pathogens

MDPI

Systematic Review

Meta-Analysis of the Prevalence of Porcine Zoonotic Bacterial Pathogens in India: A 13-Year (2010–2023) Study

Swaraj Rajkhowa [1,*,†], Joyshikh Sonowal [1,†], Udipta Borthakur [2,†], Seema Rani Pegu [1], Rajib Deb [1], Pranab Jyoti Das [1], Gyanendra Singh Sengar [1] and Vivek Kumar Gupta [1]

[1] ICAR-National Research Centre on Pig, Rani, Guwahati 781131, Assam, India; joyshikh@gmail.com (J.S.); drseemapegu@yahoo.com (S.R.P.); drrajibdeb@gmail.com (R.D.); drpranabjotidas@gmail.com (P.J.D.); gsengar71@gmail.com (G.S.S.); gupta.drvivek@gmail.com (V.K.G.)
[2] Animal Husbandry and Veterinary Department, Guwahati 781003, Assam, India; udborthakur@gmail.com
* Correspondence: swaraj.rajkhowa@gmail.com
† These authors contributed equally to this work.

Abstract: The presence of bacterial pathogens such as *Brucella* spp., *Clostridium* spp., *E. coli*, *Listeria monocytogenes*, *Salmonella* spp., *Staphylococcus* spp., and *Streptococcus suis* not only hampers pig production but also carries significant zoonotic implications. The present study aims to conduct a comprehensive meta-analysis spanning over 13 years (2010–2023) to ascertain the prevalence of these zoonotic bacterial pathogens in Indian pig populations. The study seeks to synthesize data from diverse geographic regions within India and underscores the relevance of the One Health framework. A systematic search of electronic databases was meticulously performed. Inclusion criteria encompassed studies detailing zoonotic bacterial pathogen prevalence in pigs within India during the specified timeframe. Pertinent information including authors, publication year, geographical location, sampling techniques, sample sizes, and pathogen-positive case counts were meticulously extracted. The meta-analysis of zoonotic bacterial pathogens in Indian pig populations (2010–2023) unveiled varying prevalence rates: 9% *Brucella* spp., 22% *Clostridium* spp., 19% *E. coli*, 12% *Listeria monocytogenes*, 10% *Salmonella* spp. and *Streptococcus suis*, and 24% *Staphylococcus* spp. The application of random effects further revealed additional variability: 6% *Brucella* spp., 23% *Clostridium* spp., 24% *E. coli*, 14% *Listeria monocytogenes*, 10% *Salmonella* spp. and *Streptococcus suis*, and 35% *Staphylococcus* spp. Notably, the observed heterogeneity (I^2) varied significantly from 87% to 99%. The meta-analysis findings underscore the pervasive nature of these diseases throughout India's pig populations, accentuating the substantial impact of these pathogens on pig health and the potential for zoonotic transmission. The present study reinforces the importance of the adoption of a comprehensive One Health approach that acknowledges the intricate interplay between animal, human and environmental health.

Keywords: India; meta-analysis; pig; prevalence; zoonotic bacteria

Citation: Rajkhowa, S.; Sonowal, J.; Borthakur, U.; Pegu, S.R.; Deb, R.; Das, P.J.; Sengar, G.S.; Gupta, V.K. Meta-Analysis of the Prevalence of Porcine Zoonotic Bacterial Pathogens in India: A 13-Year (2010–2023) Study. *Pathogens* **2023**, *12*, 1266. https://doi.org/10.3390/pathogens12101266

Academic Editor: Gianluca Rugna

Received: 20 September 2023
Revised: 19 October 2023
Accepted: 19 October 2023
Published: 21 October 2023

1. Introduction

The prevalence of zoonotic bacterial pathogens in animal populations poses substantial challenges to both animal and human health, calling for comprehensive assessments to inform effective management strategies. It is of particular concern for a country like India where pig husbandry plays a pivotal role in uplifting the socio-economic status of the people, especially the tribal masses for whom pig rearing is a way of life. Pork is a high-risk source of foodborne diseases worldwide. Zoonotic bacterial pathogens, such as *Brucella* spp., *Clostridium* spp., *E. coli*, *Listeria monocytogenes*, *Salmonella* spp., *Staphylococcus* spp., *Mycobacterium* spp., *Campylobacter* spp., and *Streptococcus suis* have been identified as detrimental to both pig health and public health due to their potential for zoonotic transmission. Individuals closely involved in pig farming, including pig handlers and

those who consume pork products under unhygienic conditions, are highly susceptible to infections by these zoonotic bacterial pathogens. These pathogens utilize a range of mechanisms to cause diseases, such as releasing toxins, possessing virulence factors, evading the host's immune system and establishing chronic infections within the host. In clostridial infection, *Clostridium perfringens* releases alpha toxin [1], while *Clostridium difficile* produces toxins A (TcdA, enterotoxin A) and B (TcdB, cytotoxin B), which target the colon's lining, causing colitis and severe diarrhoea [2]. Enterohemorrhagic *E. coli* (EHEC) produces Shiga toxins, specifically Shiga toxin 1 (Stx1) and Shiga toxin 2 (Stx2), leading to severe foodborne illnesses [3], while Extended Spectrum Beta-Lactamase (ESBL) *E. coli* resists many antibiotics due to enzyme production, posing treatment challenges [4,5]. *Listeria monocytogenes* produces listeriolysin O, causing listeriosis [6]. *Salmonella* spp. exhibit resilience to gastric acidity, enabling colonization of the gastrointestinal tract and subsequent invasion of the intestinal mucosa; they produce endotoxins, such as lipid A which can trigger inflammatory responses, and exotoxins, including cytotoxins and enterotoxins like stn, which can damage host cells, disrupt intestinal function, and stimulate cytokine release, contributing to gastrointestinal infections [7]. While *Staphylococcus* spp. are known to produce a wide range of toxins, including staphylococcal enterotoxins, Toxic Shock Syndrome Toxin-1 (TSST-1), exfoliative toxins (ETA and ETB), haemolysins (alpha, beta, and delta), Panton-Valentine Leukocidin (PVL), and superantigens (such as TSST-1 and various staphylococcal enterotoxins) [8,9]. The pathogenicity of Staphylococcal toxins is associated with various clinical conditions, from food poisoning to severe skin and systemic infections. *Streptococcus suis* produces a range of virulence factors, including extracellular enzymes for tissue damage and immune evasion, adhesins for host cell attachment and streptolysins, like suilysin, which induce cell lysis and tissue damage, collectively enhancing its pathogenicity [10,11]. *Streptococcus pyogenes*, on the other hand, produces toxins like streptolysins (SLO, SLG, and SLS haemolysins), pyrogenic exotoxins, streptococcal superantigens (SAgs), streptokinase, and hyaluronidase, which collectively contribute to tissue damage, immune system overstimulation, and clinical symptoms like strep throat and necrotizing fasciitis [12–14]. In contrast, *Brucella* spp. primarily cause brucellosis with toxin production playing a minor role [15]. The major virulence factors of *Brucella* are lipopolysaccharide (LPS), the Type IV Secretion System (T4SS), and the BvrR/BvrS system, to interact with host cells, create specialized vacuoles (Brucella Containing Vacuole (BVC)), and establish connections with the endoplasmic reticulum, enhancing their ability to cause chronic infection within host cells [16,17].

It is known that almost two-thirds of the pathogens that cause diseases in humans are of animal origin. Brucellosis is one of the most common, widespread zoonoses throughout the world, mainly caused by *Brucella abortus*, *Brucella melitensis* or *Brucella suis* and is transmitted to people from various animal species [18]. All Shiga-toxin-producing *E. coli* (STEC) strains are pathogenic in humans, capable of causing at least diarrhoea. Depending on the presence of certain stx subtypes and the presence/absence of the *eae* gene, all STEC subtypes may be associated with severe outcomes, i.e., haemolytic uraemic syndrome (HUS), bloody diarrhoea (BD), kidney failures, hospitalizations, and deaths [19]. Pigs are important reservoirs of STEC. The entrance of these strains into the food chain implies a risk to consumers because of the severity of haemolytic uremic syndrome [20]. *Clostridium difficile* is a well-established pathogen of both humans and animals that contaminates foods and the environment. To manage *Clostridium difficile* infections (CDI), a One Health approach with the collaboration of clinicians, veterinarians, environmentalists, and policymakers is paramount. Listeriosis, a zoonotic disease caused by *Listeria monocytogenes*, is a major public health problem and one of the most common notifiable foodborne diseases [21]. It has also been observed that pigs are an important reservoir for *L. monocytogenes* and in particular, younger animals are at risk for asymptomatic carriage [22]. Salmonellosis is one of the most serious zoonotic diseases in the world and pigs are one of the most common sources of *Salmonella* infections in humans [23]. *Streptococcus suis* is considered one of the most important pathogens affecting pig production worldwide and is also an emerging

zoonotic agent in humans [24]. Methicillin-resistant *Staphylococcus aureus* (MRSA) infections can occur in both humans and pigs, leading to a range of illnesses, from skin and soft tissue infections to more severe systemic infections [25]. ESBL *E. coli* and MRSA's resistance to multiple antibiotics complicates treatment, and it poses a public health concern due to its potential for community- and hospital-acquired infections [26,27]. The emergence of multi-drug-resistant pathogens in pig populations, driven by genetic mutations and selective pressures from antimicrobial use, threatens both animal health and public safety. Resistant bacteria of pig origin can be transmitted to humans through direct contact, environmental contamination, and the consumption of pork and its products, raising significant concerns about the spread of antimicrobial resistance. Addressing this issue requires judicious use of antibiotics in pig farming, improved biosecurity measures, and a One Health approach that recognises the interconnectedness of animal, environmental, and human health.

In this context, conducting a meta-analysis to determine the prevalence of various zoonotic bacterial pathogens in Indian pig populations is very much essential. Meta-analysis offers a powerful approach to synthesise data from various studies, providing a comprehensive overview of the prevalence landscape. By collating and analysing prevalence data from different geographic regions within India, this study aims to establish a clear understanding of the extent of prevalence of these pathogens in the pig population. This analysis not only aids in quantifying the extent of the issue but also contributes to the identification of potential trends and patterns that can guide targeted interventions and preventive measures. By exploring the prevalence rates of *Brucella* spp., *Clostridium*, spp., *E. coli*, *Listeria monocytogenes*, *Salmonella* spp., *Staphylococcus* spp., and *Streptococcus suis* within the Indian pig population, this meta-analysis seeks to provide valuable insights into the distribution and potential impacts of these pathogens.

2. Materials and Methods

2.1. Literature Retrieval and Data Compilation

The process encompassed the accumulation of published studies, facilitating a methodical evaluation of the prevalence and associated risk factors of zoonotic bacterial pathogens in pigs, spanning the years 2010 to 2023. These published works were sourced from a diverse array of online search engines, such as NCBI-PubMed, Science Direct, Google Scholar, Research Gate, etc. Subsequently, an extensive review of these studies was conducted, ensuring both their quality and relevance. This review adhered to the guidelines outlined in the Preferred Reporting Items for Systematic Review and Meta-Analysis (PRISMA) and the Meta-analysis of Observational Studies in Epidemiology (MOOSE) protocols. The procedural flow is depicted in Figure 1, delineating the meticulous steps taken throughout this systematic review process.

The criteria guiding the incorporation and exclusion of studies were devised in accordance with the specifications outlined in Table 1. The relevant details within the published studies, including author details, year of publication, study location (regional designation), sample dimension, sample types, and instances of positive occurrences, were methodically extracted to facilitate the meta-analytical process. The determination of the collective prevalence of zoonotic bacterial pathogens in pigs within India was carried out distinctly for each distinct pathogen.

