



NATIONAL INSTITUTE FOR
COMMUNICABLE DISEASES

Division of the National Health Laboratory Service

GERMS-SA ANNUAL SURVEILLANCE REVIEW





Annual Surveillance Training



Meeting 24-25 October 2024

The background of the entire page is a microscopic view of numerous bacteria, likely E. coli, characterized by their rod-like shape, dense covering of flagella, and long, thin, wavy appendages. The image is rendered in a monochromatic teal/cyan color scheme.

2024

**GERMS-SA: ANNUAL
SURVEILLANCE REVIEW**

THE GERMS-SA ANNUAL REVIEW 2024 WAS COMPILED BY THE NATIONAL INSTITUTE FOR COMMUNICABLE DISEASES, A DIVISION OF THE NATIONAL HEALTH LABORATORY SERVICE, JOHANNESBURG, SOUTH AFRICA.

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FOREWORD

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GERMS-SA: REFLECTING ON 21 YEARS OF SURVEILLANCE IMPACT AND LOOKING TO THE FUTURE

In 2024, the NICD's flagship GERMS-SA surveillance programme celebrated its 21st anniversary. GERMS-SA is co-ordinated by the Division of Public Health Surveillance and Response, providing strategic information on diseases of public health importance. The programme measures the impact of vaccines and new treatments (like pneumococcal conjugate vaccine (PCV) and flucytosine), tracks antimicrobial resistance in pathogens, monitors HIV-associated infections such as cryptococcal meningitis, and keeps watch on outbreak-prone diseases like typhoid fever. Surveillance has grown to include neglected tropical diseases (schistosomiasis

and soil-transmitted helminths) and congenital rubella syndrome.

GERMS-SA is primarily laboratory-based, relying on NHLS and private labs to report laboratory-confirmed cases. NICD reference laboratories confirm these cases and conduct specialised testing like serotyping and antimicrobial susceptibility testing. At 30 enhanced sentinel sites, clinical data are also collected through interviews and medical record reviews. Importantly, the network forms a vital link between microbiologists, clinicians, and NICD reference centres.

HOW DID GERMS-SA START?

GERMS-SA began in 1999 with a letter in the South African Medical Journal, endorsed by the Department of Health's Expanded Programme on Immunisation (EPI). The goal was to establish surveillance to measure the impact of the newly introduced *Haemophilus influenzae* type b (Hib) vaccine. A sustainable system

was needed to justify the investment, detect programme failures, determine booster needs, and potentially expand surveillance to other pathogens. Drawing on the US CDC's ABCs model, the full GERMS-SA programme launched in 2003 and continues to this day.

KEY MILESTONES

By 2006, surveillance had expanded nationally, covering nine bacterial and fungal pathogens causing pneumonia, meningitis, and enteric diseases. By 2009, GERMS-SA data were actively informing policy, including HIV-related guideline changes, PCV introduction and a Hib booster in the EPI, and nested studies were initiated, including a case-control study on PCV effectiveness and a post-discharge cryptococcosis outcomes study. From 2015, the programme strengthened quality and integrated into the NICD operational budget. Various syndromic surveillance programmes

were added (severe respiratory illness, influenza -like illness, diarrhoeal disease, TB/HIV, STIs, Acute Febrile Illness, and zoonotic diseases), leveraging GERMS-SA's permanent infrastructure.

Through the years, GERMS-SA has tracked the impact of vaccines (PCV7, PCV13, Hib booster, and rotavirus), antiretroviral scale-up, national reflex CrAg screening, and evolving antifungal regimens. We have monitored declines in vaccine-related invasive paediatric disease (including diarrhoeal disease).

During COVID-19, GERMS-SA was flexible enough to rapidly pivot the respiratory surveillance platforms to include SARS-CoV-2, and this is now the platform for ongoing SARS-CoV-2 surveillance. Through a nested study, GERMS-SA was able to demonstrate prolonged viral shedding of SARS-CoV-2 in hospitalised people living with HIV.

Other highlights include a university meningococcal carriage study which revealed a 200% spike in meningococcal carriage in students during their first week at university, contributions to the WHO “Defeating Meningitis by 2030” initiative, and a pathogen aetiology assessment of sepsis in neonates, Baby GERMS-SA. This surveillance model approach focusing on specific at-risk populations has been expanded to a pathogen aetiology study on adults presenting with advanced HIV, ADVANCE GERMS-SA. GERMS-SA is a valuable platform from which many surveillance systems and research studies have leveraged, giving rise to over 250 publications and numerous master’s and PhD dissertations. Together with public and private sector partnerships, we have built up a critical mass of expertise (including specialists in microbiology, public health medicine, and epidemiology) who feed into an important pool of shared knowledge towards improving health for all.

