Electronic Journal of Medical Research
https://respublishers.com/journals/ejmr
ISSN: 3106-1362/3106-1370

Review article

From Surveillance to Disease Burden: Evidence Gaps for WHO Priority Bacterial Pathogens in South Asia and the Eastern Mediterranean

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Article information:
Received: 19-09-2026
Revised: 21-10-2026
Accepted: 23-10-2026
Published: 24-10-2026

Academic Editor:
Dr. Naveed Ahmed

Keywords:
Antimicrobial resistance
GLASS
Disease burden
Surveillance
South Asia
Eastern Mediterranean

Abstract: Antimicrobial resistance (AMR) is assessed through laboratory surveillance, which measures resistance among tested isolates, and burden estimation, which quantifies associated and attributable mortality and disability. This structured narrative review examines what these evidence streams establish about WHO Bacterial Priority Pathogens List 2024 pathogens in South Asia and the WHO Eastern Mediterranean Region, where their connection remains uncertain, and priorities for strengthening it. Global and regional surveillance reports, modeled burden analyses, and peer-reviewed studies available through August 2026 were reviewed. Reported median resistance across infection types reached 30.0% in the Eastern Mediterranean Region and 31.1% in the WHO South-East Asia Region in 2023; the latter is not geographically equivalent to South Asia. Burden estimates indicate approximately 380,000 AMR-associated deaths in the Eastern Mediterranean Region in 2021 and a projected 11.8 million AMR-attributable deaths in South Asia during 2025–2050. However, surveillance and burden estimates remain incompletely connected. Hospital-based sampling, particularly in tertiary centres, limits population representativeness. Population denominators, infection incidence, care-seeking patterns, blood-culture utilization, and outcomes by resistance status are insufficiently measured, requiring modeling assumptions and externally derived parameters. Higher reported resistance in countries with weaker surveillance further complicates interpretation. The central gap is therefore insufficient linking data to translate resistance proportions into population-level disease burden. Priorities include surveillance within defined population catchments, linking microbiological and clinical outcomes, measuring diagnostic utilization, harmonizing reporting across WHO regional boundaries, and transparently communicating modeling assumptions and uncertainty. These improvements are essential for translating AMR evidence into defensible regional policy and investment priorities.

Article citation: Saeed, R. & Yaseen, A. From Surveillance to Disease Burden: Evidence Gaps for WHO Priority Bacterial Pathogens in South Asia and the Eastern Mediterranean. Electron J Med Res. 2026. 2(4): 81-93. https://doi.org/10.64813/ejmr.2026.148

Introduction

Antimicrobial resistance is simultaneously one of the best-documented and one of the most poorly measured threats in global health. It is well documented in the sense that laboratories in more than a hundred countries now report the proportion of bacterial isolates that are resistant to defined antibiotics, and that these reports are aggregated annually into a global dataset. It is poorly measured in the sense that, for most of the world's population, nobody knows how many people acquire a resistant infection in a year, how many of them reach a facility capable of diagnosing it, or how many die because the

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organism was resistant rather than because they were severely ill [1].

These two statements are not in tension. They describe two different evidence streams that are frequently conflated. The first is laboratory surveillance, which answers the question: of the organisms we tested, what fraction were resistant? The second is burden estimation, which answers a different question: how much death and disability does resistance cause in a population? The first is a proportion with a laboratory denominator. The second is a rate with a population denominator. Converting the first into the second requires a chain of additional parameters: incidence, care-seeking, diagnostic capture, case fatality with and without resistance, and it is in that chain, rather than in the resistance proportions themselves, that the evidence is thinnest [2].

The question matters because policy is increasingly written against burden estimates rather than against resistance proportions. The 2024 United Nations General Assembly high-level meeting on AMR, national action plans, research priority-setting and investment cases all rest on projections of deaths averted. When those projections are built on parameters that have not been measured in the regions to which they are applied, the resulting policy is being steered by numbers whose provenance deserves scrutiny [3].

This review examines that chain for the pathogens named in the WHO Bacterial Priority Pathogens List (BPPL) 2024 in two regions that together account for a large share of the global burden and uncertainty: South Asia and the WHO Eastern Mediterranean Region. It asks what the published evidence establishes, what it does not establish, and what would be required to close the gap [4].

Scope and approach

This is a structured narrative review rather than a systematic review. The objective is to characterize the relationship between two bodies of evidence and to locate the points at which inference fails, which is a question about the architecture of the evidence base rather than about the magnitude of any single effect. Quantitative pooling across surveillance reports and modeled estimates would not produce an interpretable summary statistic, because the two are not estimates of the same quantity [5].

We retrieved sources up to August 2026, including WHO global and regional publications; Global Burden of Disease analyses and their regional derivatives; national surveillance reports from the regions concerned; and peer-reviewed systematic reviews and primary studies addressing BPPL pathogens in South Asia and the Eastern Mediterranean. Priority was given to sources reporting primary data or transparent methodology. Where a figure is quoted in this review, it is drawn from a source listed in the reference list and retrieved in full; estimates circulating in secondary reporting without a traceable primary source are not reproduced.

