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Mini review

One Health surveillance of certain zoonotic bacterial pathogens in South Asia: current status, challenges, and future directions

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Abstract

Zoonotic bacterial pathogens impose a substantial and unevenly documented burden on public health, animal health, and food safety. South Asia is home to roughly a quarter of the world's people, and one of the densest livestock populations on earth, yet the epidemiology, antimicrobial resistance, and genomic diversity of its zoonotic bacteria remain poorly characterized. This mini-review synthesizes published evidence from 2000 to 2026 on six pathogen groups of regional priority: *Brucella* spp., *Listeria* spp., *Klebsiella pneumoniae*, *Leptospira* spp., *Bacillus anthracis*, and *Salmonella* spp., with *Campylobacter* spp. considered alongside *Salmonella* across Pakistan, India, Bangladesh, Nepal, and Sri Lanka. Evidence is distributed unevenly across these five countries. Brucellosis seroprevalence ranges from 2.0–18.75% in Pakistani livestock, 15% in Nepalese sheep, and 8.4% among Sri Lankan adults. Human leptospirosis in Sri Lanka is estimated at 300.6 per 100,000 population, with a 7.0% case fatality rate. In Bangladesh, 26 cutaneous anthrax outbreaks produced 1,210 suspected human cases between 2013 and 2016. Resistance is severe where measured: 73.5% of *Klebsiella pneumoniae* isolates from a referral hospital in Kathmandu, Nepal, were multidrug-resistant (MDR), and 97.1% of *Campylobacter* isolates from Bangladeshi chicken farms met MDR criteria. Sequencing capacity exists in the region and has been applied to typhoidal *Salmonella* in Bangladesh and Nepal, to *Brucella melitensis* and *Listeria monocytogenes* in India, to *Leptospira* in Sri Lanka, and to clinical *Klebsiella* collections. However, every such study is a discrete research output; no country operates whole-genome sequencing-based surveillance spanning the human, animal, food, and environmental sectors for the pathogens reviewed here. The gap is therefore one of integration and governance rather than of technology alone. A staged, costed roadmap is proposed, with priority actions, responsible institutions, and indicative timelines, drawing on models from other low- and middle-income regions where genomic surveillance has been established under comparable constraints.

Keywords: Antimicrobial resistance, Genomic surveillance, One Health, South Asia, Whole-genome sequencing, Zoonotic bacterial pathogens

Introduction

One Health treats human, animal, and environmental health as a single, interdependent system. The framework has gained traction over the past two decades as successive outbreaks have exposed the limits of surveillance organized along sectoral lines [1, 2]. About 75% of emerging pathogens and 60% of all known human pathogens originate in animals [3]. Bacterial zoonoses are particularly notable because they are host-adapted, can acquire and spread antimicrobial resistance (AMR), and directly affect livestock productivity.

This review covers Pakistan, India, Bangladesh, Nepal, and Sri Lanka, which together are home to nearly two billion people and some of the highest reported rates of human–livestock contact. Rural livelihoods and food security in the region are supported by cattle, buffaloes, sheep, goats, and poultry [4]. Farm conditions essential to livestock livelihoods also facilitate pathogen movement: livestock are kept in close proximity, veterinary and diagnostic services are inadequate, and antimicrobial use is often unsupervised. Pathogens known to be present at high rates in the region include *Brucella* (B.) spp., *Listeria* spp., *Klebsiella* (*K.*) *pneumoniae, Leptospira* spp., *Bacillus anthracis*, and *Salmonella* spp. [5].

Pathogen selection for this review was based on three criteria: documented zoonotic or One Health relevance in South Asia, primary data available in at least two of the five countries, and presence in the WHO priority lists for AMR. *Campylobacter* spp. are included with *Salmonella* spp. due to their common reservoirs in poultry and the support infrastructure for surveillance. There are several agents of undoubted regional importance that are not included here. For example, *Coxiella burnetii* is a widespread pathogen with a pooled human seroprevalence of 9.2% and a pooled herd-level seroprevalence of 77.3% in ruminants across 112 studies [6], and is an obligate intracellular pathogen with a distinct laboratory pathway for diagnosis, culture, and sequencing that differs from those of the diseases discussed here. Members of the *Mycobacterium* (*M.*) *tuberculosis* complex, such as *M. bovis* and *M. orygis*, also warrant special attention. *M. orygis* has been genomically characterized in Indian wild ungulates [7]. Bovine tuberculosis control is not part of general zoonotic disease surveillance but rather of the national tuberculosis program. The exclusions do not imply that the excluded topics are unimportant; they are simply not the focus of a mini-review.

Zoonoses are among the most significant regional public health challenges, but information on their prevalence, molecular epidemiology, and genomic diversity remains incomplete. Most published work relies on serological or single-locus molecular methods, which resolve neither transmission pathways nor the genetic basis of resistance [8]. Whole-genome sequencing (WGS) has reorganized infectious disease surveillance in settings where it has been adopted at scale, supporting outbreak reconstruction, source attribution, and characterization of resistance and virulence determinants [9, 10].

South Asia's position is more nuanced than a simple absence of sequencing capacity. Genomic methods have been applied in the region to typhoidal *Salmonella, B. melitensis* in India, *Leptospira* in Sri Lanka, *Mycobacterium orygis* in wildlife, Nipah virus, and individual collections of clinical *K. pneumoniae* [7, 11, 12, 13, 14, 15]. What has not been established is the prospective, joint application of sequencing across human, animal, food, and environmental sectors for the zoonotic bacteria reviewed here. This review therefore does not rest on the proposition that sequencing is unavailable. Its contributions are threefold: it assembles country-resolved prevalence and resistance evidence for five countries and identifies where that evidence is absent; it examines how uninterpretable resistance phenotypes have entered the regional literature and distorted the picture of the AMR burden; and it converts general calls for capacity building into a staged roadmap with named actors, sequencing entry points, and indicative costs.

Pakistan exemplifies the broader pattern. The country supports more than 240 million people and more than 200 million livestock heads, and the livestock sector accounts for a substantial share of agricultural value added [16]. Despite that scale, published genomic work on zoonotic bacteria is limited to clinical isolates, and no integrated surveillance system links veterinary and human health data [17, 18]. Similar constraints apply across the region, where research on zoonotic bacterial pathogens remains sparse, unevenly funded, and institutionally fragmented [19, 20].

Literature search strategy

This article is a narrative mini-review. It does not follow the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) statement, was not conducted under a registered protocol, and does not report stage-by-stage record counts or formal risk-of-bias scoring. The search strategy is described here so readers can assess the basis of the evidence presented and reproduce the searches if they wish.

PubMed, Web of Science, and Google Scholar were searched for material published between January 2000 and June 2026. Search terms combined pathogen names (*Brucella*, *Listeria*, *Klebsiella pneumoniae*, *Leptospira*, *Bacillus anthracis*, *Salmonella*, *Campylobacter*) with the terms "zoonotic", "One Health", "antimicrobial resistance", "whole genome sequencing", "surveillance", and the names of the five countries, using Boolean operators. Reference lists of retrieved articles were screened for additional sources.