Challenges along the way

GERMS-SA depends entirely on laboratory participation. In recent years, isolate submissions have declined due to centralisation, staff shortages, renovations, supply issues, and workload pressure. Field staffing is costly, and budget constraints and frozen posts affect data quality. Moving from paper to digital systems has been challenging when infrastructure is unable to stay ahead.

What’s next?

We will continue delivering high-quality surveillance data for public health action and work with NICD IT and the NMC platform toward a more integrated national surveillance system.

A message to partners

Isolate submission remains critical, especially for monitoring serogroup/serotype changes (a practice only routinely performed by the NICD reference laboratories). NICD reference laboratories rely on isolate collection to monitor the impact of vaccine changes (e.g., change from PCV13 to PCV10 (SII) in 2024) across the population. All data are securely stored at the NICD and belong to South Africans. They are available for students, researchers, and future public health leaders.

After 21 years, I may be the “mother” of GERMS-SA (and proud granny of Baby GERMS-SA!), but its success rests on our community: laboratories, clinicians, collaborators, analysts, and supporters nationwide. Thank you for your commitment to keeping South Africans safe and healthy. We hope you are as proud of GERMS-SA as we are.

INTRODUCTION

In 2024, the GERMS-SA surveillance programme, co-ordinated by the National Institute for Communicable Diseases (NICD), marked 21 years of laboratory-based infectious disease surveillance in South Africa. The programme continues to play a central role in tracking disease trends, monitoring antimicrobial resistance, and assessing the impact of public health interventions such as pneumococcal conjugate vaccines and antifungal therapy for cryptococcal meningitis.

Despite challenges including the NHLS cyberattack, supply shortages, and transport delays, surveillance activities remained uninterrupted through strong collaboration between laboratories, surveillance officers, and NICD staff. Integration with the Surveillance Data Warehouse (SDW) and the Notifiable Medical Conditions (NMC) system improved data completeness and the timeliness of reporting.

In 2024, GERMS-SA broadened its scope to include neglected tropical diseases (NTDs), launching a pilot project in Limpopo and Mpumalanga focusing on schistosomiasis and soil-transmitted helminthiasis (STH). This expansion strengthens national monitoring of diseases that disproportionately affect underserved communities.

Looking ahead, GERMS-SA will continue to focus on improving data quality, interoperability, and collaboration to ensure reliable, actionable surveillance data that informs public health action in South Africa.

METHODS

In 2024, diseases under surveillance included:

1. Opportunistic infections associated with HIV, e.g., cryptococcosis
2. Epidemic-prone diseases, e.g., *Neisseria meningitidis*, *Salmonella enterica* serotype Typhi, *Salmonella enterica* serotype Paratyphi A, B, and C, Nontyphoidal *Salmonella* species, *Shigella* species, *Vibrio cholerae*, *Listeria* species, and *Streptococcus pyogenes*.
3. Vaccine-preventable diseases, e.g., *Haemophilus influenzae* type b (Hib), *Streptococcus pneumoniae*, and *Streptococcus agalactiae*.
4. Neglected tropical diseases (NTDs), e.g., schistosomiasis (*Schistosoma* species) and soil-transmitted helminthiasis (*Ascaris lumbricoides*, *Trichuris trichiura*, *Necator americanus*, *Ancylostoma duodenale*, *Strongyloides stercoralis*).

The methods applied by the GERMS-SA surveillance programme have been previously described in detail (1).

In brief, approximately 222 South African clinical microbiology laboratories participated in the surveillance programme in 2024. The estimated population under surveillance in 2024 was 63 million (Table 1). Diagnostic laboratories reported case patients to the NICD using laboratory case report forms, according to standard case definitions. If available, isolates from case patients were submitted on Dorset transport media to the NICD for further phenotypic and genotypic characterisation. From 01 September 2022, *Cryptococcus* isolates from NHLS laboratories

with flucytosine (5FC) access, including all the Western Cape laboratories, were submitted to the NICD for susceptibility testing. Submission from 5FC-access sites ended on 01 July 2024, and cases are now identified through retrospective audits. For this annual report, only data from the current and immediate previous year were analysed. Thus, some fraction of cases reported as incidents in these 2 years might be misclassified because they were not cross-checked against a complete line list of individuals who had cryptococcal meningitis, other culture-positive cryptococcal disease, or antigenaemia in the years prior to the analysis period. This could lead to an overestimation of the disease incidence in these 2 years. Cryptococcal antigenaemia cases were excluded, partly because samples from patients with prior cryptococcal disease may remain CrAg-positive for years, making it difficult to distinguish new disease from previous illness.