The limitations of this approach are set out in the limitations section and should be read before the conclusions are relied upon [6].

Two regions, three definitions: a problem that precedes the data

A difficulty specific to this topic arises before any data are examined. "South Asia" and "the Eastern Mediterranean Region" are not drawn from the same map.

The Eastern Mediterranean Region is a World Health Organization administrative region, comprising a defined set of member states from Morocco to Pakistan and including Afghanistan, Egypt, Iran, Iraq, Pakistan, Saudi Arabia, Somalia, Sudan, Yemen, and the Gulf states. Surveillance data flow through WHO regional structures, so this is the unit in which GLASS reports regional summaries [7].

"South Asia" is a Global Burden of Disease super-region, comprising India, Pakistan, Bangladesh, Nepal and Bhutan. It is the unit in which GBD and the Global Research on Antimicrobial Resistance program report burden estimates.

These two units overlap but do not coincide. Pakistan and Afghanistan belong to the WHO Eastern Mediterranean Region but are, geographically and epidemiologically, part of South Asia; India, Bangladesh, Nepal, Bhutan, and Sri Lanka belong to the WHO South-East Asia Region. The consequence is that the region in which burden is estimated, and the region in which surveillance is aggregated, are different regions, and a reader moving between a GLASS regional figure and a GBD regional figure is moving between different populations without being told so [8].

This is not a pedantic point. Pakistan is a country of substantial population with a documented burden of extensively drug-resistant typhoid, and whether its data appear under "South Asia" or "Eastern Mediterranean" materially changes both regional summaries. Any synthesis across the two evidence streams must therefore state explicitly which geography it is using, and this review does so

throughout: figures sourced from GLASS are labeled by WHO region, and figures sourced from GBD analyses are labeled by GBD region [9].

What the Bacterial Priority Pathogens List asks of the evidence

The WHO Bacterial Priority Pathogens List was updated in May 2024, superseding the 2017 list. It identifies fifteen pathogen–antibiotic combinations across three priority categories, intended to direct research and development, surveillance and infection prevention investment.

Four combinations are designated critical priority: carbapenem-resistant *Acinetobacter baumannii*; third-generation cephalosporin-resistant Enterobacterales; carbapenem-resistant Enterobacterales; and rifampicin-resistant *Mycobacterium tuberculosis*. Seven are designated high priority: fluoroquinolone-resistant *Salmonella* Typhi; fluoroquinolone-resistant *Shigella* spp.; vancomycin-resistant *Enterococcus faecium*; carbapenem-resistant *Pseudomonas aeruginosa*; fluoroquinolone-resistant non-typhoidal *Salmonella*; third-generation cephalosporin- and fluoroquinolone-resistant *Neisseria gonorrhoeae*; and methicillin-resistant *Staphylococcus aureus*. Four are designated medium priority: macrolide-resistant group A streptococci; macrolide-resistant *Streptococcus pneumoniae*; ampicillin-resistant *Haemophilus influenzae*; and penicillin-resistant group B streptococci [10].

Several changes from the 2017 list bear on the regions considered here. Third-generation cephalosporin-resistant Enterobacterales were elevated to a standalone critical category. Carbapenem-resistant *P. aeruginosa* was moved down from critical to high priority, reflecting reported global declines. Group A and group B streptococci entered the list for the first time, at medium priority. Rifampicin-resistant *M. tuberculosis* was included in the critical category following a separate analysis using an adapted multi-criteria decision analysis.

The prioritization drew on the global burden of disease caused by each organism, its capacity to resist treatment and to transmit resistance determinants, its burden in low- and middle-income countries, the difficulty it poses in healthcare settings, and its effect on vulnerable populations. The list therefore embeds a burden judgment, and in doing so it inherits whatever uncertainty attaches to burden estimation in the regions where that burden is concentrated. This is the first point at which the two evidence streams become entangled: a list intended to direct surveillance investment is itself partly derived from burden models that depend on surveillance data [11].

What surveillance currently delivers

Global aggregation

The WHO Global Antimicrobial Resistance and Use Surveillance System is the principal international mechanism for aggregating laboratory data. Its 2025 report represents a substantial expansion: by the end of 2024, 127 countries and three territories were enrolled, and 104 countries reported AMR data for 2023, compared with 25 countries in 2016. The dataset drew on more than 23 million bacteriologically confirmed infections [7].

The headline finding was that approximately one in six laboratory-confirmed bacterial infections worldwide were resistant to the antibiotics assessed. Median resistance was approximately one in three for urinary tract infections, one in six for bloodstream infections, one in fifteen for gastrointestinal infections, and one in 125 for urogenital gonorrhoea. Resistance to third-generation cephalosporins was 44.8% (95% CI 39.3–50.4) in *Escherichia coli* and 55.2% (48.5–61.7) in *Klebsiella pneumoniae* bloodstream infections. Between 2018 and 2023, resistance increased in 40% of monitored pathogen–antibiotic combinations, with imipenem resistance in *K. pneumoniae* rising by a median 15.3% per year (12.7–18.1) [12].