Peer-reviewed English-language articles reporting primary data on prevalence, molecular characterization, AMR, or genomic surveillance in Pakistan, India, Bangladesh, Nepal, or Sri Lanka were prioritized. Systematic reviews and meta-analyses were used when they provided pooled regional estimates. Studies from outside South Asia were cited only when they provided a methodological standard, a regulatory framework, or a comparator relevant to the regional discussion. In this context, they are identified as comparators. Material published as preprints, conference abstracts, theses, or non-peer-reviewed material was excluded. If the resistance phenotype cannot be determined based on existing clinical breakpoints, the limitation is indicated in conjunction with the figure, not as a figure.

The evidence presented is based on a purposive, not an exhaustive, selection of the literature and should therefore be understood as an informed synthesis rather than a complete enumeration of the literature. The consequences of this design for the conclusions drawn are outlined in the critical discussion and limitations section.

Zoonotic bacterial pathogens in South Asia

Brucella spp.

Brucellosis remains one of the most prevalent bacterial zoonoses worldwide and is endemic in cattle, buffaloes, sheep, and goats in South Asia [21]. *B. abortus* and *B. melitensis* are the most common brucellae to infect livestock, while *B. melitensis* is the most common species infecting humans, accounting for most cases of disease [22]. The negative impact on reproductive performance due to infection can be seen in abortion, stillbirth, and reduced fertility, and can be directly attributed to smallholder producers [23]. The clinical picture of human brucellosis is non-specific, with fever, malaise, arthralgia, and a delayed diagnosis, leading to a tendency toward empirical treatment [24].

The seroprevalence rates for livestock vary from 2 to 18.75%, and for occupationally exposed workers, it is 9.8% in Pakistan. In small ruminants, a cross-sectional study conducted in Punjab revealed 2.0% seropositivity and 9.8% in livestock workers [25]. A molecular survey of cattle in Khyber Pakhtunkhwa (KP) found a 3.1% positivity rate for *B. melitensis*, compared with 9% in humans [26]. A serological survey of the region reported 18.75% positivity in cattle, whereas indirect ELISA showed 8% positivity [27]. There is well-documented human brucellosis in India with a predilection for rural

areas and occupation groups exposed to livestock [28]. In some surveys, the prevalence among sheep and goats in Bangladesh was reported to exceed 20% [29].

There is less evidence, but the direction is clear from Nepal and Sri Lanka. In Rupandehi district of south-western Nepal, 15% of sheep and 1.1% of goats were seropositive by the Rose Bengal test, and 31.6% of farm-based flocks were seropositive, with sheep over 18 months of age and herds larger than 100 animals being the highest-risk groups [30]. A study of 1,294 healthy individuals from four provinces in Sri Lanka found a seropositivity rate of 8.4%, with farm-animal ownership and full-time livestock work independently correlated with seropositivity [31]. Table 1 summarizes prevalence estimates by country across the region.

Control faces obstacles that are as much logistical as technical. Live attenuated vaccines such as *B. abortus* S19 and *B. melitensis* Rev.1 are available but deployed inconsistently because of cost, cold-chain requirements, and limited producer awareness [32]. Characterization of circulating strains, which would allow vaccine and field strains to be distinguished and transmission to be traced, has been achieved in only one of the five countries. Whole-genome sequencing of 24 *B. melitensis* isolates from human and animal sources across India identified sequence type ST8 as predominant and resolved regional phylogenetic structure and virulence gene content [11]. No comparable work has been published from Pakistan, Bangladesh, Nepal, or Sri Lanka, where characterization remains serological or single-locus. Work in other endemic settings shows what such data yield: genotyping of *Brucella* isolates in Turkey and Egypt has resolved the lineage structure and transmission pathways between animal and human hosts, which is cited here as a methodological comparator rather than as regional evidence [33, 34].

Listeria spp.

Listeriosis is caused principally by *Listeria* (*L.*) *monocytogenes*, with the closely related *L. ivanovii* implicated mainly in disease in ruminants [35]. Invasive human listeriosis affects older adults, pregnant women, neonates and immunocompromised patients, and carries a case fatality rate of 20–30% [36]. In animals, the organism causes encephalitis, abortion, septicemia and subclinical carriage across livestock, companion animals and wildlife [37].

South Asian data derive overwhelmingly from food-safety investigations. Across sources sampled in Kashmir, India, L. monocytogenes was recovered at an overall rate of 6.34%, with the highest prevalence in ovine clinical cases (13.33%), followed by mutton (7.5%), chicken (5%), and raw milk (5%) [38]. Environmental sampling on Bangladeshi cattle farms recovered *Listeria* spp. from water, feed, raw milk, cow dung, and soil, confirming that the on-farm environment sustains the organism between production cycles [39]. Detection of the pathogen in bovine milk in Pakistan established its presence in the domestic dairy chain [40]. Prevalence figures for food and animal samples are compiled in Table 1.

Four features of the regional picture deserve specific comment. First, serotype and lineage structure are better resolved than is generally recognized. Serotypes 1/2a, 1/2b, and 4b account for the overwhelming majority of human disease globally, and in India, serotype 4b of sequence type 328 (ST328) has been recovered repeatedly from unrelated sources, locations, and time periods, indicating a disseminated and persistent clone rather than sporadic introductions [41]. Comparable serotyping has not been reported in Pakistan, Bangladesh, Nepal, or Sri Lanka, so it is unknown whether the same clone circulates region-wide.

Second, the regulatory framework governing *L. monocytogenes* in ready-to-eat foods is effectively absent from the regional literature. Comparative analyses of regulatory systems set out the risk-based European criteria, which permit up to 100 colony-forming units (cfu)/g at the end of shelf life for products that do not support growth and require absence in 25 g otherwise, alongside the zero-tolerance approach applied in the United States and the Codex framework [42]. These analyses do not extend to South Asia, and no harmonized regional criterion, verification program, or environmental monitoring requirement has been described for the five countries considered here.

Third, ambient conditions across much of South Asia place unusual strain on chilled distribution. *L. monocytogenes* grows at refrigeration temperatures, so the public health consequence of a cold-chain failure differs in kind from that for mesophilic pathogens: an interruption does not merely fail to prevent growth but selects for an organism that competitors cannot match at low temperature. Informal retail of milk, meat and dairy products without continuous refrigeration is widespread in the region, yet no published study has quantified *L. monocytogenes* growth along a South Asian distribution chain.

Fourth, clinical evidence is limited to isolated reports. Neonatal meningitis and sepsis attributable to *L. monocytogenes* have been reported from Indian centers, but no case series, sentinel hospital network, or laboratory-based surveillance system for human listeriosis operates in any of the five countries. Invasive listeriosis in the region is therefore likely to be recorded as culture-negative sepsis or undifferentiated febrile illness, and the regional incidence cannot be estimated from the available literature [43].

Genomic characterization of *Listeria* isolates has been undertaken in India, where sequencing from food, clinical,

Table 1: Country-resolved prevalence and reservoirs of zoonotic bacterial pathogens reviewed in South Asia.