Table 1. Details of inclusion and exclusion criteria used in the study.

Sl. No.	Criteria	Inclusion Criteria	Exclusion Criteria
1	Study design	Observational	Reviews, editorials, commentaries, and non-observational studies (e.g., experimental, or interventional studies
2	Geographical area	Specified to India only	Study radius outside India
3	Publication year	From 2010 to 2023	Studies other than said period (Before 2009 and after 2023)

Table 1. *Cont.*

Sl. No.	Criteria	Inclusion Criteria	Exclusion Criteria
4	Selection of bacteria	Having zoonotic importance and at least 6 publications within the study range	Non-zoonotic bacteria and less than 6 numbers of publication within the study range
5	Specified for the organisms	*Brucella* spp., *Clostridium* spp., *E. coli*, *Listeria monocytogenes*, *Salmonella* spp., *Staphylococcus* spp., *Streptococcus suis*	Other than mentioned organisms
6	Sample size	More than 2 samples	Less than 2 samples
7	Target animal	Swine	Other than mentioned animal
8	Publication type	Peer-Reviewed	Non-peer-reviewed articles, conference abstracts, or unpublished data
9	Language	English	Non-English language publications
10	Sample source	Blood, tissue, body fluids, stool samples, farm waste and environmental samples etc.	Samples from human and other animals

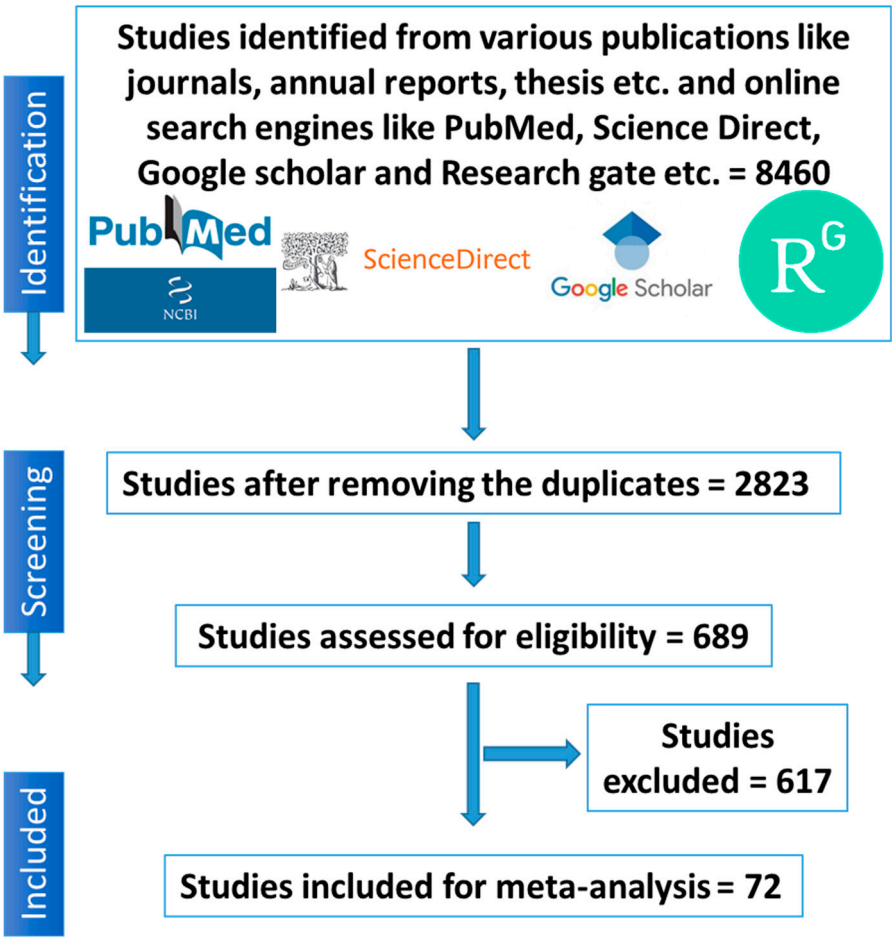

Figure 1. Schematic depiction of the literature selection procedure for the systematic review of the prevalence of zoonotic bacterial pathogens in swine of India from 2010 to 2023.

2.2. Methods Used for Meta-Analysis

Utilizing R-software, the prevalence of zoonotic bacterial pathogens in pigs was computed through the application of meta-analysis tools. This encompassed the systematic analysis of 73 published studies conducted across India, spanning the timeline from 2010 to 2023. A funnel plot generated using the 'dplyr' package in R was employed to visually assess publication bias and the potential influence of small-study effects. This plot aids in identifying any asymmetry in the distribution of effect sizes and offers insights into the

presence of bias within the included studies. The presentation of a funnel plot involves the plotting of the logit proportion against the standard error. The emergence of signs suggesting publication bias implies the appropriateness of employing the random effects model for the analysis of this dataset (Figure 2).

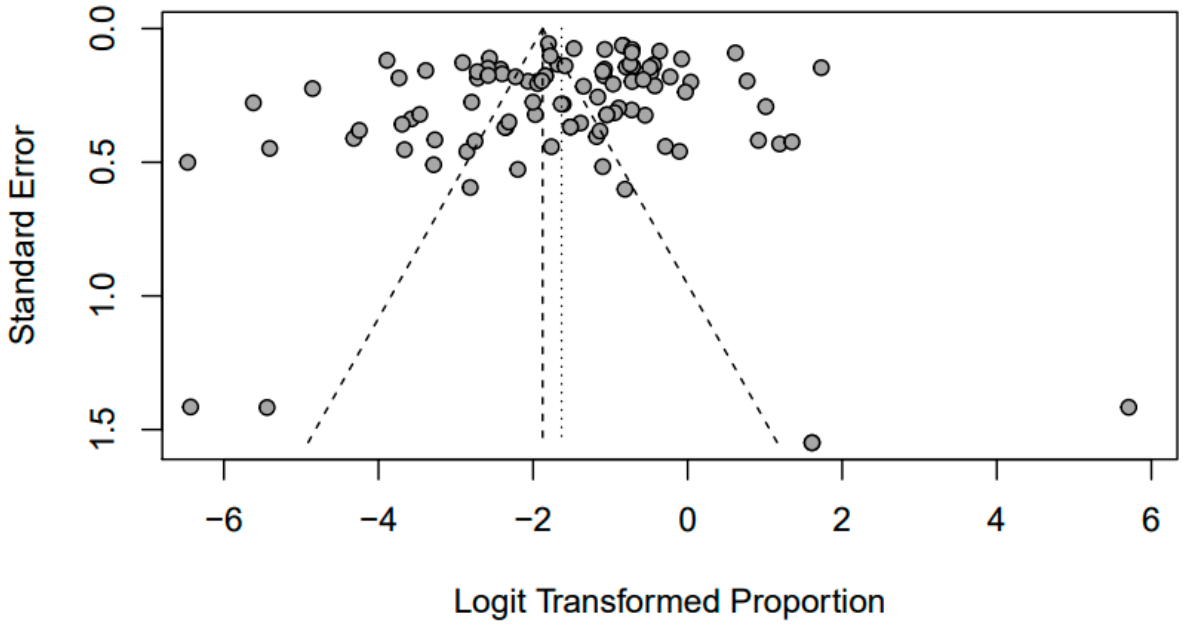

Figure 2. Funnel plot that elucidates potential publication bias in prevalence of zoonotic bacterial pathogens in India from 2010 to 2023.

The analysis was subdivided pathogen-wise, such as *Brucella* spp., *Clostridium* spp., *E. coli*, *Listeria monocytogenes*, *Salmonella* spp., *Staphylococcus* spp., and *Streptococcus suis* separately. The list of studies included in the meta-analysis of zoonotic bacterial pathogens in pigs is given in Table 2. The 'meta' package in R was employed to generate a forest plot, an effective visual tool for presenting the effect sizes and corresponding confidence intervals of individual studies. Two distinct models were employed to estimate the proportion of positive samples in relation to the sample size using Forest plots: the common effect model was used to estimate the overall prevalence of zoonotic bacterial pathogens across all studies, assuming homogeneity among the studies; the random effects model, accounting for potential heterogeneity, provided a more conservative estimate. Heterogeneity among the studies was assessed using the I^2 statistic, which quantifies the proportion of variability attributable to true heterogeneity rather than chance. The presence of heterogeneity was considered significant at I^2 values greater than 50%. The τ^2 (tau-square) value was calculated to estimate the extent of true differences contributing to the observed heterogeneity.

Table 2. List of published research articles and details of studies included in the meta-analysis of zoonotic bacterial pathogens of pigs in India from 2010–2023.

Sl. No.	Author's Name	Year of Publication	Sample Size	Organism	Number of Positives	Percent Positive	Study Area	References
1	Shome et al., 2019	2019	575	*Brucella*	236	41.04	Southern India	[28]
2	Shome et al., 2019	2019	575	*Brucella*	47	8.17	Southern India	[28]
3	Gogoi et al., 2017	2017	115	*Brucella*	0	0.00	North Eastern India	[29]
4	Kalleshamurthya et al., 2019	2019	1121	*Brucella*	5	0.45	North East India	[30]
5	Jindal et al., 2017	2017	330	*Brucella*	9	2.73	Northern India	[31]
6	Jindal et al., 2017	2017	330	*Brucella*	8	2.42	Northern India	[31]
7	Jindal et al., 2017	2017	330	*Brucella*	10	3.03	Northern India	[31]
8	Jindal et al., 2017	2017	40	*Brucella*	4	10.00	Northern India	[31]
9	Kaur et al., 2020	2020	34	*Brucella*	8	23.53	Northern India	[32]
10	Kaur et al., 2020	2020	90	*Brucella*	15	16.67	Northern India	[32]