The two regions

Both regions reported resistance well above the global median. In the Eastern Mediterranean Region, median resistance across all infection types was 30.0%, approaching one in three infections; methicillin resistance in *S. aureus* bloodstream infections was the highest of any region at 50.3% (39.8–60.8); and ceftriaxone resistance in *N. gonorrhoeae* was 2.5% (0.8–7.7), a figure whose significance lies not in its magnitude but in the fact that ceftriaxone is the last reliable empirical option for that infection [13].

In the South-East Asia Region, median resistance was 31.1%. Fluoroquinolone resistance in *Shigella* spp. reached 75.5% (58.1–87.3) and carbapenem resistance in *K. pneumoniae* bloodstream infections reached 41.2% (30.3–53.1). Both figures concern BPPL pathogens, and both describe organisms for which the remaining therapeutic options are narrow and expensive. These regional values are shown alongside global comparators in Figure 2A [14].

National systems: the Indian example

National surveillance networks supply the data that regional summaries aggregate, and their design determines what those summaries can mean. The Indian Council of Medical Research Antimicrobial Resistance Surveillance Network provides the most detailed published national series in South Asia. Its 2024 report, the eighth in the series, analyzed 99,027 culture-positive isolates from a network of regional centers [15].

The reported resistance is severe. Meropenem resistance in *A. baumannii* was 91.0%. Susceptibility of *K. pneumoniae* to imipenem was 31.2% and to meropenem 35.1%, implying carbapenem resistance in roughly two-thirds of isolates. Susceptibility of *E. coli* to ceftazidime was 27.5%. Methicillin resistance in *S. aureus* was reported as having risen to approximately half of isolates, from about a third in 2017. Fluoroquinolone resistance in *Salmonella* Typhi exceeded 95% [16].

The report is explicit about what these figures do and do not represent. The data come from tertiary care hospitals, and the report states that they do not reflect community resistance levels in the country and should not be extrapolated to community settings. It further notes that approximately 1% of isolates came from stool specimens, so diarrheal pathogens are poorly represented [17].

This candor is a strength of the report, and it should be read as a general statement about the regional evidence base rather than as a limitation peculiar to one network. Surveillance of this design answers the question a clinician asks what is likely to work in my hospital? and does so well. It does not answer the question a health ministry asks when costing a national program, because it has no population denominator [18].

Table 1. Reported antimicrobial resistance in the two regions and globally, 2023, with the surveillance characteristics that condition each figure.

Indicator	Eastern Mediterranean Region	South-East Asia Region	Global	Source
Median resistance, all infection types	30.0%	31.1%	~1 in 6 infections	GLASS 2025
MRSA, bloodstream infection	50.3% (39.8–60.8); highest of any region	Not separately reported	—	GLASS 2025
Carbapenem-resistant *K. pneumoniae*, bloodstream	Not separately reported	41.2% (30.3–53.1)	—	GLASS 2025
Fluoroquinolone-resistant *Shigella* spp.	Not separately reported	75.5% (58.1–87.3)	—	GLASS 2025
3rd-generation cephalosporin-resistant *E. coli*, bloodstream	—	—	44.8% (39.3–50.4)	GLASS 2025
3rd-generation cephalosporin-resistant *K. pneumoniae*, bloodstream	—	—	55.2% (48.5–61.7)	GLASS 2025
Ceftriaxone-resistant *N. gonorrhoeae*	2.5% (0.8–7.7)	Not separately reported	—	GLASS 2025
Countries reporting AMR data for 2023	—	—	104 of 194 member states	GLASS 2025
National data completeness score	—	—	53.8%	GLASS 2025
Countries with all WHO core surveillance components	—	—	46.2% (48 of 104)	GLASS 2025

Dashes indicate that the indicator is not reported for that geography in the source. "Not separately reported" indicates that the regional value was not published even though the global value was. Values are modeled estimates with 95% credible intervals. GLASS regional groupings follow WHO administrative regions and do not correspond to the Global Burden of Disease super-region "South Asia".

What burden estimation requires, and where it breaks

The inferential chain

Converting a resistance proportion into an estimate of deaths requires, at minimum: the incidence of infection in the population; the proportion of infections that present to care; the proportion of presentations from which a specimen is taken and successfully cultured; the resistance proportion among those cultured; the case fatality of infection with a resistant organism; and the counterfactual case fatality had the same organism been susceptible. Surveillance measures one of these six quantities directly [4].

Figure 1 sets out the chain as a sequence of narrowing stages, each with the evidence available on what is lost at that point. Three stages deserve particular attention in these regions.