Pathogen	Major species	Country	Population sampled	Reported prevalence	Reservoir	Source
Brucella spp.	*B. abortus*, *B. melitensis*	Pakistan	Small ruminants and livestock workers, Punjab	2.0% animals; 9.8% workers	Cattle, buffaloes, sheep, goats; unpasteurized dairy	[25]
		Pakistan	Cattle and humans, Khyber Pakhtunkhwa	3.1% cattle; 9% humans		[26]
		Pakistan	Cows and buffaloes	18.75% (RBPT); 8% (iELISA)		[27]
		India	Humans, occupational and rural	Endemic; systematic review		[28]
		Bangladesh	Sheep and goats	> 20% in some surveys		[29]
		Nepal	Sheep and goats, Rupandehi	15% sheep; 1.1% goats		[30]
		Sri Lanka	Healthy adults, four provinces (n = 1,294)	8.4%		[31]
Listeria spp.	*L. monocytogenes*, *L. ivanovii*	India	Foods of animal origin and ovines, Kashmir	6.34% overall; 13.33% ovine clinical; 7.5% mutton; 5% chicken; 5% raw milk	Raw milk, meat, dairy products; farm environment	[38]
		India	Multiple sources, national synthesis	Serotype 4b (ST328) recurrent across sources and years		[41]
		Bangladesh	Cattle farm environment	Detected in water, feed, raw milk, dung and soil		[39]
		Pakistan	Bovine milk, Hyderabad	Detected		[40]
		Nepal, Sri Lanka	—	No published data retrieved		—
Klebsiella pneumoniae	*K. pneumoniae* (ESKAPE)	Pakistan	Bovine milk, subclinical mastitis (n = 305)	11.8%	Human clinical; livestock, milk, food products	[56]
		Pakistan	Human clinical isolates	ESBL and carbapenemase genes characterized		[51]
		India	Human clinical isolates	Multidrug-resistant; genomically characterized		[53]
		Bangladesh	Human clinical, urinary tract infection	Pan-drug-resistant isolates recovered		[12]
		Nepal	Human clinical, Kathmandu	28.5% of culture-positive specimens		[55]
		Sri Lanka	—	No published data retrieved		—
Leptospira spp.	*L. interrogans*, *L. borgpetersenii*	Sri Lanka	National, human	300.6 per 100,000 total burden; 52.1 per 100,000 hospitalized; 7.0% case fatality	Rodents, livestock, contaminated water	[60]
		India	Human, outbreak settings	Recurrent outbreaks; endemic		[59]
		Region	Livestock	Limited data		[58]
Bacillus anthracis	*B. anthracis*	Bangladesh	Human, seven districts, 2013–2016	26 outbreaks; 1,210 suspected cutaneous cases; 20% attack rate	Livestock, wildlife, soil	[63]
		Region	Livestock and wildlife	Endemic; outbreaks reported		[61]
Salmonella spp.	*S. enterica* serovars	India	Poultry	Resistance figures in Table 2	Poultry, meat, eggs, contaminated food	[66]
		Region	Livestock and poultry	Resistance figures in Table 2		[67]
Campylobacter spp.	*C. jejuni*, *C. coli*	Bangladesh	Chicken farms (n = 84), Mymensingh and Gazipur	40.5% farm-level positivity	Poultry, livestock, contaminated water	[71]
		Pakistan, Nepal, Sri Lanka	—	No farm-level data retrieved		—

Entries marked "no published data retrieved" indicate that the search returned no primary study for that pathogen–country combination. “Region” indicates a finding reported for South Asia as a whole, or for more than one country, that cannot be attributed to a single national dataset. ESBL = extended-spectrum β-lactamase; iELISA = indirect enzyme-linked immunosorbent assay; n = number sampled; RBPT = Rose Bengal plate test; ST = sequence type.

environmental, and seafood sources established the persistent ST328 lineage described above [41], but not elsewhere in the region. Sustained sequencing-based *Listeria* surveillance in Germany, where systematic characterization of animal isolates has clarified transmission to humans, indicates what prospective application of the same methods can deliver, and is cited as a comparator [44]. *L. ivanovii* remains largely outside surveillance frameworks despite sharing virulence determinants with *L. monocytogenes* [45].

Klebsiella pneumoniae

Klebsiella pneumoniae is a Gram-negative member of the *Enterobacteriaceae* and one of the most consequential antimicrobial-resistant organisms worldwide [46]. It belongs to the ESKAPE group, responsible for a large share of hospital-acquired infections [47], and causes urinary tract infections, pneumonia, bacteremia, and pyogenic liver abscess in humans [48]. In animals, it is associated with bovine mastitis, neonatal septicemia in foals, and infections in companion species [49].

The classification of *K. pneumoniae* as a zoonotic pathogen requires qualification, and the term is not used here in the sense applied to *Brucella* or *Leptospira*. Direct animal-to-human transmission of *K. pneumoniae* has not been demonstrated conclusively. A One Health assessment of bovine mastitis-associated strains concluded that, while direct zoonotic transmission remains unproven, *Klebsiella* populations and their mobile genetic elements circulate among connected animal, human and environmental reservoirs, and hybrid IncFIB–IncFIIk plasmids carrying both resistance and virulence determinants have been recovered from cattle and from humans [50]. *K. pneumoniae* is included in this review on that basis: as a One Health pathogen whose resistance determinants move across the human–animal–environment interface through shared reservoirs and mobile elements, rather than as a classical zoonosis transmitted directly from animal hosts.

Resistance in the region is extensive. Extended-spectrum β-lactamase (ESBL) and carbapenemase genes have been characterized in clinical isolates from major Pakistani cities [51]. A study from Karachi reported multidrug resistance (MDR) in 90.2% of clinical isolates, with a strong association between resistance and virulence traits, including biofilm formation and efflux pump activity [52]. In Bangladesh, pan-drug-resistant (PDR) *K. pneumoniae* has been recovered from patients with urinary tract infection [12], and MDR clinical isolates from India have been characterized genomically [53]. A survey of *K. pneumoniae* across South and Southeast Asia identified a broad complement of virulence genes, along with high carriage of resistance genes [54]. Data from Nepal reinforce the pattern: among 49 isolates from a Kathmandu neurological referral center, 73.5% were MDR and 73.5% produced extended-spectrum β-lactamases, with $bla_{\text{NDM-1}}$ detected in 58.6% of carbapenem-resistant isolates [55]. Resistance figures are compiled in Table 2.

Non-clinical reservoirs have received far less attention, but the regional evidence base is no longer empty. Among 305 milk samples from six Pakistani dairy farms, *K. pneumoniae* was recovered from 11.8% of samples, with prevalence varying markedly by breed. Complete resistance to ampicillin and 80.5% resistance to amoxicillin were observed. The *blaTEM* gene was detected in 91.6% of isolates, while cefotaxime, meropenem, and ciprofloxacin retained activity [56]. No comparable study has examined food-chain or environmental *K. pneumoniae* in India, Bangladesh, Nepal or Sri Lanka, and no genomic comparison of animal, food and human isolates has been published from any of the five countries. Work outside the region indicates that resistance genes detected genotypically are not always expressed phenotypically, which argues for paired genomic and phenotypic characterization rather than either alone [57].