Table 2. *Cont.*

Sl. No.	Author's Name	Year of Publication	Sample Size	Organism	Number of Positives	Percent Positive	Study Area	References
11	Kaur et al., 2020	2020	90	*Brucella*	11	12.22	Northern India	[32]
12	Kavya et al., 2017	2017	225	*Brucella*	88	39.11	Southern India	[33]
13	Kavya et al., 2017	2017	225	*Brucella*	74	32.89	Southern India	[33]
14	Tadepalli et al., 2011	2011	1184	*Brucella*	221	18.67	Southern India	[34]
15	Tadepalli et al., 2011	2011	1184	*Brucella*	359	30.32	Southern India	[34]
16	Tadepalli et al., 2011	2011	1184	*Brucella*	356	30.07	Southern India	[34]
17	Shakuntala et al., 2016	2016	2583	*Brucella*	20	0.77	North Eastern India	[35]
18	Shakuntala et al., 2016	2016	2583	*Brucella*	4	0.15	North Eastern India	[35]
19	Shakuntala et al., 2020	2019	3597	*Brucella*	13	0.36	North Eastern India	[36]
20	Shakuntala et al., 2020	2019	3597	*Brucella*	72	2.00	North Eastern India	[36]
21	Shome et al., 2016	2016	2576	*Brucella*	365	14.17	mix	[37]
22	Kavya et al., 2017	2017	225	*Brucella*	70	39.11	Southern India	[33]
23	Fahrion et al., 2014	2014	53	*Brucella*	3	5.66	North Eastern India	[38]
24	Yadav et al., 2018	2018	111	*Clostridium*	4	3.60	Southern India	[39]
25	Das et al., 2017	2017	41	*Clostridium*	15	36.59	North Eastern India	[40]
26	Hazarika et al., 2023	2023	41	*Clostridium*	6	14.63	North Eastern India	[41]
27	Yadav et al., 2017	2017	154	*Clostridium*	59	38.31	Eastern India	[42]
28	Hussain et al., 2016	2016	233	*Clostridium*	29	12.45	North Eastern India	[43]
29	Hussain et al., 2021	2021	116	*Clostridium*	38	32.76	North Eastern India	[44]
30	Hussain et al., 2017	2017	2	*Clostridium*	2	100.00	North Eastern India	[45]
31	Kataria et al., 2014	2014	100	*E. coli*	51	51.00	North Eastern India	[46]
32	Kylla et al., 2019	2019	457	*E. coli*	6	1.31	North Eastern India	[47]
33	Regon et al., 2014	2014	150	*E. coli*	150	100.00	North Eastern India	[48]
34	Tamta et al., 2020	2020	124	*E. coli*	55	44.35	mix	[49]
35	Tamta et al., 2020	2020	21	*E. coli*	9	42.86	Southern India	[49]
36	Lalruatdiki et al., 2018	2018	228	*E. coli*	58	25.44	North Eastern India	[50]
38	Kumar et al., 2021	2021	37	*E. coli*	9	24.32	North Eastern India	[51]
39	Kumar et al., 2021	2021	49	*E. coli*	16	32.65	North Eastern India	[51]
40	Debbarma et al., 2020	2020	420	*E. coli*	66	15.71	North Eastern India	[52]
41	Begum et al., 2013	2013	1260	*E. coli*	65	5.16	North Eastern India	[53]
42	Tamta et al., 2020	2020	71	*E. coli*	35	49.30	Northern India	[54]
43	Tamta et al., 2020	2020	84	*E. coli*	20	23.81	Southern India	[54]
44	Nirupama et al., 2018	2018	741	*E. coli*	243	32.79	mix	[55]
45	Samanta et al., 2015	2015	200	*E. coli*	76	38.00	Eastern India	[56]
46	Puii et al., 2019	2019	164	*E. coli*	6	3.66	North Eastern India	[57]
47	Rajkhowa et al., 2014	2014	782	*E. coli*	113	14.45	North Eastern India	[58]
48	Mandakini et al., 2015	2015	170	*E. coli*	43	25.29	North Eastern India	[59]
49	Kumar et al., 2019	2019	531	*E. coli*	345	64.97	mix	[60]
50	Kylla et al., 2020	2020	1286	*E. coli*	30	2.33	North Eastern India	[61]
51	Kylla et al., 2020	2020	1286	*E. coli*	42	3.27	North Eastern India	[61]
52	Lalruatdiki et al., 2018	2018	867	*E. coli*	221	25.49	North Eastern India	[50]
53	Mandakini et al., 2020	2020	258	*E. coli*	83	32.17	North Eastern India	[62]
54	Mandakini et al., 2020	2020	258	*E. coli*	29	11.24	North Eastern India	[62]
55	Raorane et al., 2015	2015	501	*Listeria*	31	6.19	Western India	[63]
56	Suryawanshi et al., 2017	2017	92	*Listeria*	15	16.30	Western India	[64]
57	Suryawanshi et al., 2017	2017	92	*Listeria*	5	5.43	Western India	[64]
58	Suryawanshi et al., 2017	2017	92	*Listeria*	8	8.70	Western India	[64]
59	Vaidya et al., 2018	2018	50	*Listeria*	10	20.00	Central India	[65]
60	Fahrion et al., 2014	2014	91	*Listeria*	36	39.56	North Eastern India	[38]
61	Sarangi et al., 2012	2012	13	*Listeria*	4	30.77	Eastern India	[66]
62	Raorane et al., 2014	2014	215	*Listeria*	27	12.56	Northern India	[67]
63	Sharma et al., 2013	2013	55	*Salmonella*	16	29.09	Northern India	[68]
64	Kumar et al., 2014	2014	50	*Salmonella*	9	18.00	Southern India	[69]
65	Kumar et al., 2014	2014	93	*Salmonella*	8	8.60	Northern India	[70]
66	Chaudhary et al., 2015	2015	270	*Salmonella*	37	13.70	Western India	[71]
67	Kylla et al., 2016	2016	20	*Salmonella*	5	25.00	North Eastern India	[72]
68	Chaudhary et al., 2016	2016	270	*Salmonella*	37	13.70	Western India	[73]
69	Kalambhe et al., 2016	2016	100	*Salmonella*	6	6.00	Western India	[74]
70	Latha et al., 2017	2017	310	*Salmonella*	0	0.00	Southern India	[75]
71	Das et al., 2018	2018	200	*Salmonella*	5	2.50	North Eastern India	[76]
72	Lalruatdiki et al., 2018	2018	228	*Salmonella*	30	13.16	North Eastern India	[50]
73	Chakraborty et al., 2019	2019	50	*Salmonella*	9	18.00	North Eastern India	[77]
74	Mahindroo1 et al., 2019	2019	208	*Salmonella*	52	25.00	Northern India	[78]
75	Kylla et al., 2019	2019	457	*Salmonella*	38	8.32	Northern India	[79]
76	Borah et al., 2022	2022	1231	*Salmonella*	88	7.15	North Eastern India	[80]
77	Kumar et al., 2014	2014	50	*Staphylococcus*	14	28.00	Southern India	[69]
78	Fahrion et al., 2014	2014	19	*Staphylococcus*	9	47.37	North Eastern India	[38]
79	Zehra et al., 2017	2017	28	*Staphylococcus*	20	71.43	Northern India	[81]
80	Rajkhowa et al., 2016	2016	698	*Staphylococcus*	49	7.02	North Eastern India	[82]
82	Yaiphathoi et al., 2020	2020	50	*Staphylococcus*	13	26.00	North Eastern India	[83]
83	Latha et al., 2017	2017	310	*Staphylococcus*	149	48.06	Southern India	[75]
84	Kalai et al., 2020	2020	60	*Staphylococcus*	44	73.33	North Eastern India	[84]
85	Zehra et al., 2019	2019	131	*Staphylococcus*	27	20.61	Northern India	[85]
86	Yaiphathoi et al., 2019	2019	50	*Staphylococcus*	13	26.00	North Eastern India	[86]
88	Savariraj et al., 2018	2018	120	*Staphylococcus*	82	68.33	Southern India	[87]
89	Baruah et al., 2016	2016	349	*Staphylococcus*	34	9.74	North Eastern India	[88]
90	Devi et al., 2017	2017	497	*Streptococcus*	7	1.41	North Eastern India	[89]
91	Anand et al., 2016	2016	100	*Streptococcus*	9	9.00	Northern India	[90]

Table 2. *Cont.*

Sl. No.	Author's Name	Year of Publication	Sample Size	Organism	Number of Positives	Percent Positive	Study Area	References
92	Dinesh et al., 2020	2020	243	*Streptococcus*	14	5.76	Northern India	[91]
93	Dinesh et al., 2022	2022	664	*Streptococcus*	41	6.17	Northern and North Eastern India	[92]
94	Pegu et al., 2020	2020	116	*Streptococcus*	32	27.59	North Eastern India	[93]
95	Sonowal et al., 2014	2014	126	*Streptococcus*	15	11.90	North Eastern India	[94]
96	Rajkhowa et al., 2021	2021	365	*Streptococcus*	62	16.99	North Eastern India	[95]
97	Rajkhowa et al., 2017	2017	34	*Streptococcus*	27	79.41	North Eastern India	[96]
98	Devi et al., 2017	2017	497	*Streptococcus*	35	7.04	North Eastern India	[97]
99	Vishva et al., 2022	2022	563	*Streptococcus*	184	32.68	Northern India	[98]

3. Results

3.1. Meta-Analysis

The prevalence of *Brucella* spp., *Clostridium*, *E. coli*, *Listeria monocytogenes*, *Salmonella* spp., *Staphylococcus* spp., and *Streptococcus suis* were calculated separately for pigs. The meta-analysis for these organisms was carried out using 73 published studies from India, which included 23 studies on *Brucella* spp., 7 studies on *Clostridium* spp., 23 studies on *E. coli*, 8 studies on *Listeria monocytogenes*, 14 studies on *Salmonella* spp., 11 studies on *Staphylococcus* spp., and 10 studies on *Streptococcus* suis on pig from India (Figure 3).

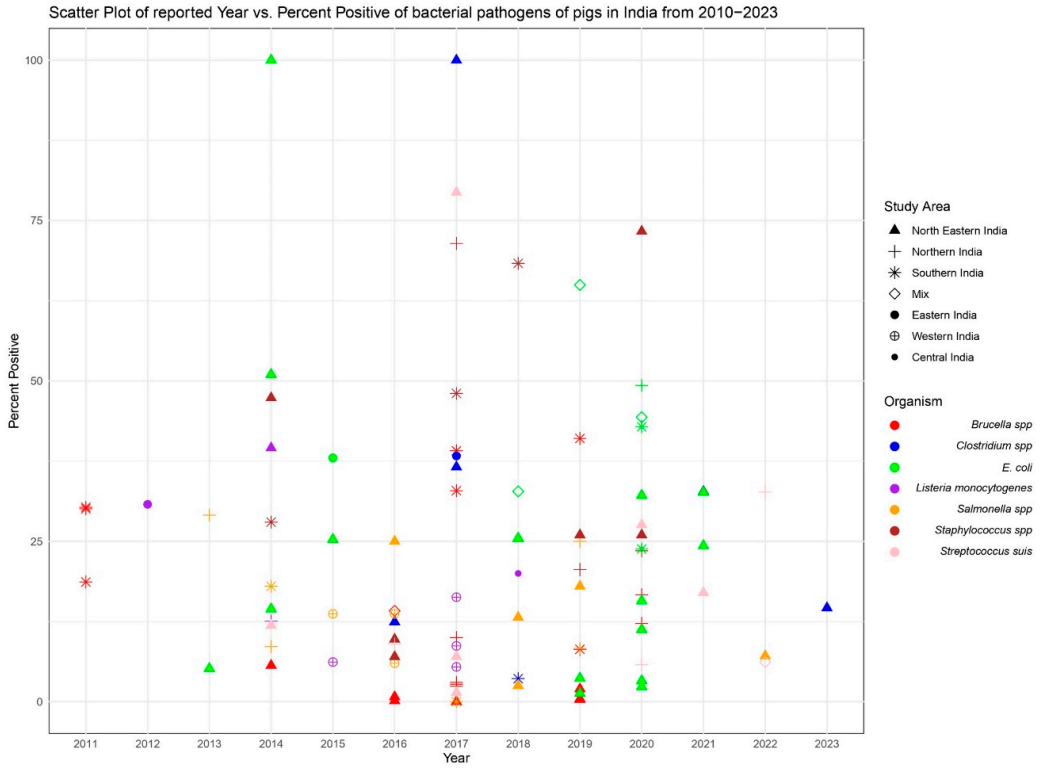

Figure 3. Representation of a scatter plot, depicting the positive percentage trends in the prevalence of different zoonotic bacterial pathogens among Indian swine. The data spans the years from 2010 to 2023 and includes samples from different regions across India.

3.2. Meta-Analysis of the Prevalence of Brucellosis in Pigs

In this meta-analysis of the prevalence of *Brucella* spp. in pigs across India (2010–2023), a total of 22,846 events were included (Figure 4). The common effect model yielded an estimated overall prevalence proportion of nine percent (95% CI: [8%; 9%]), suggesting that approximately 9 out of every 100 pigs were infected with *Brucella* spp. in India. On the other hand, the random effects model, which accounts for potential heterogeneity among the studies, yielded an estimated proportion of six percent (95% CI: [3%; 13%]).