Enteric fever, listeriosis, and cholera are category 1 NMCs, and reporting of all cases through the NMC platform by healthcare workers and laboratorians is mandatory. The Centre for Enteric Diseases oversees active surveillance for each condition, following up every notification by liaising with diagnostic laboratories to facilitate isolate referral and with healthcare professionals or Department of Health officials to complete case investigation forms (CIFs). GERMS-SA Surveillance officers at enhanced surveillance sites assist with completing investigation forms for cases identified at their sites.

In January 2024, GERMS-SA launched a pilot laboratory-based surveillance project for schistosomiasis and soil-transmitted helminths (STH) in Limpopo and Mpumalanga to assess diagnostic quality at NHLS laboratories and evaluate *Schistosoma* egg characteristics. Positive samples were re-tested at the Parasitology Reference Laboratory (PRL) using microscopy and PCR, with data verified through the SDW and analysed by province and laboratory to identify trends.

For 2024, at ESS (30 hospitals in 9 provinces), surveillance officers completed clinical case investigation forms electronically using the REDCap database on tablets for patients with eleven laboratory-confirmed diseases: cryptococcosis, invasive pneumococcal disease, invasive meningococcal disease, invasive *Haemophilus influenzae* disease, invasive Group A streptococcus disease, invasive Group B streptococcus disease, invasive *Salmonella* Typhi disease, Paratyphi A,B,C, shigellosis, and listeriosis by case patient interview or hospital medical record review to obtain additional clinical details, including antimicrobial use, vaccination history, HIV status, and patient outcome. Case patients were followed up only for the duration of the hospital admission. Data management was centralised at the NICD. Laboratory, clinical and demographic data from

case patients were recorded on a Microsoft Access database. A surveillance audit was performed for NHLS laboratories in all provinces using the NHLS SDW. For all diseases under surveillance, except cryptococcosis, the audit was designed to obtain basic demographic and laboratory data from additional case patients with laboratory-confirmed disease not already reported to GERMS-SA by participating laboratories. Data from case patients, detected by audit, were included on the surveillance database and have been included in this report. Incidence was calculated using mid-year population estimates for 2023 and 2024 from Statistics South Africa (Table 1) (2). Incidence in the HIV-infected and AIDS populations was calculated for 2023 and 2024, using the Thembisa Model (3) (Table 1). All reported incidence is expressed as cases per 100 000 population, unless otherwise stated. Reported p-values were calculated using the Mantel-Haenszel chi-squared test and p-values <0.05 were considered significant throughout. Ethics approval for the ongoing activities of the surveillance programme was obtained from the Human Research Ethics Committee (Medical), University of Witwatersrand, and from relevant university and provincial ethics committees for other enhanced surveillance sites. Surveillance activities were funded by the NICD/NHLS.

Table 1. Population denominators used to calculate incidence rates, South Africa, 2023 and 2024

Province	General population*		HIV-infected population**	
	2023	2024	2023	2024
Eastern Cape	7 150 858	7 176 230	893 175	905 292
Free State	3 022 882	3 044 050	420 817	421 695
Gauteng	15 639 891	15 931 824	1 963 580	1 994 720
KwaZulu-Natal	12 161 867	12 312 712	1 958 570	1 964 150
Limpopo	6 335 306	6 402 594	647 126	656 596
Mpumalanga	4 984 096	5 057 662	742 786	749 634
Northern Cape	1 356 580	1 372 943	95 686	96 641
North West	4 091 587	4 155 303	524 163	528 951
Western Cape	7 437 324	7 562 588	500 317	511 780
South Africa	62 180 391	63 015 904	7 746 220	7 829 459

Data source: *Statistics South Africa, **Thembisa model

OPERATIONAL REPORT

Co-ordination of meetings

In 2024, GERMS-SA staff involved in both syndromic and laboratory-based surveillance attended a combined annual training workshop held from 24–25 October at the Birchwood Conference Centre in Johannesburg. The workshop marked two important milestones: 15 years of pneumonia surveillance and 21 years of GERMS-SA laboratory-based surveillance in South Africa, recognising the significant contributions of surveillance staff to national public health monitoring. The training aimed to reinforce case definitions, standardise procedures across sentinel sites, and strengthen quality control practices to ensure data accuracy and integrity. Sessions also addressed common data collection challenges and provided practical solutions to improve the completeness of daily reporting.