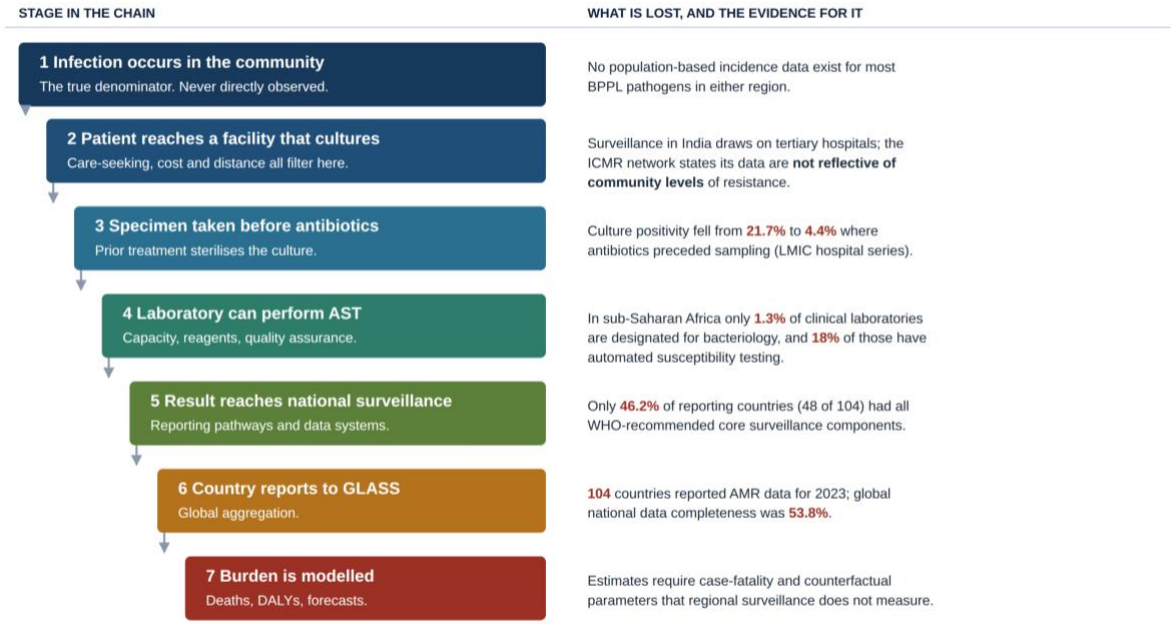


Figure 1. Where evidence is lost between infection and burden estimate. Each stage narrows the population captured, and resistance proportions are measured only on what survives to the later stages. Figures shown beside each stage are drawn from the sources cited in this review. The laboratory-capacity values are reported for sub-Saharan Africa and are included as the best available quantification of a constraint that is described, but not comparably measured, for South Asia and the Eastern Mediterranean. AST, antimicrobial susceptibility testing; BPPL, WHO Bacterial Priority Pathogens List; GLASS, Global Antimicrobial Resistance and Use Surveillance System.

Diagnostic capture

Resistance proportions are calculated on cultured isolates, so anything that selectively prevents culture distorts them. Prior antibiotic exposure is the most direct such mechanism: in one recent hospital series from a low- and middle-income setting, blood culture positivity was 21.7% among patients who had not received antibiotics before sampling and 4.4% among those who had, a difference that reflects sterilized cultures rather than absent infection [19]. In settings where antibiotics are widely available without prescription, a documented feature of both regions, this filter operates at scale and in a direction that is not easily predicted, since it removes both susceptible and resistant organisms but may not remove them equally [20].

Laboratory capacity imposes a second filter. The GLASS 2025 report notes that in sub-Saharan Africa only 1.3% of clinical laboratories are designated for bacteriological testing, and that 18% of those have automated susceptibility testing systems [8]. Comparable quantification is not available for South Asia or the Eastern Mediterranean, which is itself a finding: the capacity constraint is described qualitatively in regional literature but has not been measured in a form that permits comparison [21].

The selection problem

The most consequential observation in the GLASS 2025 report for present purposes is also the least intuitive. Countries with lower surveillance coverage reported *higher* median resistance, with a correlation of r = −0.74 between coverage and reported resistance [22].

There are two candidate explanations, and they have opposite policy implications. The first is that resistance genuinely is higher where health systems are weaker, through poorer infection control, less regulated antibiotic access and limited therapeutic options [23]. The second is that sparse surveillance systems sample preferentially from tertiary referral centers and from patients whose initial therapy has already failed, so that the isolates reaching the laboratory are enriched for resistance. Both mechanisms are plausible, both are probably operating, and the available data do not separate them [24].

Until they are separated, a regional resistance proportion from a low-coverage setting cannot be interpreted as an unbiased estimate of resistance in that population. This is not an argument for discounting such data; it is an argument for reporting coverage alongside resistance, so that the reader can judge [25].

Outcome parameters

The final links in the chain, case fatality with resistance and the counterfactual without it, are the least well measured and most influential in any burden model. A systematic review and meta-analysis of the impact of AMR on bloodstream infection outcomes in low- and middle-income countries reported a 58% increase in mortality, a doubling of the odds of intensive care admission, roughly a week of additional hospital stay, and approximately US$12,000 in additional direct medical cost per case [26].

The geographic distribution of that evidence base is the problem. Of 109 included publications, 96 came from upper-middle-income countries, and 49 of those 96 came from a single country. One study came from a low-income country and four from Africa. The accompanying commentary noted that pooled estimates rested on crude rather than adjusted comparisons, that patients with resistant infections differ systematically from those with susceptible infections in ways that independently raise mortality, and that these biases have most likely resulted in an overestimation of the impact of resistance [27].