The considerable heterogeneity observed in the random effects model, indicated by an I^2 value of 99%, underscores the diversity in the study outcomes beyond what could be attributed to chance. This indicates the presence of factors influencing *Brucella* prevalence differences across the studies, such as variations in sample collection methods, geographical regions, management practices and testing protocols. The associated *p*-value of zero further confirms the statistical significance of this heterogeneity. The calculated τ^2 value of 3.4092 highlights the extent to which true differences in *Brucella* prevalence rates among the studies contribute to the observed heterogeneity.

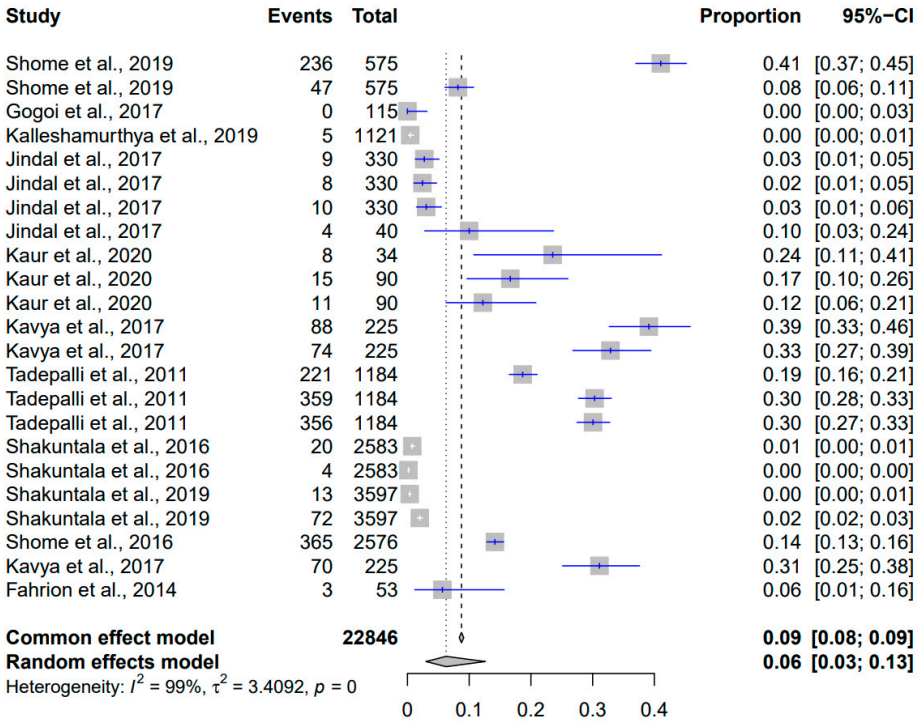

Figure 4. Forest plot showing the result of 23 studies reporting the prevalence of brucellosis in pigs in India from 2010 to 2023.

3.3. Meta-Analysis of the Prevalence of Clostridium spp. in Pigs

The meta-analysis of the prevalence of *Clostridium* spp. in Indian pigs (2010–2023) based on 698 events revealed an estimated overall proportion of 22% (95% CI: [0.19; 0.25]) using the common effect model and 23% (95% CI: [0.11; 0.41]) using the random effects model (Figure 5). Heterogeneity was substantial (I^2 = 90%, $p < 0.01$), suggesting diverse factors contributing to the observed variation. The τ^2 value of 1.0815 highlighted the degree of true differences between studies.

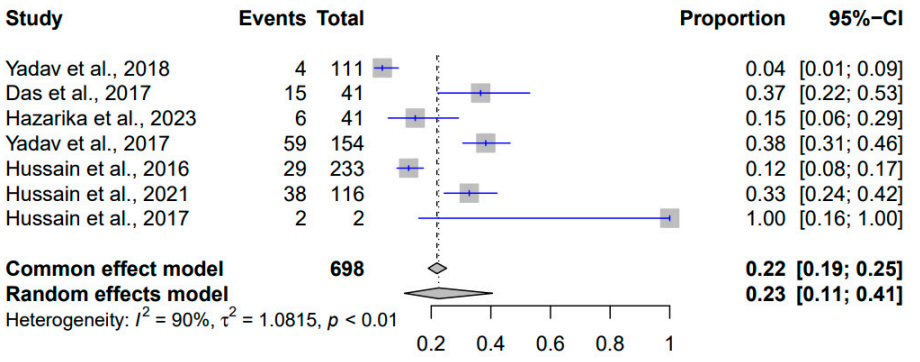

Figure 5. Forest plot showing the result of 7 studies reporting the prevalence of *Clostridium* spp. in pigs in India from 2010 to 2023.

3.4. Meta-Analysis of the Prevalence of E. coli in Pigs

In the present study, the meta-analysis of the prevalence of *E. coli* in pigs in India between 2010 and 2023 employed two distinct models to estimate the proportion of positive cases (Figure 6). The common effect model yielded an estimated prevalence of 19% (95% CI: [18%; 19%]), suggesting that about 19% of cases were associated with *E. coli* infection in the pig population during this period. The random effects model, which considers study variability, provided a slightly higher estimate of 24% (95% CI: [13%; 40%]), reflecting potential differences across studies. Heterogeneity was pronounced, with an I^2 value of 98%, signifying significant variation beyond chance. The τ^2 value of 3.1956 further quantified true differences contributing to heterogeneity.

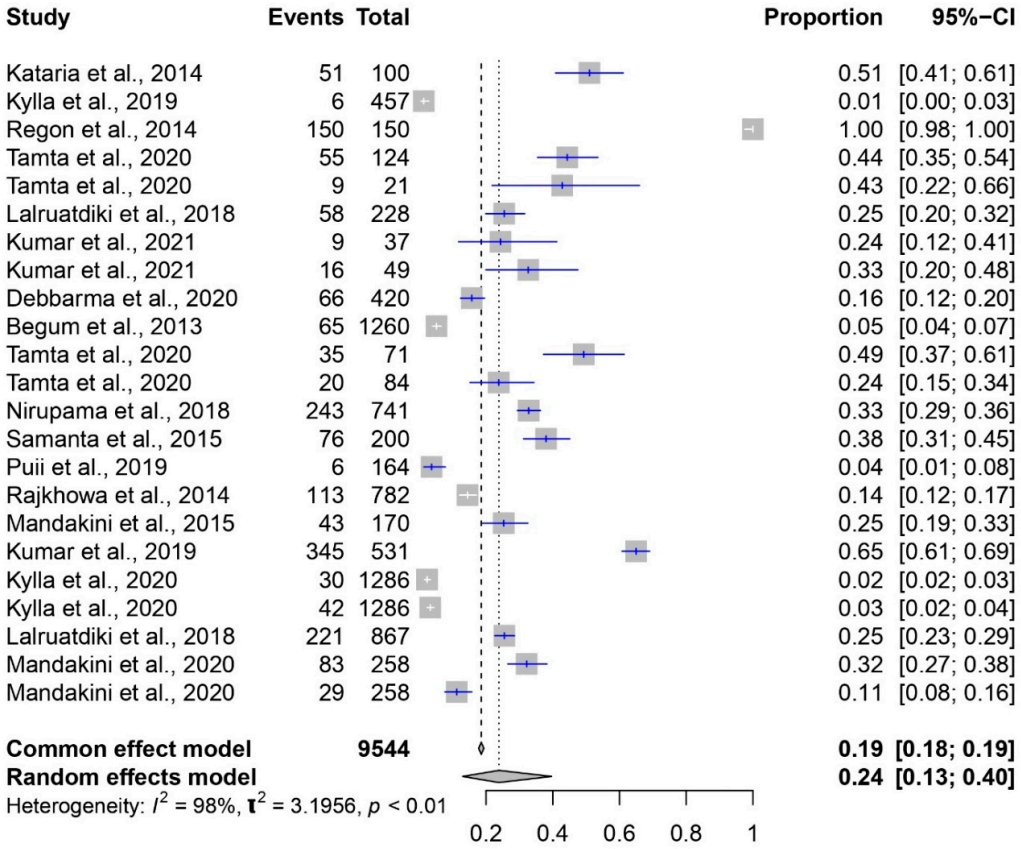

Figure 6. Forest plot showing the result of 23 studies reporting the prevalence of *E. coli* in pigs in India from 2010 to 2023.

3.5. Meta-Analysis of the Prevalence of Listeria monocytogenes in Pigs

The results of the meta-analysis of the prevalence of *Listeria monocytogenes* in Indian pigs from 2010 to 2023 are shown in Figure 7. With a total of 1146 events, the common effect model estimated a prevalence of 12% (95% CI: [10%; 14%]), suggesting that approximately 12% of pigs were affected. The random effects model estimated a prevalence of 14% (95% CI: [8%; 22%]), indicating potential study variations. Heterogeneity was significant (I^2 = 91%), denoting substantial variation beyond chance. The *p*-value below 0.01 affirmed this heterogeneity's statistical significance. A τ^2 value of 0.5654 quantified genuine differences contributing to the variation.

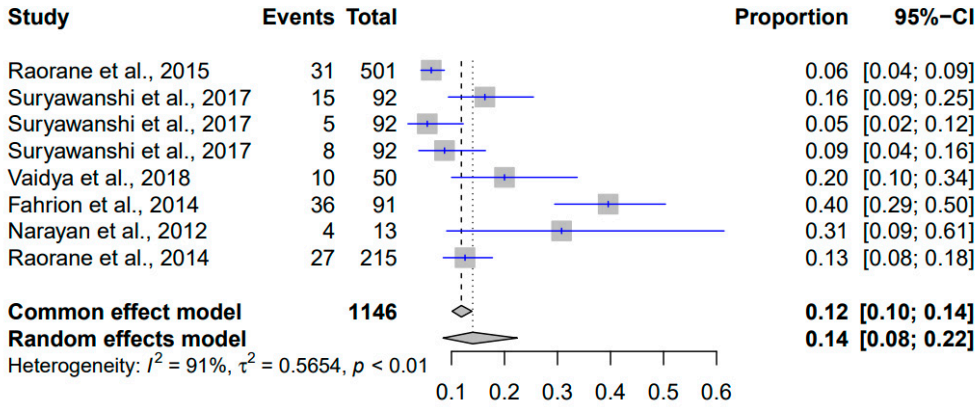

Figure 7. Forest plot showing the result of 8 studies reporting the prevalence of *Listeria monocytogenes* in pigs in India from 2010 to 2023.

3.6. Meta-Analysis of the Prevalence of Salmonella spp. in Pigs

The results of the meta-analysis of the prevalence of *Salmonella* spp. in Indian pigs spanning 2010 to 2023 are shown in Figure 8. With a total of 3542 events, the common effect model estimated a prevalence of ten percent (95% CI: [9%; 11%]), implying that approximately ten percent of pigs were infected. Interestingly, the random effects model produced a comparable estimate of ten percent (95% CI: [6%; 16%]), accommodating potential variations in study approaches. Substantial heterogeneity was observed (I^2 = 87%), implying significant variation beyond chance. This heterogeneity's statistical significance was reaffirmed by the *p*-value less than 0.01. A τ^2 value of 1.1165 quantified the extent of authentic differences contributing to this observed variation.