Leptospirosis

Leptospirosis is endemic across South Asia and concentrated in areas subject to heavy rainfall and flooding [58]. Human infection ranges from undifferentiated fever to severe pulmonary hemorrhage and renal failure, and outbreaks recur throughout the region [59]. The Sri Lankan situation is the most comprehensive in the entire South Asian region. A systematic review estimated an annual caseload of 10,423, a hospitalization rate of 52.1 per 100,000 population, a total burden of 300.6 per 100,000 (95% CI 96.54–604.23), approximately 730 deaths annually, and a case fatality rate of 7.0%; renal involvement occurred in a median of 48.7% of patients [60]. The same review also noted that there had been no Sri Lankan study based on cultured specimens since 1975. Since then, complete genomes have been obtained for two strains of *Leptospira weilii* and one *Leptospira kirschneri* strain from febrile patients in different districts, and isolation has been made [15]. Three genomes cannot characterize the serovar distribution underlying a national burden of this magnitude, and the distance between a functioning clinical surveillance system and systematic characterization of the organisms it detects remains substantial. In livestock, leptospirosis causes reproductive failure and production loss, but prevalence and molecular data from the region remain limited.

Anthrax

Anthrax is endemic in South Asia, and outbreaks happen frequently in livestock and occasionally in humans, caused by *Bacillus anthracis* [61]. Systemic infections in humans have high case fatality, and its potential as a bioterrorism threat puts it under international watch [62].

Table 2: Antimicrobial resistance in zoonotic bacterial pathogens from South Asia, with an assessment of clinical interpretability.

Pathogen	Host or source	Country	Antimicrobial or resistance type	Reported resistance	Clinically interpretable?	Source
Klebsiella pneumoniae	Human clinical	Pakistan, India	Multidrug resistance	60–90%	Yes	[51, 53]
Klebsiella pneumoniae	Human clinical	Pakistan	ESBL production	50–70%	Yes	[51]
Klebsiella pneumoniae	Human clinical	Bangladesh, Pakistan	Carbapenem resistance	10–30%	Yes	[12, 51]
Klebsiella pneumoniae	Human clinical	Nepal	Multidrug resistance	73.5% (36/49)	Yes	[55]
Klebsiella pneumoniae	Human clinical	Nepal	ESBL production	73.5% (36/49)	Yes	[55]
Klebsiella pneumoniae	Human clinical	Nepal	$bla_{\text{NDM-1}}$ among carbapenem-resistant isolates	58.6% (17/29)	Yes (genotypic)	[55]
Klebsiella pneumoniae	Bovine milk, subclinical mastitis	Pakistan	Ampicillin	100%	Yes	[56]
Klebsiella pneumoniae	Bovine milk, subclinical mastitis	Pakistan	Amoxicillin	80.5%	Yes	[56]
Klebsiella pneumoniae	Bovine milk, subclinical mastitis	Pakistan	bla_{TEM} carriage	91.6%	Yes (genotypic)	[56]
Salmonella spp.	Poultry	India	Ampicillin	95.71–100%	Yes	[66]
Salmonella spp.	Poultry	India	Tetracycline	76.27–100%	Yes	[66]
Salmonella spp.	Poultry	India	Ciprofloxacin	Up to 82.56%	Yes	[66]
Salmonella spp.	Poultry	India	Third-generation cephalosporins	18.75–79.66%	Yes	[66]
Salmonella spp.	Livestock and poultry	South Asia (pooled)	Erythromycin	94.04%	**No.***	[67]
Escherichia coli	Livestock and poultry	South Asia (pooled)	Ampicillin	70–90%	Yes	[67]
Escherichia coli	Livestock and poultry	South Asia (pooled)	Tetracycline	60–85%	Yes	[67]
Campylobacter spp.	Chicken farms	Bangladesh	Erythromycin	91.2%	Yes **	[71]
Campylobacter spp.	Chicken farms	Bangladesh	Ciprofloxacin	88.2%	Yes	[71]
Campylobacter spp.	Chicken farms	Bangladesh	Tetracycline	94.1%	Yes	[71]
Campylobacter spp.	Chicken farms	Bangladesh	Multidrug resistance	97.1%	Yes	[71]
Staphylococcus aureus (MRSA) and coagulase-negative staphylococci	Livestock–human–environment interface	India	Methicillin resistance	10–40%	Yes	[76]
Brucella spp.	Raw milk and livestock feces	Pakistan	Multiple agents	Detected; variable	Interpret with caution — standardized breakpoints for *Brucella* are not established	[75]

Resistance percentages are meaningful only where recognized interpretive criteria exist for that organism–antimicrobial combination; intrinsic phenotypes are identified as such. * Enterobacterales are intrinsically resistant to macrolides, and no interpretive criteria exist for erythromycin against *Salmonella*; the figure describes an expected phenotype, not acquired resistance [70]. ** Macrolides are first-line therapy for campylobacteriosis.

Bangladesh has produced the most detailed regional evidence: an investigation of 26 outbreaks in seven districts from 2013–2016 recorded 1,210 suspected human cases, all of which were cutaneous, with an attack rate of 20% for exposed humans, and 22 animals (mainly cattle) were implicated in the outbreak. The risk was associated with butchering practices, not with casual contact with the animals, such as prior cut injuries (adjusted odds ratio, 19.04), slaughtering raw meat (5.73), mixing bones and meat (4.64), and observing slaughter (2.86) [63]. Molecular characterization of *Bacillus anthracis* in the region is limited to India, where isolates from cattle outbreaks in the state of Karnataka have been typed and their genetic relationships resolved [64]. There are no published whole-genome studies for any of the five countries; thus, the relationship among outbreak strains, soil reservoirs, and cross-border spread remains unknown.

Salmonella spp. and *Campylobacter* spp.

Salmonella spp. and *Campylobacter* spp. are leading foodborne pathogens globally, and South Asia is no exception [65]. A systematic review of AMR in *Salmonella* from Indian poultry documented ampicillin resistance exceeding 95% in several studies, tetracycline resistance between 76.27% and 100%, ciprofloxacin resistance reaching 82.56% in Uttar Pradesh isolates, and third-generation cephalosporin resistance between 18.75% and 79.66% across regions [66]. A systematic review and meta-analysis of livestock and poultry across South Asia likewise reported extensive MDR in *Salmonella* and *Escherichia coli* [67]. Human salmonellosis and campylobacteriosis are common, and poultry products are the principal recognized source [68]. MDR non-typhoidal *Salmonella* has been documented in food-producing animals, retail meat and humans across neighboring South-East Asia [69].

Resistance data for these organisms require interpretive care, and one figure that has entered the regional literature illustrates the problem. Erythromycin resistance of 94.04% in *Salmonella* has been reported from South Asian livestock and poultry [67]. *Enterobacterales*, including *Salmonella* and *E. coli*, are intrinsically resistant to macrolides, and this phenotype is listed as expected rather than acquired in international expert rules [70]. Neither the Clinical and Laboratory Standards Institute (CLSI) nor the European Committee on Antimicrobial Susceptibility Testing (EUCAST) provides interpretive criteria for erythromycin against *Salmonella*; azithromycin criteria exist only for *Salmonella enterica* serovar Typhi and for *Shigella*. A near-universal erythromycin resistance rate in *Salmonella*, therefore, reflects the normal phenotype of the genus and provides no information about acquired resistance, treatment options, or selection pressure from antimicrobial use. It should not be presented as an antimicrobial resistance signal, and clinically interpretable agents — fluoroquinolones, third-generation cephalosporins, ampicillin and, for typhoidal serovars, azithromycin — should be reported in its place. Table 2 distinguishes interpretable from non-interpretable entries on this basis.