The opposite result has also been reported. In a prospective study across eight sub-Saharan African hospitals, Enterobacterales bloodstream infection substantially increased mortality [28], but drug resistance was not associated with higher mortality risk, plausibly because only the most severely ill patients reached hospital at all, and because therapeutic options were constrained irrespective of susceptibility. Whatever the explanation, the finding demonstrates that the mortality effect of resistance is context-dependent, and that a parameter estimated predominantly in upper-middle-income hospitals cannot be assumed to transfer [29].

What the burden estimates say

Against that methodological background, the modeled estimates remain the best available description of the scale of the problem, and they are substantial.

Globally, the Global Research on Antimicrobial Resistance analysis of 1990–2021 estimated 1.14 million deaths attributable to bacterial AMR in 2021 and 4.71 million associated deaths. Attributable deaths are forecast to reach 1.91 million annually by 2050 and associated deaths 8.22 million, with a cumulative 39 million attributable deaths projected between 2025 and 2050 in the absence of further action. Deaths among children under five fell by approximately half between 1990 and 2021 [30], attributed principally to vaccination and improvements in water, sanitation and hygiene rather than to falling resistance; deaths among people aged 70 and over rose by more than 80% over the same period [31].

South Asia carries the highest forecast burden of any region, with 11.8 million attributable deaths projected between 2025 and 2050. Among pathogens, deaths involving methicillin-resistant *S. aureus* rose from 57,200 in 1990 to 130,000 in 2021, and deaths involving carbapenem-resistant Gram-negative organisms rose from 127,000 to 216,000.

A dedicated regional analysis of the WHO Eastern Mediterranean Region estimated approximately 380,000 deaths associated with bacterial AMR in 2021 (95% UI 332,000–426,000) and approximately 92,800 attributable to it (78,300–111,000), with forecasts of 752,000 (629,000–879,000) and 187,000 (157,000–223,000) respectively by 2050 [32]. Six pathogens accounted for most of the burden: *Streptococcus pneumoniae*, *K. pneumoniae*, *E. coli*, *S. aureus*, *A. baumannii* and *P. aeruginosa*. Attributable deaths involving *S. aureus* rose from approximately 28,200 in 1990 to approximately 49,500 in 2021, and methicillin-resistant *S. aureus* was a leading pathogen–drug combination in most countries of the region in 2021 [33]. The age pattern mirrored the global one, with associated deaths in children under five falling by 50.0% (38.2–62.0) between 1990 and 2021 while deaths in adults aged 70 and over rose by more than 85.7% (57.0–115.7). Somalia had the highest age-standardized mortality rates in both 1990 and 2021; Qatar had the lowest [34].

Table 2. WHO Bacterial Priority Pathogens List 2024 and the availability of regional evidence in South Asia and the Eastern Mediterranean.

Priority	Pathogen and resistance	Regional surveillance evidence	Population-level burden evidence	Principal gap
Critical	Carbapenem-resistant *Acinetobacter baumannii*	Dense hospital data; 91.0% meropenem resistance reported in India 2024	Included in EMR modelled burden among six leading pathogens	No community denominator; hospital-acquired fraction unknown
Critical	3rd-generation cephalosporin-resistant Enterobacterales	Dense; global bloodstream values 44.8% (*E. coli*), 55.2% (*K. pneumoniae*)	Included in modelled burden	Resistance measured on referral-centre isolates; incidence unmeasured
Critical	Carbapenem-resistant Enterobacterales	Dense; 41.2% in SEAR bloodstream *K. pneumoniae*	Included in modelled burden	Case fatality by resistance status not estimated regionally
Critical	Rifampicin-resistant *Mycobacterium tuberculosis*	Reported through separate TB programmes, not GLASS	Separate estimation pathway	Not integrated with bacterial AMR surveillance or burden models
High	Fluoroquinolone-resistant *Salmonella* Typhi	Dense in South Asia; >95% resistance reported in India 2024; 74-study regional meta-analysis available	Partial; typhoid burden modelled separately	No eligible data from Sri Lanka or Bhutan; breakpoint heterogeneity
High	Fluoroquinolone-resistant *Shigella* spp.	75.5% in SEAR; stool specimens ~1% of Indian network isolates	Minimal	Diarrhoeal pathogens structurally under-sampled
High	Vancomycin-resistant *Enterococcus faecium*	Sporadic single-centre reports	Absent	No regional aggregation
High	Carbapenem-resistant *Pseudomonas aeruginosa*	Moderate; 43% imipenem resistance reported in India 2024	Included in EMR modelled burden	Hospital-based only
High	Fluoroquinolone-resistant non-typhoidal *Salmonella*	Sparse	Absent	Requires stool and food-chain sampling not routinely performed
High	Resistant *Neisseria gonorrhoeae*	Low coverage explicitly noted in GLASS 2025; EMR ceftriaxone resistance 2.5% (0.8–7.7)	Absent	Very thin sampling base; wide credible interval
High	Methicillin-resistant *Staphylococcus aureus*	Dense; 50.3% EMR bloodstream, ~50% India 2024	Strong; leading pathogen–drug combination in most EMR countries	Community versus healthcare origin not distinguished
Medium	Macrolide-resistant group A streptococci	Minimal; new to the 2024 list	Absent	No regional incidence estimate for invasive disease
Medium	Macrolide-resistant *Streptococcus pneumoniae*	Moderate	Leading contributor to EMR modelled burden	Serotype and vaccine-impact data sparse
Medium	Ampicillin-resistant *Haemophilus influenzae*	Sparse	Absent	Requires specialised media; under-detected
Medium	Penicillin-resistant group B streptococci	Minimal; new to the 2024 list	Absent	No maternal or neonatal screening surveillance at scale