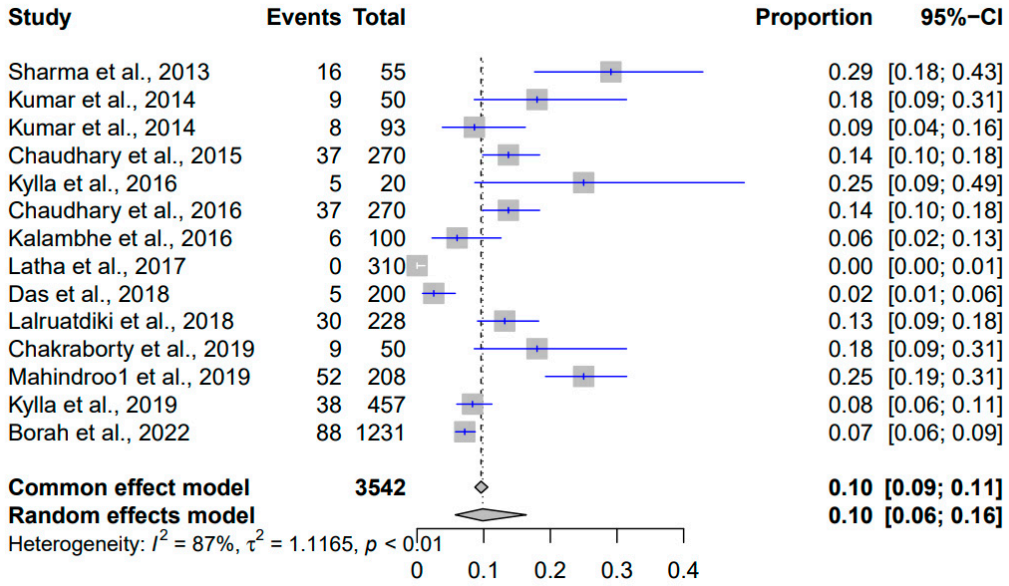

Figure 8. Forest plot showing the result of 14 studies reporting the prevalence of *Salmonella* spp. in pigs in India from 2010 to 2023.

3.7. Meta-Analysis of the Prevalence of Staphylococcus spp. in Pigs

In the current study, a meta-analysis was conducted to explore the prevalence of *Staphylococcus* spp. in Indian pigs between 2010 and 2023 (Figure 9). The dataset encompassed a total of 1865 events. The common effect model estimated a prevalence of 24% (95% CI: 22% to 26%), indicating that approximately 24% of pigs were affected by *Staphylococcus* spp. during this period. Contrastingly, the random effects model, accounting for potential study variations, presented a higher estimated prevalence of 35% (95% CI:

21% to 52%). Heterogeneity was pronounced, with an I^2 value of 97%, indicating substantial variation beyond chance. The associated *p*-value of less than 0.01 confirmed the statistical significance of this heterogeneity. The τ^2 value of 1.3396 quantified the extent to which genuine differences in *Staphylococcus* spp. prevalence rates contributed to the observed heterogeneity.

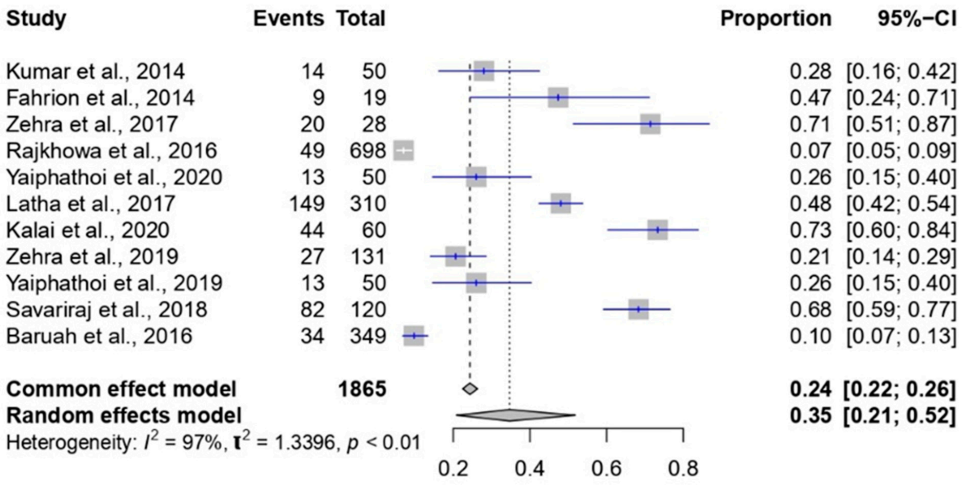

Figure 9. Forest plot showing the result of 11 studies reporting the prevalence of *Staphylococcus* spp. in pigs in India from 2010 to 2023.

3.8. Meta-Analysis of the Prevalence of Streptococcus suis in Pigs

The comprehensive meta-analysis investigating the prevalence of *Streptococcus suis* in Indian pigs from 2010 to 2023 analysed a total of 3205 events (Figure 10). The common effect model estimated a prevalence of 13% (95% CI: [12%; 15%]), suggesting that roughly 13% of pigs were affected by *Streptococcus suis* during this period. The random effects model, designed to account for potential variations between studies, yielded a similar estimated prevalence of 13% (95% CI: [6%; 27%]). Heterogeneity emerged with an I^2 value of 97%, signifying significant variation beyond chance. The associated *p*-value of less than 0.01 confirmed the statistical significance of this heterogeneity. The τ^2 value of 1.9289 provided insight into the extent to which genuine differences in *Streptococcus suis* prevalence rates contributed to the observed heterogeneity.

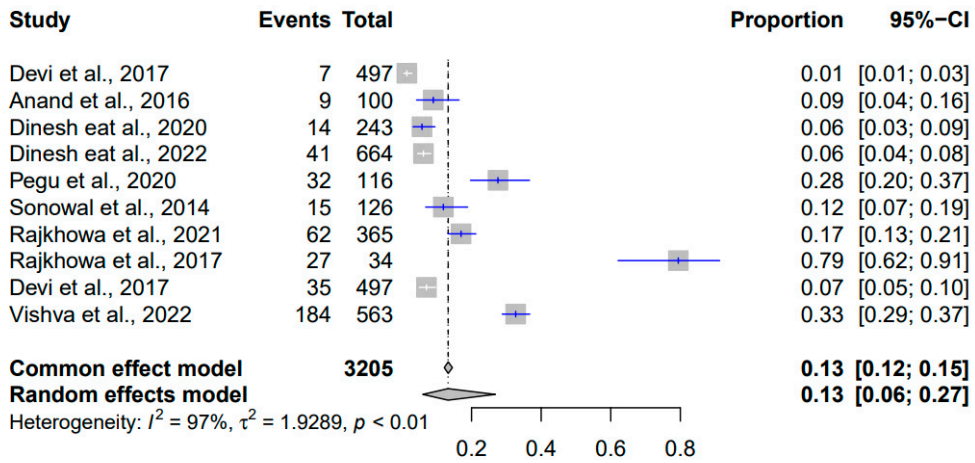

Figure 10. Forest plot showing the result of 10 studies reporting the prevalence of *Streptococcus suis* in pigs in India from 2010 to 2023.

Table 3 shows the overall meta-analysis of the prevalence patterns of various zoonotic bacterial pathogens in pig populations in India from 2010 to 2023.

Table 3. Meta-analysis of the prevalence patterns of various zoonotic bacterial pathogens in pig populations in India from 2010 to 2023.

Organism	Total Events	Common Effect		Random Effects		Heterogeneity (I^2)	Variance (τ^2)	*p*-Value
		Proportion	95% CI (Common Effect)	Proportion	95% CI (Random Effects)			
Brucella spp.	23,846	0.09	[0.08; 0.09]	0.06	[0.03; 0.13]	99%	3.4092	0
Clostridium spp.	698	0.22	[0.19; 0.25]	0.23	[0.11; 0.41]	90%	1.0815	<0.01
E. coli	9544	0.19	[0.18; 0.19]	0.24	[0.13; 0.40]	98%	3.1956	<0.01
Listeria monocytogenes	1146	0.12	[0.10; 0.14]	0.14	[0.08; 0.22]	91%	0.5654	<0.01
Salmonella spp.	3542	0.1	[0.09; 0.11]	0.1	[0.06; 0.16]	87%	1.1165	<0.01
Staphylococcus spp.	1865	0.24	[0.22; 0.26]	0.35	[0.21; 0.52]	98%	1.3396	<0.01
Streptococcus suis	3205	0.13	[0.12; 0.15]	0.13	[0.06; 0.27]	97%	1.9289	<0.01

4. Discussion

Zoonotic bacterial pathogens within the pig production system represent a significant public health concern due to their potential to transmit diseases to humans. In this study, we performed a systematic meta-analysis of 73 published studies conducted across India, spanning between 2010 to 2023 to assess the prevalence patterns of various zoonotic bacterial pathogens in pigs. The findings have provided some valuable insights into the distribution and prevalence of these pathogens, along with their potential implications for public health and veterinary interventions.

The present analysis revealed distinct patterns of prevalence across different bacterial pathogens, which have zoonotic importance. *Staphylococcus* spp. exhibited the highest estimated prevalence with a random effects proportion of 0.35 (95% CI: [0.21; 0.52]), followed by *Clostridium* spp. with a random effects proportion of 0.23 (95% CI: [0.11; 0.41]). The prevalence of *Staphylococcus* spp. was notably consistent with previous studies, closely aligning with Latha et al. (2017) at 48%, Fahrion et al. (2014) at 47%, Kumar et al. (2014) at 28%, Yaiphathoi et al. (2020) at 26%, and Zehra et al. (2019) at 21% [38,69,75,83,85]. Similarly, the prevalence of *Clostridium* spp. closely corresponded to the findings of previous studies, aligning notably with Das et al. (2017) at 37%, Hussain et al. (2021) at 33%, and Hazarika et al. (2023) at 15% [40,41,44]. In contrast, *Brucella* spp. and *Salmonella* spp. showed lower estimated random effects proportions of 0.06 (95% CI: [0.03; 0.13]) and 0.1 (95% CI: [0.06; 0.16]), respectively. The prevalence of *Brucella* spp. in the present study corroborated the findings of Jindal et al. (2017), Shome et al. (2019), and Fahrion et al. (2014) which showed the prevalence to be ten, eight, and six percent, respectively [28,31,38]. The prevalence of *Salmonella* spp. was consistent with the findings of several prior studies, including Kumar et al. (2014) at 18% and 9%, Chaudhury et al. (2015) at 14%, Chaudhary et al. (2016) at 14%, Kalambhe et al. (2016) at 6%, Lalruatdiki et al. (2018) at 13%, and Kylla et al. (2019) at 8% [47,50,70,71,73,74]. *E. coli* exhibited a moderate estimated prevalence in pig populations with a random effects proportion of 0.24 (95% CI: [0.13; 0.40]). Similarly, *Listeria monocytogenes* and *Streptococcus suis* also demonstrated moderate prevalence levels with random effects proportions of 0.14 (95% CI: [0.08; 0.22]) and 0.13 (95% CI: [0.06; 0.27]), respectively. The prevalence of *E. coli* closely resembled the findings of previous studies, aligning notably with Mandakini et al. (2020) at 32%, Mandakini et al. (2015) at 25%, Tamta et al. (2020) at 25%, Lalruatdiki et al. (2018) at 24%, and Kumar et al. (2021) at 24% and 33% [50,51,54,59,62]. The prevalence of *Listeria monocytogenes* in the present study was consistent with the findings of Suryawanshi et al. (2017) at 16% and 9%, Vaidya et al. (2018) at 20%, and Raorane et al. (2014) at 13% [64,65,67]. In the present study, it was also observed that the prevalence of *Streptococcus suis* was on par with the findings of several researchers [90,94,96].

The study also revealed that heterogeneity was a common feature among the studies, with I^2 values exceeding 50% for all of the pathogens. This indicated substantial variability among the included studies. Furthermore, funnel plots were used to assess publication bias, and in some cases, asymmetry was observed, suggesting the potential influence of small-study effects or publication bias.