The contrast with *Campylobacter* makes the point precisely. Macrolides are first-line therapy for campylobacteriosis, so erythromycin resistance in this genus is clinically decisive rather than intrinsic. Evidence from the region is no longer absent. Sampling of 84 chicken farms across Mymensingh and Gazipur districts in Bangladesh found 40.5% farm-level positivity for *Campylobacter* spp., with 91.2% of isolates resistant to erythromycin, 88.2% to ciprofloxacin and 94.1% to tetracycline; 97.1% met MDR criteria, and 50% were extensively drug resistant (XDR), and ten resistance genes were characterized, including bla_{TEM} in 97.1% of isolates [71]. Resistance to both first-line therapeutic classes within a single food-animal population is the most consequential finding identified in this review, and it comes from a single pair of districts in one country. Comparable farm-level data are unavailable from Pakistan, Nepal, and Sri Lanka.

Antimicrobial resistance and surveillance gaps

Resistance burden across the region

South Asia is disproportionately affected by antimicrobial resistance. Inappropriate and excessive antibiotic use in humans and animals, weak regulatory enforcement, limited infection prevention and control, and thin surveillance combine to accelerate both the emergence and spread [72, 73]. Resistance rates in zoonotic bacteria from the region are among the highest reported anywhere [67]. Findings are summarized in Table 2.

Country-level evidence is uneven yet consistent in direction. A systematic review and meta-analysis of food animals in Pakistan outlined the national resistance profile across the principal food-producing species [74], and antimicrobial-resistant *Brucella* spp. have been isolated from raw milk and livestock feces in the same country [75]. MDR *Salmonella* is recurrent in Indian poultry [66], and resistance in clinical *K. pneumoniae* is severe in Bangladesh [12] and Nepal [55].

Two organisms in Table 2 warrant explicit treatment in the text. Methicillin-resistant *Staphylococcus aureus* has been recovered across the livestock–human–environment interface in Karnataka, India, alongside methicillin-resistant coagulase-negative staphylococci, and the isolates carried both resistance and virulence determinants [76]. *Staphylococcus aureus* is not a classical zoonosis, but livestock-associated lineages move between animal and human hosts, and its inclusion here follows the same One Health logic applied to *K.*

pneumoniae. *E. coli*, cited throughout the resistance literature as a sentinel organism, shows ampicillin and tetracycline resistance of 70–90% and 60–85%, respectively, in South Asian livestock and poultry [67]; commensal *E. coli is* monitored not because every isolate is pathogenic but because it indexes selection pressure across the food chain.

One of the major contributors is livestock production. Antibiotics are used extensively in growth promotion, prophylaxis, and therapy, and third-generation cephalosporins, macrolides, and fluoroquinolones are commonly used without veterinary supervision [77, 78]. This selection pressure will favor resistance determinants that reach humans via the food chain, occupational contact, and environmental contamination [67, 79].

Gaps in current surveillance systems

The surveillance of zoonotic bacterial diseases in South Asia is neither comprehensive, well-resourced, nor applied uniformly. Multisectoral (human, animal, food, and environmental) One Health surveillance is not reported in the region at any level of the country [19]. Human surveillance is mostly clinical, and laboratory confirmation is limited to tertiary centers [20]. Passive reporting and irregular sampling form the basis of animal surveillance [80]. Food surveillance is based on only a few prevalence studies [81], and environmental surveillance is almost nonexistent [82].

The country-specific assessments outline the same structural issues. Pakistan lacks a national surveillance program; instead, surveillance is conducted on an ad hoc basis by academic and research institutes [17], and there is limited integration between the veterinary and human health sectors [18]. A policy content analysis of surveillance systems in Gujarat, India, identified issues with information sharing, sampling, communication with decision makers, and external dissemination [20]. In Nepal, gaps span infection prevention and control, laboratory readiness, wildlife and livestock surveillance, and cross-border coordination [19].

The main shortcoming is genomic monitoring. The reference technique for high-resolution pathogen characterization, outbreak detection, source attribution, and resistance profiling is whole-genome sequencing [9, 10]. It has not been systematically integrated into detection and control plans in any sector of any South Asian country for zoonotic bacteria. Networks capable of supporting its integration would make a material difference in the region's capacity to detect and contain outbreaks and the emergence of resistance.

Genomic surveillance using whole-genome sequencing

Regional application of sequencing

Whole-genome sequencing has restructured infectious disease surveillance where implemented at scale, enabling high-resolution pathogen characterization, identification of transmission pathways, and detection of resistance determinants [9, 83]. European programs routinely apply it to *Listeria, Salmonella,* and *K. pneumoniae*, improving outbreak detection and source attribution [44, 84].

The South Asian position is one of capacity without integration. Sequencing infrastructure exists and has been used productively across the region. Genomic epidemiology of *Salmonella enterica* serovars Typhi and Paratyphi A in Bangladesh and Nepal has resolved pathogen diversity and the transmission of resistance at a national scale [13]. *Mycobacterium orygis* has been sequenced from Indian wild ungulates [7], and a culture-independent workflow for sequencing Nipah virus has been developed in Bangladesh [14]. Among the bacteria reviewed here, whole-genome data exist for *B. melitensis* and *L. monocytogenes* in India [11, 41], for *Leptospira* in Sri Lanka [15] and for clinical *K. pneumoniae* in India and Bangladesh [12, 53]. Each is a discrete research output rather than a surveillance stream: none samples humans, animals, food, and the environment concurrently; none is repeated on a defined schedule; and none reports to a national system. The distribution of this evidence across the seven pathogens and five countries is set out in Figure 1. Of the 35 pathogen–country combinations, 14 have no country-specific primary study at all, and only seven have reached whole-genome sequencing. The deficiency is therefore neither uniform across the region nor total. It is concentrated in particular pathogens and particular countries, and is a deficiency in coverage and continuity rather than in capability.

The limiting factor is therefore organizational rather than technical. Constraints reported include infrastructure, sequencing and bioinformatics costs, shortage of trained personnel and limited domestic research funding [19, 85]. International partnership and structured capacity development offer a route through these constraints [86].

Comparison with other regions

Comparing South Asia with other regions clarifies both the size of the gap and the realistic path to closing it. In Europe, coordinated genomic surveillance of zoonotic pathogens is routine across human, animal, and food isolates [84], and sequencing-based surveillance of *Listeria* in Germany has resolved outbreaks and identified routes of animal-to-human transmission [87]. Egypt and Turkey have applied sequencing to *Brucella* and *K. pneumoniae*, with results that informed regional control [33, 34, 88].