Evidence density is characterized qualitatively from the sources cited in this review and is intended as an orientation rather than a formal appraisal. "Absent" denotes that no regional population-level estimate was identified during this review, not that none exists.

These estimates are shown in Figure 2B. Their internal structure is worth noting: the analysis covered 11 infectious syndromes, 22 bacterial pathogens and 84 pathogen–drug combinations, with uncertainty intervals derived from 500 draws. The uncertainty intervals are wide, and they quantify parameter uncertainty within the model. They do not quantify the structural uncertainty introduced by the chain, which is larger and is not reported as an interval anywhere [35].

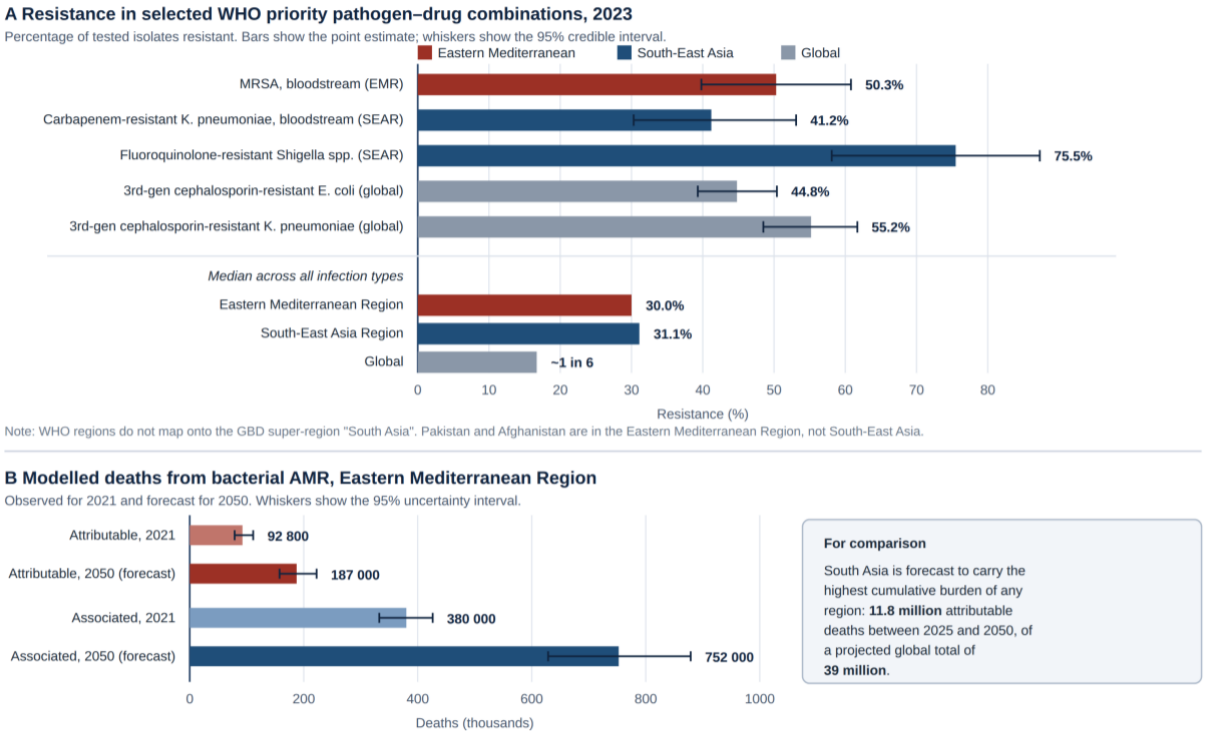


Figure 2. Reported resistance and modeled burden in the two regions. (A) Resistance in selected WHO priority pathogen-drug combinations in 2023, with 95% credible intervals, together with the median across all infection types for each region. (B) Modeled deaths from bacterial antimicrobial resistance in the WHO Eastern Mediterranean Region, observed for 2021 and forecast for 2050, with 95% uncertainty intervals. Deaths attributable to resistance are those that would not have occurred had the organism been susceptible; deaths associated with resistance are those occurring in people with a resistant infection. Note that panel A uses WHO administrative regions while the South Asia comparison in panel B uses the Global Burden of Disease super-region, which are not the same geography. EMR, Eastern Mediterranean Region; MRSA, methicillin-resistant *Staphylococcus aureus*; SEAR, South-East Asia Region.