The higher prevalence of zoonotic bacterial pathogens as observed in the present study, such as *Staphylococcus* spp. and *Clostridium* spp. underscores the need for continued surveillance, targeted interventions and control measures both at the farm and processing levels to reduce the risk of zoonotic disease transmission from pigs to humans. Serological and molecular epidemiological studies can help in elucidating the genetic diversity and evolution of these pathogens [99]. It has also been observed that the studies included in the present meta-analysis commonly used techniques like biochemical tests and PCR [44,56,97] followed by ELISA [34,37,64] and lateral flow assays [33] for the detection of bacterial pathogens. It is very much desired that longitudinal studies are needed to monitor the changes in prevalence over time and to assess the effectiveness of control measures.

5. Conclusions

The meta-analysis covering 2010 to 2023 revealed a significant prevalence of zoonotic bacterial pathogens among the pig population in India. The study elucidated the prevalence patterns of zoonotic bacterial pathogens in the Indian pig population, with *Staphylococcus* spp. emerging as the most prevalent bacterial pathogen in pigs, closely followed by *E. coli* and *Clostridium* spp., while *Brucella* spp. and *Salmonella* spp. exhibited lower prevalence rates. Additionally, *Listeria monocytogenes* and *Streptococcus suis* demonstrated moderate prevalence among zoonotic bacterial pathogens in the Indian pig population. These findings underscore the urgent need for adopting a One Health approach, which recognizes the interconnectedness of animal and human health to effectively mitigate economic losses and mitigate zoonotic risks.

Author Contributions: Concept and design of manuscript: S.R. and J.S.; literature search: J.S., S.R.P., U.B. and S.R.; data analysis: J.S.; manuscript drafting: J.S. and S.R.; proofreading and editing: U.B., S.R., J.S., S.R.P., R.D., P.J.D., G.S.S. and V.K.G. All authors have read and agreed to the published version of the manuscript.

Funding: This research received no external funding.

Institutional Review Board Statement: This meta-analysis was conducted using publicly available data from previously published studies. As such, ethical approval was not required for this study.

Informed Consent Statement: No human participants were involved in this study.

Data Availability Statement: The datasets used during the study will be available upon request to the corresponding author.

Acknowledgments: The authors are highly grateful to the Director of the ICAR-National Research Centre on Pig, Rani, Guwahati, Assam.

Conflicts of Interest: The authors declare that they have no conflict of interest.

References

1. Uzal, F.A.; Navarro, M.A.; Asin, J.; Boix, O.; Ballarà-Rodriguez, I.; Gibert, X. Clostridial diarrheas in piglets: A review. *Vet. Microbiol.* **2023**, *280*, 109691. [CrossRef] [PubMed]
2. Di Bella, S.; Ascenzi, P.; Siarakas, S.; Petrosillo, N.; di Masi, A. *Clostridium difficile* Toxins A and B: Insights into Pathogenic Properties and Extraintestinal Effects. *Toxins* **2016**, *8*, 134. [CrossRef] [PubMed]
3. Pacheco, A.R.; Sperandio, V. Shiga toxin in enterohemorrhagic *E.coli*: Regulation and novel anti-virulence strategies. *Front. Cell. Infect. Microbiol.* **2012**, *2*, 81. [CrossRef]
4. Castanheira, M.; Simner, P.J.; Bradford, P.A. Extended-spectrum β-lactamases: An update on their characteristics, epidemiology and detection. *JAC-Antimicrob. Resist.* **2021**, *3*, dlab092. [CrossRef] [PubMed]
5. Bergšpica, I.; Kaprou, G.; Alexa, E.A.; Prieto, M.; Alvarez-Ordóñez, A. Extended Spectrum β-Lactamase (ESBL) Producing *Escherichia coli* in Pigs and Pork Meat in the European Union. *Antibiotics* **2020**, *9*, 678. [CrossRef]
6. Dramsi, S.; Cossart, P. Listeriolysin O: A genuine cytolysin optimized for an intracellular parasite. *J. Cell. Biol.* **2002**, *156*, 943–946. [CrossRef] [PubMed]
7. van Asten, A.J.A.M.; van Dijk, J.E. Distribution of "classic" virulence factors among *Salmonella* spp. *FEMS Immunol. Med. Microbiol.* **2005**, *44*, 251–259. [CrossRef] [PubMed]
8. Pinchuk, I.V.; Beswick, E.J.; Reyes, V.E. Staphylococcal enterotoxins. *Toxins* **2010**, *2*, 2177–2197. [CrossRef]

9. Hennekinne, J.-A.; De Buyser, M.-L.; Dragacci, S. *Staphylococcus aureus* and its food poisoning toxins: Characterization and outbreak investigation. *FEMS Microbiol. Rev.* **2012**, *36*, 815–836. [CrossRef]
10. Tenenbaum, T.; Asmat, T.M.; Seitz, M.; Schroten, H.; Schwerk, C. Biological activities of suilysin: Role in *Streptococcus suis* pathogenesis. *Future Microbiol.* **2016**, *11*, 941–954. [CrossRef] [PubMed]
11. Kouki, A.; Pieters, R.J.; Nilsson, U.J.; Loimaranta, V.; Finne, J.; Haataja, S. Bacterial Adhesion of *Streptococcus suis* to Host Cells and Its Inhibition by Carbohydrate Ligands. *Biology* **2013**, *2*, 918–935. [CrossRef]
12. Barnett, T.C.; Cole, J.N.; Rivera-Hernandez, T.; Henningham, A.; Paton, J.C.; Nizet, V.; Walker, M.J. Streptococcal toxins: Role in pathogenesis and disease. *Cell. Microbiol.* **2015**, *17*, 1721–1741. [CrossRef] [PubMed]
13. Hynes, W.; Sloan, M. Secreted Extracellular Virulence Factors. In *Streptococcus pyogenes: Basic Biology to Clinical Manifestations*; Ferretti, J.J., Stevens, D.L., Fischetti, V.A., Eds.; University of Oklahoma Health Sciences Center: Oklahoma City, OK, USA, 2016.
14. Cunningham, M.W. Pathogenesis of Group A Streptococcal Infections. *Clin. Microbiol. Rev.* **2000**, *13*, 470–511. [CrossRef] [PubMed]
15. Głowacka, P.; Żakowska, D.; Naylor, K.; Niemcewicz, M.; Bielawska-Drózd, A. *Brucella*-Virulence Factors, Pathogenesis and Treatment. *Pol. J. Microbiol.* **2018**, *67*, 151–161. [CrossRef]
16. Celli, J.; de Chastellier, C.; Franchini, D.M.; Pizarro-Cerda, J.; Moreno, E.; Gorvel, J.P. *Brucella* evades macrophage killing via VirB-dependent sustained interactions with the endoplasmic reticulum. *J. Exp. Med.* **2003**, *198*, 545–556. [CrossRef]
17. Pizarro-Cerdá, J.; Méresse, S.; Parton, R.G.; van der Goot, G.; Sola-Landa, A.; Lopez-Goñi, I.; Moreno, E.; Gorvel, J.P. *Brucella abortus* transits through the autophagic pathway and replicates in the endoplasmic reticulum of nonprofessional phagocytes. *Infect. Immun.* **1998**, *66*, 5711–5724. [CrossRef] [PubMed]
18. World Health Organization. *Brucellosis in Humans and Animals*; WHO Press: Geneva, Switzerlad, 2006.
19. EFSA. Scientific Opinion on the pathogenicity assessment of Shiga toxin-producing *Escherichia coli* (STEC) and the public health risk posed by contamination of food with STEC. *EFSA J.* **2020**, *18*, 105.
20. Colello, R.; Cáceres, M.E.; Ruiz, M.J.; Sanz, M.; Etcheverría, A.I.; Padola, N.L. From Farm to Table: Follow-Up of Shiga Toxin-Producing *Escherichia coli* Throughout the Pork Production Chain in Argentina. *Front. Microbiol.* **2016**, *7*, 93. [CrossRef]
21. Vallejo, P.; Cilla, G.; López-Olaizola, M.; Vicente, D.; Marimón, J.M. Epidemiology and Clinical Features of Listeriosis in Gipuzkoa, Spain, 2010–2020. *Front. Microbiol.* **2022**, *13*, 894334. [CrossRef]
22. Schoder, D.; Guldimann, C.; Martlbauer, E. Asymptomatic Carriage of *Listeria monocytogenes* by Animals and Humans and Its Impact on the Food Chain. *Foods* **2022**, *11*, 3472. [CrossRef]
23. Bonardi, S. *Salmonella* in the pork production chain and its impact on human health in the European Union. *Epidemiol. Infect.* **2017**, *145*, 1513–1526. [CrossRef]
24. Werinder, A.; Aspan, A.; Backhans, A.; Sjolund, M.; Guss, B.; Jacobson, M. *Streptococcus suis* in Swedish grower pigs: Occurrence, serotypes, and antimicrobial susceptibility. *Acta. Vet. Scand.* **2020**, *62*, 36. [CrossRef]
25. Algammal, A.M.; Hetta, H.F.; Elkelish, A.; Alkhalifah, D.H.H.; Hozzein, W.N.; Batiha, G.E.; El Nahhas, N.; Mabrok, M.A. Methicillin-Resistant *Staphylococcus aureus* (MRSA): One Health Perspective Approach to the Bacterium Epidemiology, Virulence Factors, Antibiotic-Resistance, and Zoonotic Impact. *Infect. Drug. Resist.* **2020**, *13*, 3255–3265. [CrossRef] [PubMed]
26. Shaikh, S.; Fatima, J.; Shakil, S.; Rizvi, S.M.; Kamal, M.A. Antibiotic resistance and extended spectrum beta-lactamases: Types, epidemiology and treatment. *Saudi J. Biol. Sci.* **2015**, *22*, 90–101. [CrossRef]
27. Mancuso, G.; Midiri, A.; Gerace, E.; Biondo, C. Bacterial Antibiotic Resistance: The Most Critical Pathogens. *Pathogens* **2021**, *10*, 1310. [CrossRef]
28. Shome, R.; Kalleshamurthy, T.; Natesan, K.; Jayaprakash, K.R.; Byrareddy, K.; Mohandoss, N.; Sahay, S.; Shome, B.R.; Hiremath, J.; Rahman, H. Serological and molecular analysis for brucellosis in selected swine herds from Southern India. *J. Infect. Public. Health.* **2019**, *12*, 247–251. [CrossRef]
29. Gogoi, S.; Hussain, P.; Sarma, P.C.; Barua, A.; Mahato, G.; Bora, D.; Konch, P.; Gogoi, P. Prevalence of bovine brucellosis in Assam, India. *J. Entomol. Zool. Stud.* **2017**, *5*, 179–185.
30. Kalleshamurthy, T.; Yaranna, C.; Shekar, R.; Natesan, K.; Sahay, S.; Shome, B.R.; Rahman, H.; Barbuddhe, S.B.; Barman, N.N.; Das, S.K.; et al. Fluorescence polarization assay: Diagnostic evaluation for porcine brucellosis. *J. Microbiol. Methods* **2019**, *156*, 46–51. [CrossRef] [PubMed]
31. Jindal, P.; Singh, B.B.; Kaur, P.; Gill, J.P.S. Sero-prevalence and molecular detection of *Brucella* species in slaughter pigs (*Sus Scrofa*) of Punjab, India. *J. Anim. Res.* **2017**, *7*, 495–499. [CrossRef]
32. Kaur, A.; Mahajan, V.; Singh, N.; Filia, G.; Banga, H.; Leishangthem, G.; Singh, A. Patho-epidemiological and molecular diagnosis of swine brucellosis in Punjab. *Indian J. Anim. Res.* **2020**, *54*, 90–95. [CrossRef]
33. Kavya, B.; Veeregowda, B.; Kamran, A.; Gomes, A.; Triveni, K.; Padmashree, B.; Shome, R. Comparative evaluation of blood based lateral flow assay for diagnosis of brucellosis in livestock species. *Indian J. Anim. Sci.* **2017**, *87*, 1068–1070.
34. Tadepalli, M.; Rajendra, L.; Bhavesh, T.; Thiagarajan, D.; Srinivasan, V.A. Development and comparative evaluation of a competitive ELISA with rose bengal test and a commercial indirect ELISA for serological diagnosis of brucellosis. *Indian J. Microbiol.* **2011**, *51*, 528–530.
35. Shakuntala, I.; Ghatak, S.; Sanjukta, R.; Sen, A.; Das, S.; Puro, A.; Dutta, A.; Kakoty, K. Incidence of brucellosis in livestock in North-Eastern India. *Int. J. Infect. Dis.* **2016**, *45*, 474. [CrossRef]