Surveillance audit

A total of 12 028 surveillance cases were detected by GERMS-SA in 2024. Excluding the cases of cryptococcosis (n=3 729), which are all detected by audit, 2 334/8 299 (28%) of cases were detected by audit of the NHLS Corporate Data Warehouse (Table 2) 5 965/8 299 (72%, target=80%) of episodes had isolates sent by clinical microbiology laboratories to NICD for further characterisation. GERMS-SA constantly strives to reduce the number of cases detected on audit by raising awareness of the surveillance programme; this is important because GERMS-SA is unable to perform additional microbiological characterisation of isolates detected only through audit.

Table 2. Cases detected by surveillance audit by province, 2024

Surveillance case		Percentage of cases detected by audit* n1/n2 (%)	Number of cases detected by audit									
			EC	FS	GA	KZ	LP	MP	NC	NW	WC	SA
Invasive	Cryptococcosis**	3 729/3 729 (100)	623	123	825	810	321	289	62	226	450	3 729
	Non-typhoidal salmonellosis†	231/986 (23)	21	7	113	45	2	12	1	9	21	231
	Shigellosis	11/49 (22)	3	0	3	3	0	0	0	0	2	11
	Listeriosis	27/71 (38)	2	1	14	5	0	0	1	1	3	27
	Enteric fever	19/111 (17)	1	5	7	0	4	0	0	2	19	27
	Meningococcal disease	29/150 (19)	2	2	6	2	0	0	5	0	12	29
	<i>Haemophilus influenzae</i> disease	95/225 (42)	7	5	26	13	3	6	3	1	31	95
	Pneumococcal disease	607/1 927 (31)	75	39	251	71	15	27	12	26	91	607
	<i>Streptococcus pyogenes</i>	327/708 (46)	34	16	125	58	6	11	2	7	68	327
	<i>Streptococcus agalactiae</i>	494/862 (57)	24	31	213	103	12	19	5	23	64	494
Non-invasive	Non-typhoidal salmonellosis†	325/2 308 (14)	49	18	99	76	5	13	4	23	38	325
	Shigellosis	162/872 (19)	35	16	10	52	0	5	1	8	35	162
	Listeriosis	2/2 (100)	0	1	0	0	0	1	0	0	0	2
	Enteric fever	5/28 (18)	0	2	2	0	0	0	0	1	0	5
	Total (excl crypto)	2 334/8 299 (28%)	252	139	867	435	43	98	34	99	367	2 334

Percentage of cases detected by audit = number of cases detected on audit (n1)/total number of cases detected by GERMS-SA (n2) x 100;**Submission of isolates from 5FC-access sites ended on 1 July 2024, therefore all cases of cryptococcal disease are detected by LIS audit and this disease is excluded from the total; †Excludes cases of *Salmonella enterica* serovars Typhi, and serovars Paratyphi A, B and C; EC: Eastern Cape; FS: Free State; GA: Gauteng; KZ: KwaZulu-Natal; LP: Limpopo; MP: Mpumalanga; NC: Northern Cape; NW: North West; WC: Western Cape; SA: South Africa.

Enhanced surveillance site performance indicators

At Enhanced surveillance sites, the total number of cases reported to GERMS-SA declined from 4 852 in 2023 to 2 962 in 2024 partly due to *E. coli* surveillance done in 2023 and not in 2024. Despite this reduction, the proportion of completed case investigation forms (CIFs) remained consistent, with 2 666 of 2 962 cases (90%) completed in 2024 compared to 4 408 of 4 852 (91%) in 2023, achieving the annual target of 90% (Table 3). The decrease in reported cases likely reflects ongoing operational challenges, including temporary disruptions in specimen transport and data flow following the NHLS cyberattack. Delays in patient identification and reduced follow-up opportunities at affected sites also impacted the ability to obtain consent and

conduct interviews. In 2024, 1 510 CIFs (57%) were completed through patient interviews, an improvement from 2023 (44%, 1 956/4 408), though still below the target of 70%.

Since 2007, enhanced surveillance site operational reports (ESSOR) have been provided to the site co-ordinators, laboratory staff, and surveillance officers to enable the site team to regularly review site performance in comparison with set targets. The main objective of these reports is to provide information regarding the overall functioning of the surveillance site by providing indicators of laboratory participation (submission of isolates) and indicators of surveillance officer performance (completion of CIFs). By reviewing these indicators, problems with data collection can be targeted, and recommendations are provided to improve the site performance.

