooled infestation % (95% CI)	I ² (%)	Cochran's Q	Q p-value	p-value
Tick	Summer	30	2.1–82.2	16.8 (11.9–23.2)	94.8	554.22	< 0.001	0.924
	Rainy	30	0.7–63.7	17.7 (12.7–24.2)	96.8	894.66	< 0.001	
	Winter	30	1.4–71.7	18.5 (13.0–25.7)	95.5	644.09	< 0.001	
Lice	Summer	33	0.3–100.0	23.2 (13.5–36.9)	93.3	474.81	< 0.001	0.886
	Rainy	33	1.2–100.0	21.5 (11.8–35.7)	94.0	536.87	< 0.001	
	Winter	33	0.0–100.0	19.3 (11.2–31.4)	95.4	696.45	< 0.001	
Mite	Summer	12	0.0–60.0	4.5 (2.2–8.7)	91.7	132.70	< 0.001	0.581
	Rainy	12	0.7–57.1	6.8 (4.0–11.6)	84.2	69.77	< 0.001	
	Winter	12	1.0–75.0	6.9 (3.3–13.6)	89.4	103.68	< 0.001	
Flea	Summer	2	1.8–81.8	22.0 (0.1–98.4)	96.8	31.74	< 0.001	0.993
	Rainy	2	1.8–77.8	19.8 (0.1–97.7)	96.4	27.97	< 0.001	
	Winter	2	1.2–93.8	29.2 (0.0–99.8)	96.9	32.13	< 0.001	
Fly	Summer	5	1.4–5.5	3.2 (2.0–5.2)	77.4	17.68	0.001	0.428
	Rainy	5	0.7–3.8	2.4 (1.6–3.4)	49.5	7.92	0.095	
	Winter	5	0.0–4.4	2.0 (1.1–3.6)	74.0	15.38	0.004	
Unspecified	Summer	3	6.2–12.0	8.9 (5.7–13.7)	64.9	5.70	0.058	0.940
	Rainy	3	4.3–15.4	7.7 (3.3–17.1)	88.1	16.85	< 0.001	
	Winter	3	3.6–12.2	8.0 (3.6–16.7)	90.1	20.17	< 0.001	

k = number of studies; CI: confidence interval; I²(%): percentage of total variability attributable to between-study heterogeneity; Cochran's Q: test for between-study heterogeneity; Q p-value: p-value from Cochran's Q test; p-value: indicates the significance of the seasonal difference.

(89.4%), particularly in ducks (98.6%) and pigeons (73.8%), consistent with existing evidence of a higher proportion of lice infestation in an organized poultry farm (100%) in Mumbai, India and the rapid spread of chewing lice through close communal contact in flocking birds [55]. The higher lice infestation observed in ducks (98.6%) may be related to their

flocking, ground-dwelling, and communal behaviors, which increase exposure to infested hosts and contaminated environments, while the dense plumage of poultry birds provides a favorable habitat for lice [56–58]. Moreover, a recent global meta-analysis's findings on higher ectoparasite prevalence (70.2%) on chickens in backyard systems [59],