A pathogen-level view of the evidence

Examining individual BPPL pathogens shows that the gap is uneven. For some organisms, the regional evidence is reasonably dense; for others, it is close to absent.

Salmonella Typhi illustrates the denser end. A systematic review and meta-analysis of azithromycin resistance across South Asia identified 74 studies comprising 30,085 clinical isolates, reporting pooled resistance of 5% (95% CI 4–5) in *S.* Typhi and 5% (0–9) in *S.* Paratyphi, with country-level estimates of 8% in Pakistan, 7% in India and 1% in each of Nepal and Bangladesh [36]. No significant temporal trend was detected between 2005 and 2024. The review is instructive in two further respects. No eligible studies were identified from Sri Lanka or Bhutan, so two countries of the region contribute nothing to the regional estimate. And the authors note that no CLSI or EUCAST breakpoints exist for *S.* Paratyphi, that *S.* Typhi breakpoints date only from 2015, and that studies therefore applied heterogeneous criteria, a measurement problem that constrains comparability independently of any sampling issue [37].

At the opposite end, several BPPL pathogens have essentially no population-level evidence in either region. Group A and group B streptococci entered the list in 2024 [38]; neither is routinely reported in regional surveillance summaries, and there is no regional estimate of the incidence of invasive disease from either. Vancomycin-resistant *E. faecium* is reported sporadically from individual hospitals. *N.*

gonorrhoeae surveillance coverage was explicitly noted as low in the GLASS 2025 report, and the regional ceftriaxone resistance estimate for the Eastern Mediterranean rests on a correspondingly thin base, as its wide credible interval indicates [39].

Table 2 summarizes the position pathogen by pathogen. The pattern it shows is that evidence density tracks laboratory convenience rather than public health importance: organisms that grow readily from blood or urine in a hospital laboratory are well represented, while organisms requiring specialized media, molecular confirmation or community-based sampling are not [40].

Consequences

Three consequences follow from the preceding analysis, and they are practical rather than academic.

Investment may be misdirected

If resistance proportions from low-coverage settings are inflated by selection while the true population burden is understated by incomplete capture, then the two errors do not cancel. They point investment in different directions: the first toward last-line antibiotic procurement, the second away from the diagnostic and primary care capacity that would make any procurement decision rational. A region can therefore simultaneously appear to have very high resistance and have no reliable basis for estimating how many people it affects [41].

Progress cannot be detected

The 2024 political declaration on AMR commits to at least 80% of countries being able to test all GLASS pathogens for resistance by 2030. That is a capacity target, and it is measurable [42]. But an intervention that reduced infection incidence while surveillance coverage simultaneously expanded would produce a rising number of reported resistant isolates, and a surveillance system without a population denominator cannot distinguish that from a worsening epidemic. Without denominators, success and failure generate similar signals [41].

The regional boundary obscures a coherent epidemiological unit

South Asia is divided between two WHO regions. Resistant organisms, their mobile genetic elements and the people carrying them do not observe that boundary. Typhoid lineages circulate between Pakistan and India, and carbapenemase genes [43] moving with patients and with trade, are regional phenomena reported through two separate administrative channels into two separate regional summaries. No existing mechanism reconciles them [44].

What would close the gaps?

The remedies below are ordered by the ratio of evidential value to cost, which is not the same as the order in which they are usually proposed.

Report coverage alongside resistance: The single cheapest improvement is to publish, beside every resistance proportion, the number of specimens cultured per 100,000 population in the catchment and the proportion of eligible patients sampled. This requires no new laboratory capacity and immediately allows a reader to judge whether a high resistance proportion reflects epidemiology or selection. The GLASS finding that coverage and reported resistance are inversely correlated makes this a precondition for interpreting any regional figure [45].

Establish sentinel surveillance with population denominators: A small number of well-characterized catchment populations, in which the denominator is known, and all suspected cases are investigated, yields more interpretable information than a large number of hospital laboratories reporting isolates without context. Such sites would generate the incidence estimates that burden models currently import from elsewhere [46].

Measure blood-culture utilization and prior antibiotic exposure routinely: Both are recordable at the point of specimen collection, and both are required to interpret culture-based surveillance. Neither is are routinely reported in either region.

Link susceptibility to outcome: Surveillance that records the organism, its susceptibility, and the patient's outcome (survival, length of stay, escalation of care) would allow regional estimation of case-fatality parameters rather than importing them from upper-middle-income hospitals. This is the parameter to which burden estimates are most sensitive and for which regional data are weakest [47].

Harmonize reporting across the regional boundary: A reporting mechanism that presents South Asia as a single epidemiological unit, irrespective of WHO regional administration, would permit coherent regional analysis of pathogens such as *S.* Typhi whose circulation spans the boundary [48].

Standardize breakpoint reporting: Studies should state the breakpoint standard and version used, and

regional syntheses should stratify by it. The *S.* Paratyphi example demonstrates that heterogeneity of criteria can be sufficient on its own to prevent meaningful pooling [49].