Table 3. Enhanced surveillance site performance indicators, 2024

Enhanced surveillance site	Case patients, n	Completed case investigation forms*, n (%)**		Case investigation forms completed by interview, n (%)***	
Addington	45	39	87	27	69
Charlotte Maxeke Johannesburg Academic	202	197	98	137	70
Chris Hani Baragwanath/ Zola-Jabulani District	432	409	95	215	53
Dr George Mukhari	114	113	99	65	58
Edendale/ Greys/ Northdale	163	157	96	116	74
Groote Schuur/ Red Cross	371	324	87	175	54
Helen Joseph/ Rahima Moosa Mother & Child	230	206	90	147	71
Kimberley/ Robert Mangaliso Sobukwe	61	58	95	31	53
King Edward VIII	91	71	78	47	66
Klerksdorp/ Tshepong	127	104	82	70	67
Mankweng/ Polokwane/ Seshego	114	102	89	60	59
Pelonomi/ Universitas/ National district	107	90	84	35	39
Port Elizabeth/ Dora Nginza/ Livingstone	426	361	85	168	47
RK Khan	87	76	87	40	53
Rob Ferreira/ Themba	87	85	98	48	56
Steve Biko Pretoria Academic/ Tshwane District	117	98	84	47	48
Tygerberg	188	176	94	82	47
Total	2 962	2 666	90	1 510	57

Note - The percentage (in brackets) in each cell was calculated using the numerator from that cell and the corresponding denominator from the cell to the left; *increased investigation form completion rates after re-training SOs and improved monitoring/ evaluating systems at sites. Patient interviews still low at certain sites due to delayed notifications therefore patients discharged/ demised before alert. Kimberley, shared post with NMC therefore most CIFs completed by medical reviews (which are a challenge to access); **Target = 90%; ***Target = 70%.

Enhanced surveillance site quality monitoring

In 2024, as part of annual performance monitoring and ongoing efforts to improve data quality, surveillance officers underwent routine audits to assess the accuracy and completeness of CIFs. CIFs from a defined time period were randomly selected for each SO, ensuring that all pathogens were represented in the review. Medical record files were retrieved, and GERMS-SA co-

ordinating staff completed clean CIFs from the original source data, which were then compared with the surveillance officers' submitted versions. A standardised scoring system was used to evaluate performance. While results varied across surveillance officers, most discrepancies were due to missing or overlooked information rather than incorrect entries. Regular refresher training sessions were conducted to address these gaps and strengthen data accuracy.

SURVEILLANCE REPORTS

Enhanced surveillance site project

In 2024, 2 683 surveillance case patients were diagnosed at enhanced surveillance sites. Of case patients with recorded HIV status, 55% (1 181/2 149) were HIV-infected (Table 4). The proportion of case patients with confirmed HIV infection varied by surveillance disease: unsurprisingly, a very high proportion of

patients with AIDS-defining infections like cryptococcosis (96%) were HIV-infected. HIV infection amongst patients with invasive pneumococcal disease, for which HIV is a known risk factor, was 51%.

Table 4. Numbers and percentage* of patients diagnosed with laboratory-confirmed invasive disease at GERMS-SA enhanced surveillance sites, with confirmed HIV-1 infection **, South Africa, 2024

Pathogen	Case patients, n	Case patients with completed case investigation forms, n (%)*	Case patients with known HIV status, n (%)	Case patients with confirmed HIV infection, n (%)**
<i>Cryptococcus</i> species	779	682 (88)	655 (96)	628 (96)
<i>Neisseria meningitidis</i>	44	41 (93)	39 (95)	7 (18)
<i>Streptococcus pneumoniae</i> [^]	828	735 (89)	711 (97)	366 (51)
<i>Haemophilus influenzae</i> [^]	96	90 (94)	84 (93)	31 (37)
<i>Streptococcus pyogenes</i>	369	323 (88)	304 (94)	83 (27)
<i>Streptococcus agalactiae</i> [^]	412	369 (90)	356 (96)	66 (19)
Total	2 683	2 434 (91)	2 149 (88)	1 181 (55)

*The percentage (in brackets) in each cell was calculated using the numerator from that cell and the corresponding denominator from the cell to the left. **HIV infection was confirmed by an age-appropriate, laboratory test and recorded by surveillance officers at enhanced surveillance sites. [^] co-infections counted separately under each pathogen: 3 *Streptococcus pneumoniae* and *Haemophilus influenzae* mixed episodes, 1 *Streptococcus pyogenes* and *Haemophilus influenzae* mixed episode, 1 *Neisseria meningitidis* and *Haemophilus influenzae* mixed episode.