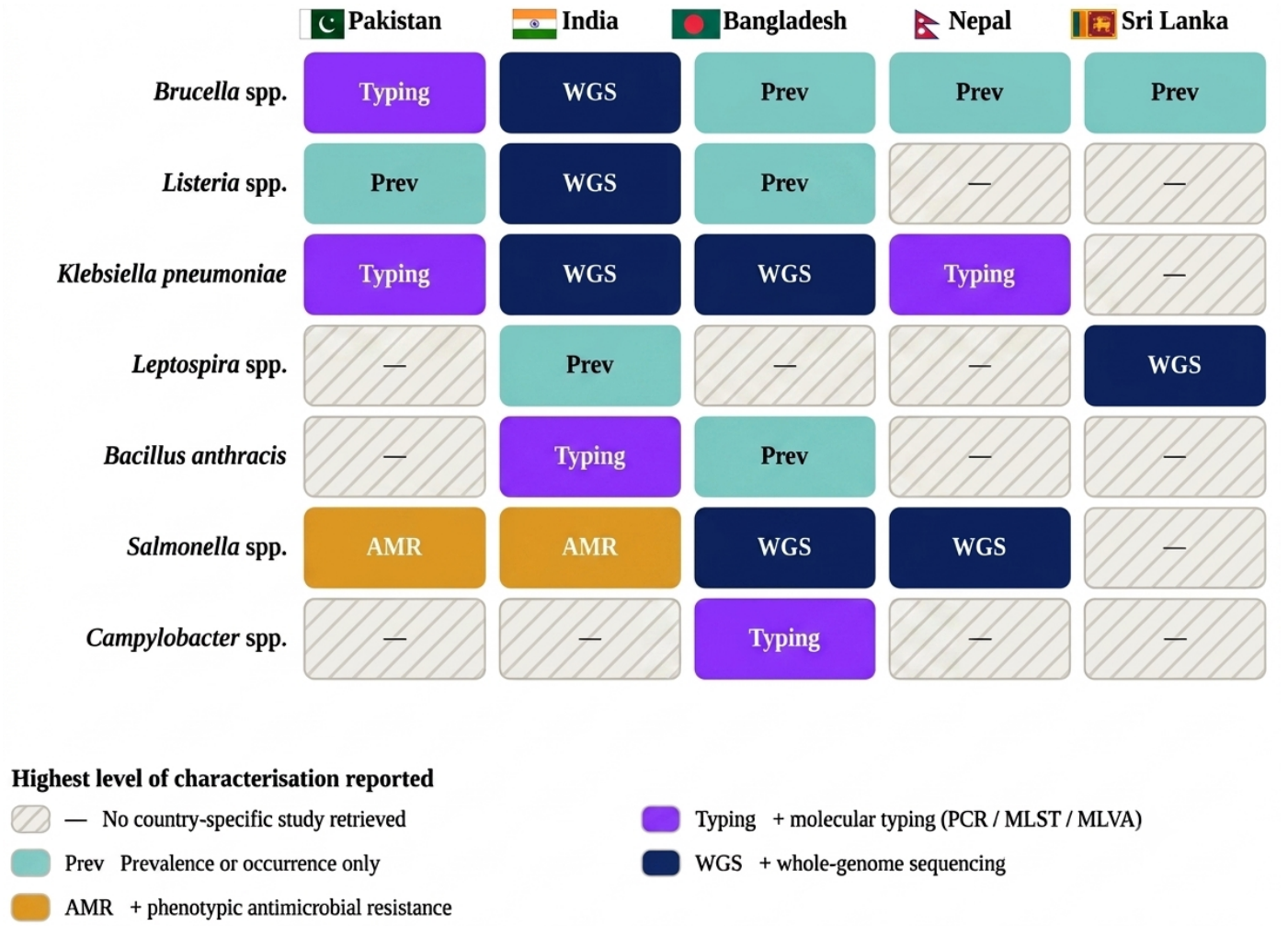

Figure 1: Level of characterization reported for each zoonotic bacterial pathogen in each South Asian country. Each cell records the highest level reached by any country-specific primary study cited in this review, on an ordered scale from no retrieved study, through prevalence or occurrence, phenotypic antimicrobial resistance and molecular typing, to whole-genome sequencing. Fourteen of the 35 pathogen–country combinations have no primary study; seven have whole-genome data, distributed across four pathogens and four countries rather than concentrated in a single country or sector. Regional pooled analyses that do not report country-level results [54, 67] are not attributed to individual countries, and the matrix reflects the purposive search described in the Literature search strategy section rather than an exhaustive enumeration. The underlying data are those compiled in Tables 1 and 2, together with the genomic studies cited in the regional application of sequencing section.

European systems are an imperfect template, however, because they rest on institutional and financial foundations that took decades to build and remain incomplete in integrating animal, food and human data. More instructive comparisons come from settings with constraints closer to those in South Asia. A PulseNet International survey of foodborne disease surveillance across 33 countries found that only 8% of participating laboratories used sequencing routinely, with a further 20% using it reactively for outbreak investigation; funding was the leading barrier for 78% of respondents, followed by expertise (61%) and analytical training (56%) [89]. Genomic surveillance in Africa has advanced through pooled regional infrastructure and coordinated capacity development rather than through parallel national build-outs [86]. These experiences suggest that regional consolidation, shared analytical infrastructure, and sustained, rather than project-based, funding matter more than the availability of instruments.

Barriers to implementation

Six constraints recur across the regional literature: (1) Infrastructure. Sequencing depends on stable electricity, cold-chain storage, reliable connectivity, and computing capacity, all of which are unevenly available in the rural districts where livestock production is concentrated [85]. (2) Cost. Instrument acquisition, reagents, bioinformatics, and data storage entail recurring costs that national research budgets in the region rarely accommodate [19, 90]. (3) Personnel. Library preparation, sequencing, and, most acutely, genomic data analysis and interpretation require skills that remain scarce, and career pathways in

bioinformatics are limited [19, 20]. (4) Sample collection and transport. Representative sequencing depends on systematic collection from animals, food, and the environment, which existing surveillance does not provide [91]. (5) Data sharing. Surveillance data are held separately by sector and by country, preventing the integrated analysis on which One Health interpretation depends [19, 20]. (6) Political commitment. Sustained genomic surveillance requires government financing and institutional ownership, and zoonotic disease competes poorly for both against more visible health priorities [19, 92].

Regional bodies, including the South Asian Association for Regional Cooperation (SAARC), provide existing mechanisms for cross-border cooperation and data exchange that could reduce the per-country cost of addressing several of these constraints [19, 93].

Challenges to integrated One Health surveillance

Seven obstacles recur across the five countries: (1) Sectoral separation. Human, veterinary, and environmental surveillance are conducted by separate agencies under different ministries, with limited data harmonization [19, 20]. (2) Limited political and financial commitment. Zoonotic disease surveillance is rarely prioritized in national budgets [19, 92]. (3) Laboratory infrastructure. Molecular diagnostic and genomic capacity is concentrated in a small number of urban institutions [85]. (4) Workforce. Shortages of trained researchers, laboratory technicians, and bioinformaticians constrain every stage, from sampling to interpretation [19, 20]. (5) Sample collection and transport. Weak field systems compromise the availability and quality of isolates [91]. (6) Interagency coordination. Limited coordination between agencies and across borders obstructs reconstruction of transmission pathways and slows outbreak response [19, 20]. (7) Regional partnership. Despite the existence of SAARC and comparable bodies, operational partnerships for zoonotic disease surveillance among South Asian countries remain scarce [93].

These constraints reinforce one another. Sectoral separation restricts data sharing; without integrated data, the evidence base for advocacy remains thin; without that evidence, zoonotic disease continues to lose out in budget allocation, which in turn perpetuates the separation. Interrupting this cycle requires simultaneous action on evidence generation, institutional arrangements, and financing rather than sequential attention to each.