Report structural uncertainty in burden models: Published uncertainty intervals quantify parameter uncertainty conditional on model structure. Sensitivity analyses showing how estimates change under alternative assumptions about diagnostic capture and case fatality would convey the uncertainty that matters most to regional users [50].

Table 3. Structural evidence gaps, their consequence for policy, and the measurement that would close each.

Gap	Why it matters	What would close it	Relative cost
No population denominator	Resistance proportions cannot be converted into incidence or burden	Sentinel sites with defined catchment populations and complete case ascertainment	Moderate
Surveillance confined to tertiary hospitals	Resistance is measured on a selected, treatment-experienced population	Inclusion of secondary and primary care facilities; explicit reporting of facility tier	Moderate
Blood-culture utilisation unmeasured	Cannot distinguish low detection from low incidence	Report specimens cultured per 100,000 population and proportion of eligible patients sampled	Low
Prior antibiotic exposure unrecorded	Sterilised cultures remove cases non-randomly	Record exposure at specimen collection and report alongside positivity	Low
Coverage not reported with resistance	High resistance in low-coverage settings cannot be interpreted	Publish coverage metrics beside every resistance proportion	Low
Outcomes not linked to susceptibility	Case-fatality parameters imported from other regions	Link laboratory results to discharge outcome in surveillance datasets	Moderate
Breakpoint heterogeneity	Pooled estimates combine incompatible definitions	Mandatory reporting of breakpoint standard and version; stratified synthesis	Low
South Asia divided between two WHO regions	Regional analysis fragmented across administrative channels	Reporting mechanism presenting South Asia as a single epidemiological unit	Low
Structural uncertainty not quantified	Published intervals understate true uncertainty	Sensitivity analyses over diagnostic capture and case-fatality assumptions	Low

Relative cost is the author's qualitative judgment of the incremental resource required given existing infrastructure, and is offered to inform sequencing rather than as a costing.

Limitations

This review has limitations that bear directly on how its conclusions should be read. It is narrative rather than systematic. Studies were not screened against pre-specified eligibility criteria by independent reviewers, and selection favoring prominent sources cannot be excluded. A formal systematic review of regional surveillance infrastructure would be a valuable complement and does not, to the author's knowledge, exist [51]. The reference base is deliberately restricted to sources retrieved in full. This protects against the propagation of mis-cited figures but means that relevant regional literature, particularly national surveillance reports from Eastern Mediterranean countries and regional analyses published in the Eastern Mediterranean Health Journal, is underrepresented relative to its importance [52]. Several comparisons are made between figures that are not strictly commensurable: GLASS regional medians, national network resistance proportions and modeled burden estimates differ in population, denominator and method. They are juxtaposed here to illustrate the disconnection that is the subject of the review, not to imply that they are interchangeable [8].

Finally, the quantitative landscape changes with each annual surveillance cycle and each GBD revision. The specific values reported here are current to August 2026 and should be refreshed against the latest releases before use [53].

Conclusion

South Asia and the Eastern Mediterranean Region report some of the world’s highest resistance proportions and are forecast to carry some of the heaviest mortality from antimicrobial resistance. Both of those statements rest on evidence, and neither is

seriously disputed. What is weakly evidenced is the relationship between them. Surveillance in these regions measures resistance among isolates that reach laboratories situated predominantly in tertiary hospitals, selected by a chain of filters: care-seeking, prior antibiotic exposure, laboratory capacity, and reporting completeness, none of which is quantified. Burden estimation requires population incidence, diagnostic capture, and resistance-specific case fatality, of which the regional evidence base supplies almost nothing. The gap between the two is bridged by assumption, and the uncertainty introduced by that bridge is larger than the uncertainty intervals published alongside the estimates. The conclusion is not that the burden estimates should be discounted. They are the best available, and they are probably directionally correct. It is that the next increment of investment in AMR evidence in these regions should be directed not at generating more resistance proportions, which are already abundant, but at measuring the quantities that would make those proportions interpretable: denominators, diagnostic capture and outcomes. Resistance data without denominators tell us what grows in our laboratories. They do not yet tell us what is happening to our populations.

Author Contributions: Conceptualization, R.S..; methodology, R.S.; validation, A.Y.; resources, A.Y.; writing—original draft preparation, R.S.; writing—review and editing, A.Y.; supervision, R.S.; project administration, R.S. Both authors have read and agreed to the published version of the manuscript.

Funding: This research received no external funding.

Data Availability Statement: This review article is based on information obtained from previously published literature and publicly available sources. No new experimental or primary datasets were generated or analyzed in this study. All relevant information and sources are appropriately cited within the manuscript and reference list. The authors are responsible for the accuracy and integrity of the information presented.

Acknowledgments: The authors gratefully acknowledge the authors and researchers whose published scientific contributions provided the foundation for this review. The authors also acknowledge the scientific databases and publicly accessible literature resources used to prepare the manuscript.

Conflicts of Interest: The authors declare no conflict of interest.

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