36. Shakuntala, I.; Ghatak, S.; Das, S.; Milton, A.P.; Sanjukta, R.; Puro, K.-U.; Dutta, A.; Kakoty, K.; Karam, A.; Lalgruaipuii, L.; et al. Seroepidemiological survey of brucellosis and isolation of *Brucella suis* from swine herds of Meghalaya, North-East India. *Indian J. Anim. Sci.* **2020**, *90*, 12–16. [CrossRef]
37. Shome, R.; Triveni, K.; Shankaranarayana, P.B.; Sahay, S.; Rao, N.; Shome, B.R.; Misri, J.; Rahman, H. Record of porcine brucellosis in India by indigenously developed indirect ELISA. *Asian Pac. J. Trop. Dis.* **2016**, *6*, 892–894. [CrossRef]
38. Fahrion, A.S.; Jamir, L.; Richa, K.; Begum, S.; Rutsa, V.; Ao, S.; Padmakumar, V.P.; Deka, R.P.; Grace, D. Food-safety hazards in the pork chain in Nagaland, North East India: Implications for human health. *Int. J. Environ. Res. Public Health* **2014**, *11*, 403–417. [CrossRef]
39. Yadav, J.P.; Das, S.C.; Dhaka, P.; Mukhopadhyay, A.K.; Chowdhury, G.; Naskar, S.; Malik, S.S. Pulsed-field gel electrophoresis of enterotoxic *Clostridium perfringens* type A isolates recovered from humans and animals in Kolkata, India. *Int. J. Vet. Sci. Med.* **2018**, *6*, 123–126. [CrossRef]
40. Das, B.; Sharma, R.; Borah, P.; Das, S.; Barkalita, L.; Devi, R.M.; Baishya, B. Molecular characterization and toxin-typing of *Clostridium difficile* isolates of dogs and pigs from Assam and Mizoram of North East India. *Curr. Sci.* **2017**, *113*, 1099–1106. [CrossRef]
41. Hazarika, R.; Sarmah, H.; Doley, M.K.; Saikia, D.P.; Hazarika, G.; Barkalita, L.M.; Deka, P.; Manoharan, S.; Sharma, R.K. *Clostridioides difficile* in food and food products of animal origin in Assam, India. *Anaerobe* **2023**, *81*, 102723. [CrossRef] [PubMed]
42. Yadav, J.P.; Das, S.C.; Dhaka, P.; Vijay, D.; Kumar, M.; Mukhopadhyay, A.K.; Chowdhury, G.; Chauhan, P.; Singh, R.; Dhama, K. Molecular characterization and antimicrobial resistance profile of *Clostridium perfringens* type A isolates from humans, animals, fish and their environment. *Anaerobe* **2017**, *47*, 120–124. [CrossRef]
43. Hussain, I.; Borah, P.; Sharma, R.; Rajkhowa, S.; Rupnik, M.; Saikia, D.; Hasin, D.; Hussain, I.; Deka, N.; Barkalita, L. Molecular characteristics of *Clostridium difficile* isolates from human and animals in the North Eastern region of India. *Mol. Cell. Probes.* **2016**, *30*, 306–311. [CrossRef]
44. Hussain, M.I.; Borah, P.; Hussain, I.; Sharma, R.K.; Kalita, M.C. Densitometric analysis of rep-PCR data: Insight into genetic variability and transmission of *Clostridium perfringens* typed with an improved multiplex PCR. *Anaerobe* **2021**, *70*, 102383. [CrossRef] [PubMed]
45. Hussain, M.I.; Borah, P.; Hussain, I.; Sharma, R.K.; Kalita, M.C. Necrotic enteritis by beta2toxin-producing *Clostridium perfringens* in doom pigs of assam, India. *Int. J. Curr. Microbiol. Appl. Sci.* **2017**, *6*, 1872–1876. [CrossRef]
46. Kataria, J.; Dutta, T.; Roychoudhury, P.; Tiwari, J. Detection and molecular characterization of Shiga toxin producing *Escherichia coli* (STEC) autoagglutinating adhesion gene (saa) from piglets in Mizoram. *Vet. World* **2014**, *7*, 373–376. [CrossRef]
47. Kylla, H.; Dutta, T.K.; Roychoudhury, P.; Subudhi, P.K. Coinfection of diarrheagenic bacterial and viral pathogens in piglets of Northeast region of India. *Vet. World* **2019**, *12*, 224. [CrossRef]
48. Regon, M.; Pathak, D.; Tamuli, S.; Baruah, G. Serotyping of *Escherichia coli* isolated from piglet diarrhea. *Vet. World* **2014**, *7*, 614–616. [CrossRef]
49. Tamta, S.; Kumar, O.R.V.; Singh, S.V.; Pruthvishree, B.S.; Karthikeyan, R.; Rupner, R.; Sinha, D.K.; Singh, B.R. Antimicrobial resistance pattern of extended-spectrum β-lactamase-producing *Escherichia coli* isolated from fecal samples of piglets and pig farm workers of selected organized farms of India. *Vet. World* **2020**, *13*, 360. [CrossRef]
50. Lalruatdiki, A.; Dutta, T.; Roychoudhury, P.; Subudhi, P. Extended-spectrum β-lactamases producing multidrug resistance *Escherichia coli*, *Salmonella* and *Klebsiella pneumoniae* in pig population of Assam and Meghalaya, India. *Vet. World* **2018**, *11*, 868. [CrossRef]
51. Kumar, S.; Gali, J.M.; Dutta, T.; Roychoudhury, P.; Subudhi, P. Development of isothermal lamp assay for detection of intimin gene (*Eae*) in *E. coli* associated with piglet diarrhea. *Indian J. Anim. Res.* **2021**, *55*, 956–959. [CrossRef]
52. Debbarma, S.; Bora, D.P.; Hazarika, R.A.; Tamuly, S.; Barua, A.G.; Das, P.; Goswami, C.; Jerry, R.J.; Sinha, S.J.I.J.o.A.R. Molecular characterization of *Escherichia coli* isolates from food animals. *Indian J. Anim. Res.* **2020**, *54*, 985–993. [CrossRef]
53. Begum, J.; Dutta, T.; Chandra, R.; Choudhary, P.R.; Varte, Z.; Bitew, M. Molecular and phenotypic characterization of shigatoxigenic *Escherichia coli* (STEC) and enteropathogenic *E. coli* (EPEC) from piglets and infants associated with diarrhoea in Mizoram, India. *Afr. J. Biotechnol.* **2014**, *13*, 1452–1461.
54. Tamta, S.; OR, V.K.; Pruthvishree, B.; Karthikeyan, R.; Rupner, R.N.; Chethan, G.; Dubal, Z.; Sinha, D.; Singh, B.R. Faecal carriage of extended spectrum beta-lactamase (ESBL) and New Delhi metallo beta-lactamase (NDM) producing *Escherichia coli* between piglets and pig farmworkers. *Comp. Immunol. Microbiol. Infect. Dis.* **2020**, *73*, 101564. [CrossRef] [PubMed]
55. Nirupama, K.; OR, V.K.; Pruthvishree, B.; Sinha, D.; Murugan, M.S.; Krishnaswamy, N.; Singh, B. Molecular characterisation of blaOXA-48 carbapenemase-, extended-spectrum β-lactamase-and Shiga toxin-producing *Escherichia coli* isolated from farm piglets in India. *J. Glob. Antimicrob. Resist.* **2018**, *13*, 201–205. [CrossRef]
56. Samanta, I.; Joardar, S.N.; Mahanti, A.; Bandyopadhyay, S.; Sar, T.K.; Dutta, T.K. Approaches to characterize extended spectrum beta-lactamase/beta-lactamase producing *Escherichia coli* in healthy organized vis-a-vis backyard farmed pigs in India. *Infect. Genet. Evol.* **2015**, *36*, 224–230. [CrossRef] [PubMed]
57. Puii, L.; Dutta, T.; Roychoudhury, P.; Kylla, H.; Chakraborty, S.; Mandakini, R.; Kawlni, L.; Samanta, I.; Bandopaddhay, S.; Singh, S. Extended spectrum beta-lactamase producing Shiga-toxin producing-*Escherichia coli* in piglets, humans and water sources in North East region of India. *Lett. Appl. Microbiol.* **2019**, *69*, 373–378. [CrossRef]