A staged roadmap for South Asia

General appeals for capacity building have not measurably advanced the region over the past two decades. The recommendations below are therefore specified by pathogen, actor, and timeframe, and ordered by priority. Indicative costs are drawn from published implementations rather than from list prices: bacterial genome sequencing has been delivered at a consumable cost below USD 10 per isolate, with a throughput of up to 768 samples per day, using pooled library preparation and automation [94], which places the marginal cost of sequencing within reach of existing national reference laboratory budgets. The binding constraints are not the sequencing reaction but the sampling frame, the analytical workforce, and the governance arrangement that connects them. Table 3 sets out the roadmap.

Four priorities carry the greatest expected return.

Sequence the isolates already held

National reference laboratories and veterinary research institutes in all five countries maintain archived collections of *Brucella, Salmonella, Campylobacter,* and *K. pneumoniae*. Retrospective sequencing of these collections requires no new field infrastructure, can be completed within twelve to eighteen months, and would establish a baseline population structure against which prospective surveillance can be interpreted. This is the lowest-cost entry point and should precede any instrument procurement.

Establish sentinel sites rather than national coverage

Two or three districts per country, selected for high livestock density and access to functioning laboratories, sampling humans, animals, food, and water at defined intervals for a defined pathogen panel, would generate interpretable One Health data at a fraction of the cost of national systems. Sri Lankan leptospirosis surveillance demonstrates that clinical reporting can be robust while isolate characterization remains marginal; a national burden of this size rests on three published genomes [15, 60]; pairing existing clinical systems with routine isolate characterization is more efficient than building new reporting structures.

Consolidate analysis regionally

Given the workforce constraint identified across the region and confirmed in comparable settings [89], a shared bioinformatics facility serving all five countries, with distributed sequencing and centralized analysis, would use scarce expertise more efficiently than five parallel national units. SAARC and the WHO South-East Asia Regional Office provide existing mechanisms for convening [19, 93].

Correct the resistance evidence base

Intrinsic phenotypes should not be included in national antimicrobial resistance surveillance protocols, as they lack clinical meaning, according to accepted expert guidelines [70]. This is free and will help avoid the recurrence of phenomena like macrolide resistance in

Table 3: Staged roadmap for One Health genomic surveillance of zoonotic bacterial pathogens in South Asia, ordered by priority. Timelines are in months from program start. Cost entries identify the principal cost driver rather than a full budget.

Priority	Action	Target pathogens	Responsible actors	Timeline (months)	Principal cost driver	Feasibility notes
1	Revise national antimicrobial resistance reporting panels to specify clinically interpretable agents and exclude intrinsic phenotypes	All *Enterobacterales*; *Campylobacter* spp.	National AMR coordinating committees; reference microbiology laboratories	0–6	Negligible; protocol revision only	Implementable within existing national action plans [95]
2	Retrospective whole-genome sequencing of archived isolate collections	*Brucella*, *Salmonella*, *Campylobacter*, *K. pneumoniae*	National reference laboratories; veterinary research institutes	0–18	Sequencing consumables, reported below USD 10 per isolate at pooled high throughput [94]; unit cost rises substantially at low volume	Requires prior audit of isolate viability, metadata and accessibility
3	Targeted risk communication for high-exposure occupational groups	*B. anthracis*, *Brucella* spp., *Listeria* spp.	District public health and veterinary services; livestock and butchers' associations	0–12	Materials and field staff time	Risk concentrates in defined practices rather than general contact [63]
4	Establish two to three One Health sentinel districts per country sampling humans, animals, food and water	*Brucella*, *Listeria*, *Salmonella*, *Campylobacter*, *Leptospira*	Ministries of health and livestock; district laboratories	6–36	Field sampling, cold chain, transport, laboratory staffing	Site on existing functioning laboratories rather than new construction
5	Scale isolate characterizations from proof of concept to routine	*Leptospira* (Sri Lanka); *Listeria* (all countries except India); *Brucella* (all except India)	National reference laboratories; academic partners	12–30	Culture and reference typing capacity	Sri Lankan *Leptospira* isolation has been demonstrated but rests on three published genomes [15]
6	Data-sharing framework covering data sovereignty, privacy and authorship	All	Ministries; national ethics bodies; regional organizations	6–24	Legal and governance costs	Should precede procurement of technical platforms
7	Workforce development in genomic epidemiology and bioinformatics	All	Universities; national institutes; international partners	6–48	Fellowships, in-service training and retention posts	Workforce, not instrumentation, is the binding constraint [89]
8	Regional bioinformatics hub with distributed sequencing and centralized analysis	All	SAARC; WHO South-East Asia Regional Office; national reference laboratories	12–48	Shared analytical staff and computing infrastructure	Avoids five parallel national units; requires intergovernmental agreement [93]

Salmonella, which overestimate resistance burden without providing treatment and/or policy guidance. The natural vehicle [95] is the alignment with the existing national action plans on antimicrobial resistance.

Supporting measures include structured data-sharing agreements, addressing data sovereignty and patient privacy issues before designing technical platforms, and engaging with farmers, butchers, veterinarians, and clinicians, whose practices determine exposure. The Bangladeshi anthrax findings illustrate how risk was concentrated in certain butchering practices rather than in general livestock contact, opening the door to targeted intervention. Equitable international collaboration should involve South Asian investigators in study design, analysis, and authorship, rather than only in the supply of isolates. It should be accompanied by an economic appraisal at each stage, as returns can be demonstrated for both the health and livestock sectors in the case of cross-sectoral surveillance [96]. The WHO global genomic surveillance strategy 2022–2032 establishes an international framework for positioning national plans [97]. The relationship of these four sectors, namely human, animal, food, and environment, and how they are linked together with sequencing is shown in Figure 2.