are relevant to backyard and smallholder poultry production systems in Bangladesh, with limited biosecurity, inadequate cleaning of poultry houses and litter may contribute to the persistence of ectoparasites [56, 60–63]. However, these factors were not consistently measured across the included studies and should be considered possible explanations rather than confirmed determinants. The pooled infestation proportion of fleas was comparable to that of lice due to their overlapping confidence intervals. The predominance of the flea genus *Ctenocephalides*, particularly *C. felis* and *C. canis* consistent with a previous study from Ethiopia and Egypt [64,65]. Among hosts, flea infestation was higher in cats (34.3%), which is consistent with the close association of *Ctenocephalides felis* with feline hosts, although the wide confidence interval reflects substantial uncertainty due to the limited number of contributing studies. Although approximately 1–5% of the adult cat flea population remains on the host at any given time [66], fleas can adversely affect animal hosts through blood loss and anemia, allergic dermatitis, and the transmission of pathogens and parasites [67,68]. Among mite species, *Dermanyssus gallinae* (42.8%) and *Sarcoptes scabiei* (37.3%) had the highest pooled proportion. *D. gallinae* is linked to poultry farming, where heavy infestations can harm animal health and reduce productivity. The pooled proportion of mange infestation (9.2%) was higher than the 2.37% prevalence reported in a study in Pakistan [69]. The disparity may be linked to Bangladesh's climate and differences in housing, hygiene, control measures, and surveillance practices [70,71]. However, this meta-analysis did not quantitatively evaluate climatic variables; therefore, climate-specific analyses are needed to confirm these potential associations. Poultry had a substantially higher pooled infestation proportion of mites, particularly in chickens, followed by rabbits, although these estimates were based on very few studies. In contrast, cattle and sheep had comparatively low pooled infestation proportions. These differences may partly reflect host-specific mite assemblages and differences in susceptibility, husbandry, housing, grooming behavior, and opportunities for transmission. The particularly high infestation among poultry is also consistent with the species-level finding for *Dermanyssus gallinae* and suggests that poultry production systems may represent an important setting for mite infestation. However, the limited number of studies reporting host-specific infestation proportions warrants caution when making direct comparisons among hosts. The lowest pooled infestation proportion for flies may be due to their facultative or transient character and tendency to fly during close inspection. Exceptions in this group include wingless louse flies and bat flies (Hippoboscoidea), which are permanent ectoparasites on their hosts, more similar to fleas. Thus, prevalence estimates can be quite high (>50%), as evidenced by the bat fly study covered in this meta-analysis (species: *Cyclopodia sykesii*). Among flies, *Musca domestica* showed a relatively high pooled infestation proportion (51.6%), whilst myiasis (maggot) was frequently detected in host animals ($k = 15$). Although we have included *Musca domestica* in this review, it is considered a facultative ectoparasite [72,73]. They occasionally cause myiasis and feed on blood and wound exudate from open skin lesions [74–76], as they only have sponging mouthparts and lack the skin-piercing apparatus for blood feeding, which is common in other obligate ectoparasites [77]. The frequent documentation of myiasis (maggot) across the included studies likely reflects inadequate wound care in animals and poor sanitation practices in livestock rearing [74,78]. Among the commonly represented hosts, livestock, notably goats, had the highest proportion of flies (7.0%), whereas cats had the lowest (2.7%). These findings indicate that variation in the animal population or in hosts and host categories is an important moderator when interpreting variation in reported estimates of ectoparasitic infestation, as further evidenced by meta-regression.

Heterogeneity was extremely high across all five taxa (I^2 generally > 98%), and meta-regression indicated that the sources of heterogeneity differed by taxon. Host-related moderators (species, order, category) explained the largest share of variance for lice (up to 64%), a moderate proportion for mites (7–21%), and relatively little for ticks (7–8%), fleas

(3–10%), and flies (0–5%). This finding reflects the biological gradients described earlier that lice are host-obligate and highly host-specific [79], whereas tick survival is driven more by off-host environmental conditions [80,81], and fleas and flies infest a wide range of hosts and are mobile, probably making host species a weak predictor for these taxa [82,83]. Methodological moderators were the stronger predictors for ticks and lice. Sampling type (64.2%), diagnostic method (51.2%), and study design (44.4%) each explained a large share of the heterogeneity in lice; smaller but notable contributions were observed for ticks (sampling type 23.9%, diagnostic method 17.5%) and mites (sampling type 17.7%). Convenience sampling tends to inflate the apparent burden relative to population-based surveys [39,84], and non-probability sampling was associated with a higher proportion of tick infestation, consistent with selection bias. Microscopy-based diagnosis was associated with a higher proportion of lice infestation, likely reflecting its better sensitivity in detecting small lice than visual inspection alone [85]. This pattern is commonly observed in proportional meta-analyses, where non-probability or convenience sampling methods often report higher prevalence than population-based surveys, and estimates are influenced by the diagnostic method used. Sample size was inversely associated with reported infestation for lice (14.3%) and mites (16.1%), consistent with smaller studies that tend to report larger estimates [86]. Study quality was significant only for lice, explaining 30.7% of the between-study variation. Multivariable meta-regression further demonstrated that the influence of methodological and host characteristics differed among ectoparasite taxa. The models explained 28.4%, 82.9%, and 39.9% of the between-study heterogeneity for ticks, lice, and mites, respectively, indicating that the selected moderators captured a substantial proportion of variation, particularly for lice. Nevertheless, considerable residual heterogeneity remained in all three models, with residual I^2 values of 99.57%, 99.03%, and 97.56% for ticks, lice, and mites, respectively. However, high residual I^2 is expected in proportional meta-analyses and does not by itself indicate a poorly specified model [84]. These regression findings underscore that methodological and host-related characteristics contributed to variation in reported ectoparasite infestations, with their influence particularly evident for lice and ticks. However, substantial residual heterogeneity remained across taxa, indicating that the measured moderators did not fully account for the observed variation. Other factors, including host characteristics, environmental and ecological conditions, epidemiological differences, and study-specific features, may therefore also contribute to the variation in infestation estimates.