58. Rajkhowa, S.; Sarma, D.K. Prevalence and antimicrobial resistance of porcine O157 and non-O157 Shiga toxin-producing *Escherichia coli* from India. *Trop. Anim. Health. Prod.* **2014**, *46*, 931–937. [CrossRef]
59. Mandakini, R.; Dutta, T.K.; Chingtham, S.; Roychoudhury, P.; Samanta, I.; Joardar, S.N.; Pachauau, A.R.; Chandra, R. ESBL-producing Shiga-toxigenic *E. coli* (STEC) associated with piglet diarrhoea in India. *Trop. Anim. Health Prod.* **2015**, *47*, 377–381. [CrossRef]
60. Kumar, V.O.; Singh, B.; Sinha, D.; Pruthvishree, B.; Tamta, S.; Dubal, Z.; Karthikeyan, R.; Rupner, R.N.; Malik, Y. Risk factor analysis, antimicrobial resistance and pathotyping of *Escherichia coli* associated with pre-and post-weaning piglet diarrhoea in organised farms, India. *Epidemiol. Infect.* **2019**, *147*, e174.
61. Kylla, H.; Dutta, T.K.; Roychoudhury, P.; Subudhi, P.K.; Tolenkhomba, T.; Mandakini, R.; Kawlni, L. Antimicrobial Drug Resistance of *Escherichia coli* Isolated from Piglets in North East India. *Curr. J. Appl. Sci. Technol.* **2020**, *39*, 195–205. [CrossRef]
62. Mandakini, R.; Roychoudhury, P.; Subudhi, P.; Kylla, H.; Samanta, I.; Bandyopadhayay, S.; Dutta, T. Higher prevalence of multidrug-resistant extended-spectrum β-lactamases producing *Escherichia coli* in unorganized pig farms compared to organized pig farms in Mizoram, India. *Vet. World* **2020**, *13*, 2752. [CrossRef]
63. Raorane, A.V.; Doijad, S.P.; Poharkar, K.V.; Pathak, A.; Bhosle, S.; Barbuddhe, S. Isolation and genotypic characterization of *Listera monocytogenes* from pork and pork products. *Int. J. Curr. Microbiol. App. Sci.* **2015**, *4*, 788–798.
64. Suryawanshi, R.D.; Malik, S.V.S.; Jayarao, B.; Chaudhari, S.P.; Savage, E.; Vergis, J.; Kurkure, N.V.; Barbuddhe, S.B.; Rawool, D.B. Comparative diagnostic efficacy of recombinant LLO and PI-PLC-based ELISAs for detection of listeriosis in animals. *J. Microbiol. Methods* **2017**, *137*, 40–45. [CrossRef]
65. Vaidya, G.; Chaudhary, S.; Zade, N.; Khan, W.; Shinde, S.; Patil, A.; Kalambhe, D.J.I.J.o.C.M.; Sciences, A. Prevalence, virulence and antibiotic susceptibility of *Listeria monocytogenes* recuperated from slaughtered goats and pigs of Nagpur, Central India. *Int. J. Curr. Microbiol. App. Sci.* **2018**, *7*, 1566–1578. [CrossRef]
66. Sarangi, L.N.; Panda, H. Isolation, characterization and antibiotic sensitivity test of pathogenic *Listeria* species in livestock, poultry and farm environment of Odisha. *Indian J. Anim. Res.* **2012**, *46*, 242–247.
67. Raorane, A.; Doijad, S.; Katkar, S.; Pathak, A.; Poharkar, K.; Dubal, Z.; Barbuddhe, S. Prevalence of *Listeria* spp. in animals and associated environment. *Adv. Anim. Vet. Sci.* **2014**, *2*, 81–85. [CrossRef]
68. Sharma, I.; Bist, B. Antibiotic Sensitivity of *Salmonella* Isolated from Retail Raw Meats of Goat, Pig and Poultry. *Indian Vet. J.* **2013**, *90*, 42–43.
69. Kumar, P.; Rao, J.; Haribabu, Y. Microbiological quality of meat collected from municipal slaughter houses and retail meat shops from Hyderabad Karnataka region, India. *APCBEE Procedia* **2014**, *8*, 364–369. [CrossRef]
70. Kumar, T.; Rajora, V.; Arora, N. Prevalence of *Salmonella* in pigs and broilers in the Tarai region of Uttarakhand, India. *Indian J. Med. Microbiol.* **2014**, *32*, 99. [CrossRef]
71. Chaudhary, J.; Nayak, J.; Brahmbhatt, M.; Makwana, P. Virulence genes detection of *Salmonella* serovars isolated from pork and slaughterhouse environment in Ahmedabad, Gujarat. *Vet. World* **2015**, *8*, 121. [CrossRef] [PubMed]
72. Kylla, H.; Dutta, T.K.; Roychoudhury, P.; Mandakini, R.; Subudhi, P.K. *Salmonella daarle* and *Salmonella hiduddify* associated with acute gastroenteritis in piglets in India. *Microbes Health* **2016**, *5*, 1–3. [CrossRef]
73. Chaudhary, J.; Nayak, J.; Brahmbha, M.; Parmar, B. Antibiogram of *Salmonella* Species isolated from pork and slaughter house environment in Ahmedabad, Gujarat. *Life Sci. Leafl.* **2016**, *71*, 117–124.
74. Kalambhe, D.; Zade, N.; Chaudhari, S.; Shinde, S.; Khan, W.; Patil, A. Isolation, antibiogram and pathogenicity of *Salmonella* spp. recovered from slaughtered food animals in Nagpur region of Central India. *Vet. World* **2016**, *9*, 176. [CrossRef] [PubMed]
75. Latha, C.; Anu, C.; Ajaykumar, V.; Sunil, B. Prevalence of *Listeria monocytogenes*, *Yersinia enterocolitica*, *Staphylococcus aureus* and *Salmonella enterica Typhimurium* in meat and meat products using multiplex polymerase chain reaction. *Vet. World* **2017**, *10*, 927. [CrossRef]
76. Das, M.; Motina, E.; Deka, D.; Dutta, T.; Singh, N.; Das, P.; Ghosh, S. Studies on incidence and antibiogram of *Salmonella* serovars isolated from raw pork in Aizawl and Imphal, India. *Explor. Anim. Med. Res.* **2018**, *8*, 40–44.
77. Chakraborty, S.; Roychoudhury, P.; Samanta, I.; Subudhi, P.; Das, M.; De, A.; Bandyopadhayay, S.; Joardar, S.; Mandal, M.; Qureshi, A. Molecular detection of biofilm, virulence and antimicrobial resistance associated genes of *Salmonella* serovars isolated from pig and chicken of Mizoram, India. *Indian J. Anim. Res.* **2020**, *54*, 608–613. [CrossRef]
78. Mahindroo, J.; Thanh, D.P.; Nguyen, T.N.T.; Mohan, B.; Thakur, S.; Baker, S.; Taneja, N. Endemic fluoroquinolone-resistant *Salmonella enterica* serovar Kentucky ST198 in northern India. *Microb. Genom.* **2019**, *5*, e000275. [CrossRef]
79. Kylla, H.; Dutta, T.; Roychoudhury, P.; Subudhi, P.; Lalsiamthara, J. Prevalence and molecular characterization of *Salmonella* species associated with piglet diarrhea in North East India. *Pol. J. Vet. Sci.* **2019**, *22*, 793–797. [CrossRef]
80. Borah, P.; Dutta, R.; Das, L.; Hazarika, G.; Choudhury, M.; Deka, N.K.; Malakar, D.; Hussain, M.I.; Barkalita, L.M. Prevalence, antimicrobial resistance and virulence genes of *Salmonella* serovars isolated from humans and animals. *Vet. Res. Commun.* **2022**, *46*, 799–810. [CrossRef]
81. Zehra, A.; Singh, R.; Kaur, S.; Gill, J. Molecular characterization of antibiotic-resistant *Staphylococcus aureus* from livestock (bovine and swine). *Vet. World* **2017**, *10*, 598. [CrossRef]
82. Rajkhowa, S.; Sarma, D.; Pegu, S. SCC *mec* typing and antimicrobial resistance of methicillin-resistant *Staphylococcus aureus* (MRSA) from pigs of Northeast India. *Vet. Res. Commun.* **2016**, *40*, 117–122. [CrossRef]

83. Yaiphathoi, S.; Sharma, I. Characterization and Phylogenetic Reconstruction of *MecA* and *Pvl* Genes of Methicillin Resistant *Staphylococcus aureus* from Retail Meats in North East India. *Indian J. Nat. Sci.* **2020**, *10*, 27661–27670.
84. Kalai, S.; Roychoudhury, P.; Dutta, T.; Subudhi, P.; Chakraborty, S.; Barman, N.; Sen, A. Multidrug resistant staphylococci isolated from pigs with exudative epidermitis in North eastern Region of India. *Lett. Appl. Microbiol.* **2021**, *72*, 535–541. [CrossRef]
85. Zehra, A.; Gulzar, M.; Singh, R.; Kaur, S.; Gill, J. Prevalence, multidrug resistance and molecular typing of methicillin-resistant *Staphylococcus aureus* (MRSA) in retail meat from Punjab, India. *J. Glob. Antimicrob. Reseist.* **2019**, *16*, 152–158. [CrossRef] [PubMed]
86. Yaiphathoi, S.; Sharma, I. Spa typing and prevalence of methicillin-resistant *Staphylococcus aureus* isolated in retail meats from silchar, assam, india. *Adv. Anim. Vet. Sci.* **2019**, *7*, 694–700. [CrossRef]
87. Savariraj, W.R.; Ravindran, N.B.; Kannan, P.; Paramasivam, R.; Senthilkumar, T.; Kumarasamy, P.; Rao, V.A. Prevalence, antimicrobial susceptibility and virulence genes of *Staphylococcus aureus* isolated from pork meat in retail outlets in India. *J. Food Saf.* **2019**, *39*, e12589. [CrossRef]
88. Baruah, M.S.; Phukan, A.; Sharma, R.K.; Dutta, B.; Hazarika, R.A. Clinico-Histopathological Study of Exudative Epidermitis Caused by *S. hyicus* in Swine. *Indian J. Hill Farming* **2017**, *30*, 35–40.
89. Devi, M.; Dutta, J.B.; Rajkhowa, S.; Kalita, D.; Saikia, G.K.; Das, B.C.; Hazarika, R.A.; Mahato, G. Prevalence of multiple drug resistant *Streptococcus suis* in and around Guwahati, India. *Vet. World* **2017**, *10*, 556. [CrossRef] [PubMed]
90. Anand, P.; Kumar, R.; Anoopraj, R.; Saikumar, G. *Streptococcus suis* infection in slaughtered pigs and its association with pathological lesions in the lungs, brain and tonsils. *Indian J. Vet. Pathol.* **2016**, *40*, 133–138.
91. Dinesh, M.; Thakor, J.; Vishwa, K.; Pathak, M.; Patel, S.K.; Kumar, P.; Qureshi, S.; Singh, K.; Sahoo, M. Pathology and diagnosis of *Streptococcus suis* infections in pre-weaned piglets. *Indian J. Vet. Pathol.* **2020**, *44*, 144–153. [CrossRef]
92. Dinesh, M.; Thakor, J.C.; Singh, K.P.; Singh, R.; Anbazhagan, S.; Chauhan, R.; Qureshi, S.; Sahoo, N.R.; Sahoo, M. Patho-epidemiological study of *Streptococcus suis* infections in slaughtered pigs from North and North-Eastern Region, India. *Indian J. Vet. Pathol.* **2022**, *46*, 26–32. [CrossRef]
93. Pegu, S.; Rajkhowa, S.; Choudhury, M.; Neher, S.; Yadav, A.; Barman, K.; Das, P.; Banik, S.; Deb, R.; Kumar, S. Prevalence, pathology, molecular detection and characterization of *Streptococcus suis* associated with various disease conditions in pigs in Assam. *Vet. Pract.* **2020**, *21*, 294–299.
94. Sonowal, S.; Barua, A.; Hazarika, R.; Rajkhowa, S.; Barua, C.; Bhattacharya, D. Detection of glutamate dehydrogenase gene (*gdh*) in *Streptococcus suis* isolated from pigs. *Indian J. Anim. Sci.* **2014**, *84*, 287–288.
95. Rajkhowa, S.; Rajesh, J. Virulence associated gene profiling and antimicrobial resistance pattern of *Streptococcus suis* isolated from clinically healthy pigs from North East India. *Lett. Appl. Microbiol.* **2021**, *73*, 392–397. [CrossRef] [PubMed]
96. Rajkhowa, S.; Sarma, D.; Pegu, S. Virulence markers and antimicrobial resistance of *Streptococcus suis* isolated from diseased pigs. *Indian J. Anim. Sci.* **2017**, *87*, 581–583. [CrossRef]
97. Devi, M.; Dutta, J.B.; Rajkhowa, S.; Saikia, G.; Begum, S. Molecular confirmation and detection of virulence genes of *Streptococcus suis* from Pigs in Assam. *Int. J. Chem. Stud.* **2017**, *5*, 976–980.
98. Vishva, K.; Gangwar, P.; Chaturji Thakor, J.; Dinesh, M.; Sahoo, M.; Singh, R.; Mahajan, S.; Qureshi, S.; Laddika, L.; Ranjan Sahoo, N. Carrier status of *Streptococcus suis* in the palatine tonsils of apparently healthy slaughtered pigs of India. *J. Immunoass. Immunochem.* **2022**, *43*, 557–578.
99. Rajkhowa, S.; Neher, S.; Pegu, S.; Sarma, D. Bacterial diseases of pigs in India: A review. *Indian J. Comp. Microbiol. Immunol. Infect. Dis.* **2018**, *39*, 29–37. [CrossRef]