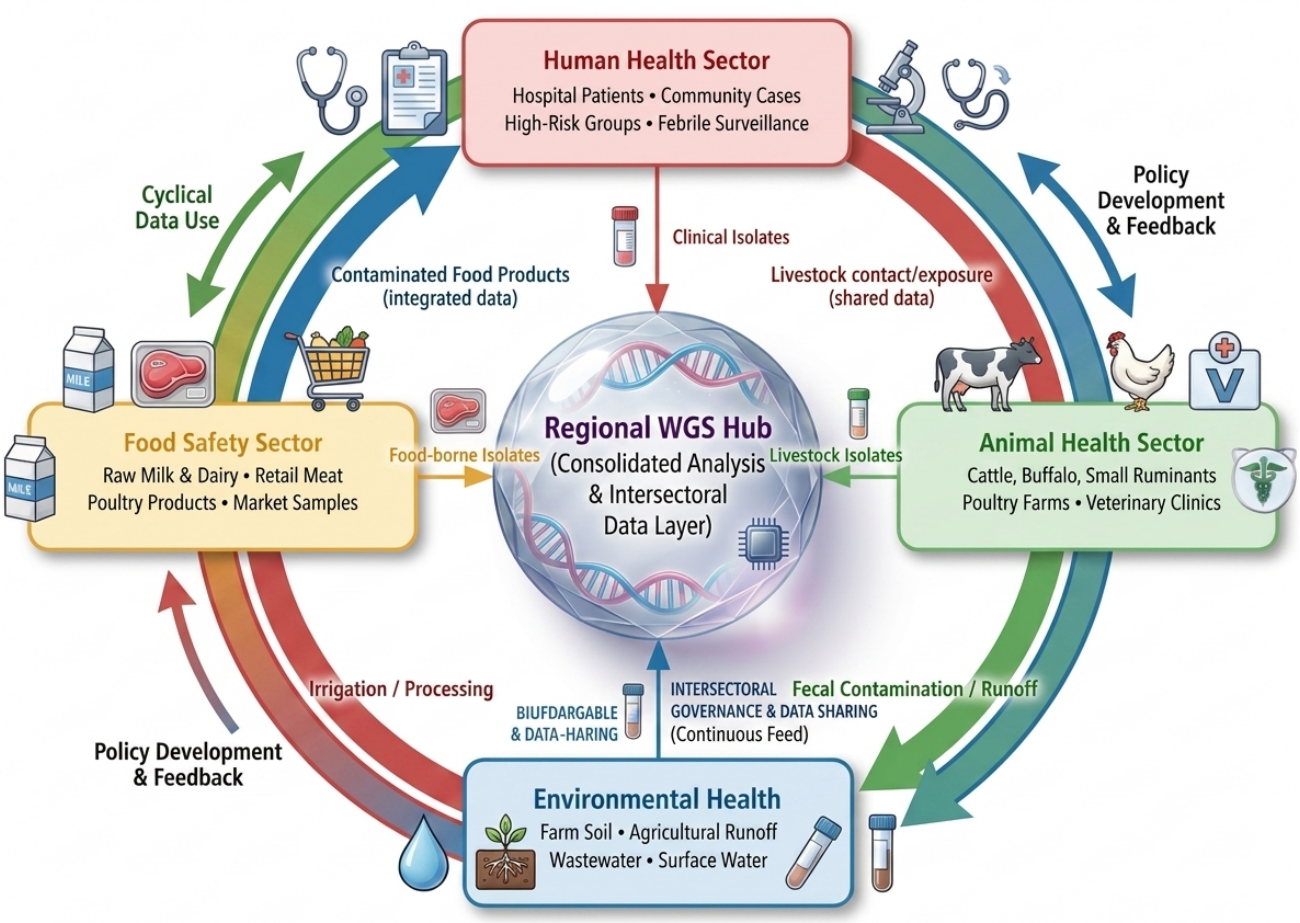

Figure 2: Proposed architecture for integrated One Health genomic surveillance in South Asia, corresponding to the roadmap in Table 3. Human, animal, food, and environmental sampling converge on a small number of sentinel districts that operate a shared schedule, pathogen panel, and metadata standard. National reference laboratories isolate, archive, and sequence, testing susceptibility only on clinically interpretable panels. Sequencing is distributed across national laboratories, while analysis is consolidated in a single regional bioinformatics hub, thereby addressing the workforce constraint rather than duplicating instrumentation across five countries. Outputs feed back into policy and practice.

Critical discussion and limitations

All the evidence brought together for this argument reinforces the central argument, but it limits the extent to which it can be said with confidence. The limits are best presented collectively, not throughout the course of the argument.

Evidence is unevenly distributed across the five countries

The majority of primary studies retrieved are from Pakistan, a significant number from India, and few from Bangladesh, Nepal, and Sri Lanka. This distribution is a discovery in and of itself, as it maps out the location of research capacity and research funding — but also shows

that the most significant regional statements fall on two countries. Data from Nepal and Sri Lanka, where available, are limited to a single district or center, and the generalizability of their findings to these countries has not been established. In Table 1 and Table 2, country attributions have been reported explicitly to enable the reader to see which claims are regionally supported or not.

Methodological heterogeneity limits comparison

Numbers of brucellosis cases are based on serological tests that might not differentiate between acute infections, past exposure, or vaccine-induced antibodies. Variation in serological tests performed on the same individual will show how the estimate is affected. Cross-sectional designs dominate, and there are no visible seasonal or temporal patterns.

The literature is skewed toward clinical and retail sampling

Evidence on *K. pneumoniae* overwhelmingly comes from tertiary hospitals, whereas evidence on *Listeria* comes from retail food products rather than the farm-to-fork continuum. Both patterns leave the reservoirs that matter most for One Health interpretation — primary production, farm environments and water — largely unsampled. Where such sampling has been done, as on Bangladeshi cattle farms and Pakistani dairy farms, it has found the organisms present, suggesting that absence of evidence reflects absence of looking.

Pathogens have been studied in isolation

Leptospira, *Bacillus anthracis*, *Salmonella*, and *Campylobacter* are investigated as separate problems by separate groups, and the resulting literature does not support the cross-sectoral synthesis that One Health requires. This review inherits that limitation: it assembles parallel evidence streams rather than integrated ones, because integrated studies have not been conducted.

Comparisons with other regions should be read cautiously

European and Middle Eastern systems are not uniformly mature, and even well-resourced programs have not fully integrated animal, food, and human data. Presenting them as models risks understating the institutional investment they required and overstating their transferability to resource-constrained settings. The comparisons with low- and middle-income implementations are more directly applicable.

The recommendations in the staged roadmap are conditional

Cost figures from high-throughput, centralized facilities may not apply to low-volume laboratories, where per-sample costs rise substantially. Retrospective sequencing of archived isolates assumes that those collections are viable, adequately documented, and accessible, a condition that has not been verified for any of the five countries. Regional consolidation of analysis presumes political agreement that does not currently exist. These proposals should be read as a prioritized agenda requiring feasibility assessment, not as a costed implementation plan.

Finally, this is a mini-review

Selection was purposive; the search was not exhaustive; a formal risk-of-bias appraisal was not undertaken; and no quantitative synthesis was attempted. Studies published in regional journals not indexed in the databases searched, or in languages other than English, will have been missed. Such sources are likely to be more numerous in Nepal and Sri Lanka than in Pakistan and India, thereby deepening rather than offsetting the geographical imbalance described above. A systematic review with a registered protocol and a prospectively documented search strategy would be required to reliably quantify the regional burden.

Conclusion

The burden of zoonotic bacterial disease and antimicrobial resistance in South Asia is significant but poorly quantified. Conditions conducive to emergence and spread are maintained by dense human–livestock interfaces, low surveillance, and high antimicrobial use in food animals. The evidence assembled here shows severe resistance where it has been measured: MDR in three-quarters of clinical *K. pneumoniae* isolates in Nepal and in almost all *Campylobacter* isolates from Bangladeshi poultry farms, as well as in whole countries for which comparable measurements do not exist.

The region's genomic deficit is one of integration rather than capability. Sequencing has been successfully applied in South Asia to typhoidal *Salmonella, M. orygis*, and selected clinical bacterial collections, but not prospectively, not across sectors, and not to the zoonotic bacteria that dominate the livestock interface. That distinction matters for policy: the requirement is not to introduce a technology but to embed an existing one within surveillance systems that currently operate separately.

Progress is more likely to come from sequencing archived collections, establishing a small number of well-characterized sentinel sites, consolidating regional analytical capacity, and correcting how resistance is reported, rather than from further general appeals for investment. Reporting practices deserve particular attention: resistance figures that reflect intrinsic phenotypes inflate the apparent burden and provide no basis for treatment or policy decisions. Applied together, these measures would begin to convert the region's silent

burden of zoonotic bacterial disease into evidence on which to build control.

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