Cryptococcus species

Results

During 2024, 4 023 episodes of laboratory-confirmed cryptococcal disease were reported. This included 3 729 first episodes (93% of total) and 294 recurrent episodes (Table 5). By comparison, 4 528 episodes were detected in 2023, of which 4 148 were incident and 380 were recurrent. Compared to 2023, a notable decrease in the monthly number of cases was observed from May to August 2024 (Figure 1). A majority (n=3 489, 93%) of the incident cases were diagnosed as cryptococcal meningitis (laboratory tests on cerebrospinal fluid positive for *Cryptococcus* species), 4% (n=151) as fungaemia (*Cryptococcus* species cultured from blood), and 2% (n=89) as culture-positive disease at other sites (Table 6). The national incidence risk of laboratory-confirmed cryptococcosis declined from 54 (95% confidence interval [CI], 52-55) in 2023 to 48 (95% CI, 46-49) cases per 100 000 people living with HIV in 2024 (Table 7). The incidence risk was stable in all provinces (as evidenced by overlapping CIs), except in the North West, where it declined. Males accounted for 61% (2 250/3 694) of the cases, and the highest incidence risk of cryptococcal disease in the general population was recorded among males aged 40-44 years. The peak incidence among females, though lower than for males, was also among those aged 40-44 years

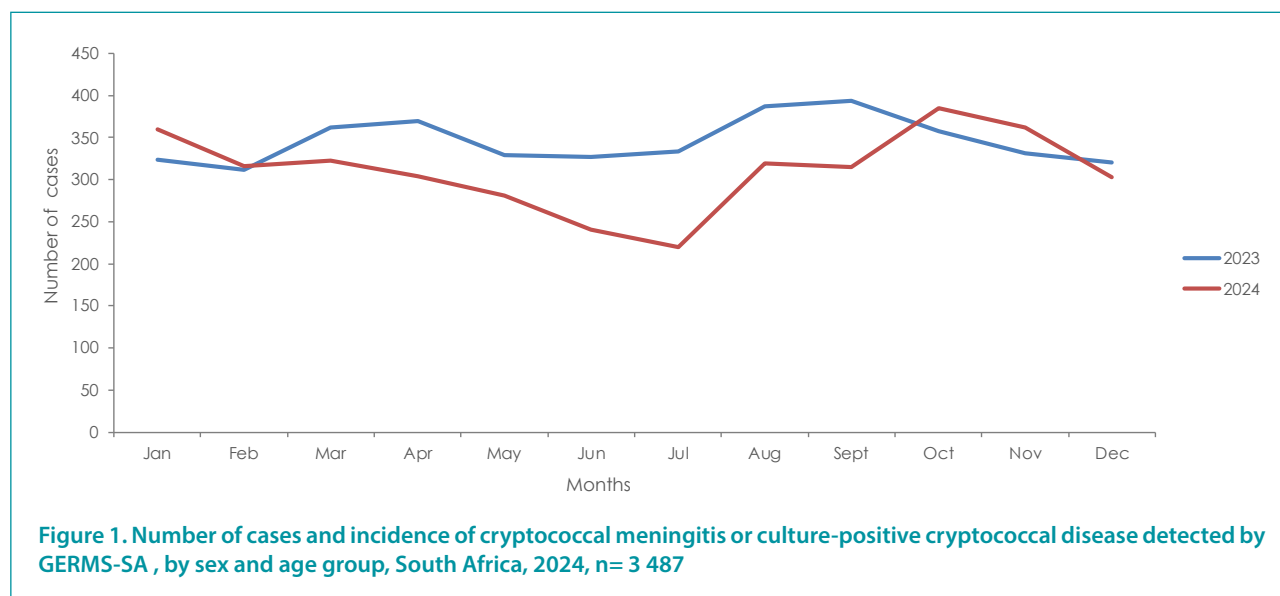
(Figure 2). Age was known for 3 514 (94%) case patients; their median age was 38 years (interquartile range [IQR], 32-46 years) and children younger than 15 years accounted for only 3% of cases (n=112).