Sensitivity analyses showed that the overall infestation estimates were generally robust. Tick and mite pooled infestation proportions remained relatively stable across sensitivity analyses, while the lice estimate increased slightly after excluding low-quality studies but remained similar overall. Conversely, flea and fly analyses showed substantial changes in the pooled proportion after excluding lower- and moderate-quality studies, although these results should be interpreted with caution because they were based on fewer studies. Furthermore, the leave-one-out analyses supported the robustness of the results, as removing any single study did not meaningfully alter the pooled estimates or heterogeneity. Egger's test detected statistically significant asymmetry only for mites, suggesting potential small-study effects for that taxon. However, given the substantial between-study heterogeneity across all taxa, funnel-plot asymmetry here is not strong evidence of publication bias on its own; it can arise from genuine between-study variability, rather than selective reporting or publication bias [87].

Seasonal differences were not statistically significant for any taxon, plausibly reflecting Bangladesh's comparatively mild, short winter and the fact that most included ectoparasites are host-dependent rather than strongly environment-dependent. This might happen in subtropical regions with mild climates like Bangladesh, where temperatures, humidity, and other climatic factors remain relatively constant throughout the year. Ectoparasites largely depend on the host rather than the environment, and the host species' nesting and movement behavior remain

mostly unchanged across such moderate seasonal fluctuations, which also favors a consistent presence of ectoparasites on hosts throughout the year. Nevertheless, some descriptive patterns were observed in the pooled proportions: ticks and mites showed gradual increases toward winter, whereas lice and flies showed declines, and fleas exhibited a higher infestation proportion in winter. These patterns should be interpreted cautiously as descriptive trends rather than evidence of significant seasonal variation.

The study areas were mostly concentrated around the country's first agricultural university in Mymensingh District and Dhaka Division, in the central region of Bangladesh, leaving the southwestern districts essentially unstudied. Since the livestock population is also concentrated in other areas of Bangladesh, beyond the adjacent areas of agricultural universities or research institutes, it is necessary to conduct studies in those areas to assess the nationwide burden of ectoparasitic infestations and implement preventive measures accordingly.

This meta-analysis has several limitations that should be considered when interpreting the results. The included studies varied in study design, host and ectoparasite species, locations, sampling methods, and diagnostic techniques used for ectoparasite identification. Moreover, some studies had small sample sizes or used non-random/convenience sampling approaches, and in several cases, they did not fully report important epidemiological information. These factors may have influenced the reliability and comparability of the pooled estimates. Additionally, hospital-based studies in this meta-analysis include only animals presented for clinical care, which may not reflect the general population and could lead to over- or underestimation of true community-level ectoparasite prevalence. This introduces selection bias and may affect the representativeness of the pooled prevalence estimates when generalizing to the wider population. Insufficient data on biological and ecological factors limited their evaluation as potential sources of between-study variability. Furthermore, this meta-analysis did not quantitatively assess climatic variables. As a result, the meta-analysis could not evaluate climate-specific effects on ectoparasite prevalence, which needs further exploration. Finally, most of the available studies were conducted in or near major cities, particularly around veterinary and agricultural university settings. Therefore, other geographic regions remain underrepresented, and future research should expand its spatial coverage to provide a more comprehensive national picture of ectoparasite prevalence.

5. Conclusion

This systematic review and meta-analysis presents a comprehensive overview of ectoparasite infestation in Bangladesh using 56 years (1968–2024) of data from 90 studies conducted on different domestic, peri-domestic, and wild animal and bird hosts. It shows that ectoparasite infestation is substantial in the country, but highly heterogeneous, driven by different ectoparasite species, which can negatively impact the animal industry. Tick infestation was highest, followed by lice and fleas, with ticks concentrated in livestock, particularly cattle, and lice in poultry birds, specifically ducks. Heterogeneity was extremely high across all taxa, and the measured host- and methodology-related moderators explained varying proportions of this variation, with the highest explanatory contribution observed for lice, followed by mites and ticks. This suggests that a complex mix of host, environmental, and study design factors influences ectoparasite infestation proportions in Bangladesh. We identified several persistent gaps in the studies on ectoparasites in Bangladesh, including limited geographical and host coverage, restricted use of molecular techniques and probability sampling, and a scarcity of longitudinal, seasonally resolved data that account for climatic and management covariates. These findings highlight the need for standardized surveillance and diagnostic approaches, along with a better understanding of host, environmental, and management-related factors, to better characterize and control ectoparasite infestations in Bangladesh.

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Declaration of Competing Interest

The authors declare no conflict of interest.

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Appendix A. Supporting information

Supplementary data associated with this article can be found in the online version at [doi:10.1016/j.pvmsr.2026.100060](https://doi.org/10.1016/j.pvmsr.2026.100060).

Data availability

All data supporting the findings of this study are available in the Open Science Framework (OSF) repository. The corresponding DOI: <https://doi.org/10.17605/OSF.IO/4VRT7>

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