There were 779 case-patients with a first episode reported at an ESS during 2024, and case report forms were completed for 88% (n=682). Among 655 patients with known HIV status, 96% (n=628) were living with HIV. More than half of patients with HIV (57% [362/628]) had previously received antiretroviral therapy (ART) or were on ART at the time of their cryptococcal disease diagnosis. The median CD4 cell count recorded close to the time of cryptococcal disease was 31 cells/ μ L (IQR, 12-70 cells/ μ L); 93% (514/553) had a CD4 cell count <200 cells/ μ L. Viral load test results were available for 408 patients; 26% (n=108) had a viral load of <400 copies/mL, 13% (n=53) had viral loads of 400-10 000 copies/mL, and 60% (n=247) had viral loads of >10 000 copies/mL. Most of the case patients received antifungal therapy in hospital (89%, 596/669); 57% (325/570) received a flucytosine-containing induction regimen. The in-hospital case-fatality ratio for patients at ESS with a first episode of cryptococcal disease was 35% (234/670). The crude in-hospital mortality was similar among individuals who did not receive a flucytosine-containing induction regimen (36% [88/243]) compared to those who did (31% [107/345]; p=0.21).

Table 5: Number of incident and recurrent episodes of cryptococcal meningitis or culture-positive cryptococcal disease detected by GERMS-SA, South Africa, 2023-2024, n=8 551

Year	Cases (incident episodes)	Total recurrent episodes*	Total episodes
2023	4 148	380	4 528
2024	3 729	294	4 023
Total	7 877	674	8 551

*Some cases had more than one recurrent episode.

**Table 6: Number and percentage of cases of cryptococcal meningitis or culture-positive cryptococcal disease detected by GERMS-SA by specimen type, South Africa, 2023-2024, n=7 877**

Site of specimen	2023		2024	
	n*	%	n*	%
Cerebrospinal fluid	3 933	95	3 489	93
Blood	145	3.49	151	4.05
Other	70	1.69	89	2.39
Total	4 148		3 729	

*These case numbers exclude 1 684 patients (968 in 2023 & 716 in 2024) who tested positive for cryptococcal antigenaemia at NHLS microbiology labs.

Table 7: Number of cases and incidence of cryptococcal meningitis or culture-positive cryptococcal disease detected by GERMS-SA by province, South Africa, 2023-2024, n=8 551

Province	2023		2024	
	n	Incidence risk (95% CI) [†]	n	Incidence risk (95% CI) [†]
Eastern Cape	683	76 (71-82)	623	69 (63-74)
Free State	131	31 (26-36)	123	29 (24-33)
Gauteng	920	47 (44-50)	825	41 (39-44)
KwaZulu-Natal	929	47 (44-50)	810	41 (38-44)
Limpopo	303	47 (42-52)	321	49 (44-54)
Mpumalanga	302	41 (36-45)	289	39 (34-43)
Northern Cape	54	56 (41-71)	62	64 (48-80)
North West	292	56 (49-62)	226	43 (37-48)
Western Cape	535	107 (98-116)	450	88 (80-96)
South Africa	4 148	54 (52-55)	3 729	48 (46-49)

*These case numbers exclude patients who tested positive for cryptococcal antigenaemia.

[†]Incidence risk was calculated using mid-year population denominators determined by the Thembeisa model and is expressed as cases per 100 000 HIV-infected persons (refer to Table 1).

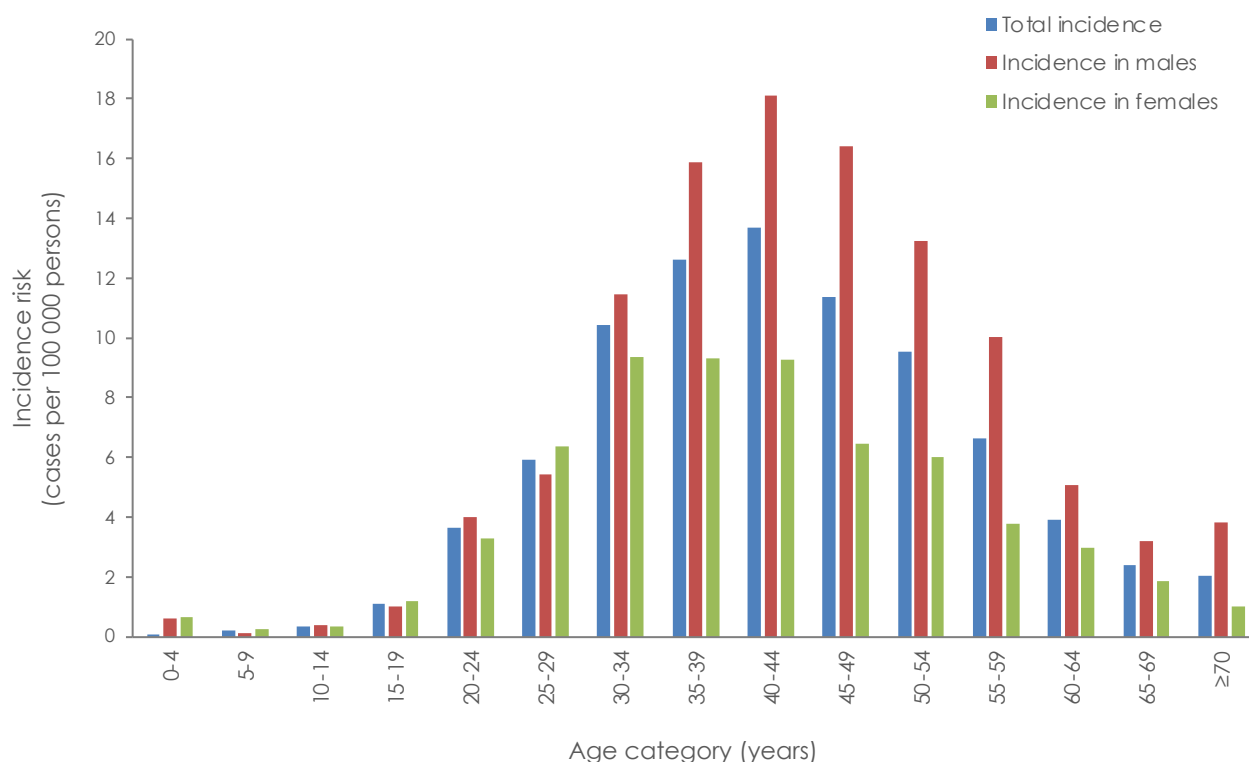


Figure 2. Number of cases of cryptococcal meningitis or culture-positive cryptococcal disease detected by GERMS-SA, by month and year, South Africa, 2023 - 2024, n= 7 877

Discussion

In 2024, the total number of episodes of cryptococcal meningitis and culture-confirmed cryptococcal disease, including recurrent disease, declined compared to 2023. The apparent decline in 2024 must be interpreted cautiously, as the NHLS laboratory information system cyberattack probably caused significant data capture disruptions, resulting in a potential underestimation of true case numbers. Despite a national-level decline in incidence risk, cryptococcosis incidence remained similar in most provinces. Males continued to account for the highest disease incidence, suggesting that current public health strategies may not be adequately reaching this key group. Development of tailored, male-specific strategies to improve testing access,

linkage to care, and ART adherence within this population is warranted. Moreover, nearly all case-patients living with HIV had advanced immunosuppression and an unsuppressed viral load, reflecting missed opportunities for earlier HIV care interventions and ART optimisation. The in-hospital case-fatality ratio at ESS was high. While it is encouraging that more than half of patients did receive a flucytosine-based induction regimen, the need to improve access to and uptake of guideline-recommended therapy must be emphasised, as persistent hindrances such as stock-outs continue. Cryptococcal disease continues to be a significant burden on patients and the healthcare system. There is an urgent need for better HIV care integration and a focus on ensuring unhindered access to early diagnosis and essential antifungal medications to reduce mortality.

Neisseria meningitidis

Results

In 2024, 150 laboratory-confirmed episodes of invasive meningococcal disease (IMD) were reported through the GERMS-SA surveillance programme, a 40% increase from 2023 (n=107). Sixty-two (41%) viable isolates were sent to the NICD for further characterisation, 59 (40%) episodes were confirmed and characterised through molecular methods only, and 29 (19%) episodes were detected through an audit of the NHLS laboratory information system (Table 2). Incidence of IMD continued to increase from 0.12 per 100 000 people in 2022 to 0.18 per 100 000 in 2023 and 0.24 per 100 000 in 2024, exceeding levels experienced in 2019 (pre-COVID-19 pandemic) (Figure 3). The Western Cape province had the highest incidence of IMD at 0.81 per 100 000 (Table 8). IMD occurred in people of all age categories; however, more than 50% of episodes were in children <15 years, with the highest peak in children <1 year of age (2.4 episodes per 100 000) (Figure 4). No clusters were reported in 2024, and most episodes occurred between May and October (Figure 5). Where sex was known, more males (81/147, 55%) were affected than females. Fifty-seven per cent (85/150) of IMD episodes were confirmed from cerebrospinal fluid, 42% (63/150) from blood and 1% (2/150) from other specimen types (joint fluid and intra-orbital fluid) (Table 9). Among episodes with isolates or specimens with serogroup results (100/150, 75%), 35% (35/100) were serogroup B, 10% (10/100) were serogroup C, 26% (26/100) were serogroup W, 26% (26/100) were serogroup Y, and 3 were non-groupable

(Table 10). Besides serogroup B dominating the <1-year age category, serogroup B, C, W, and Y distribution varied across all age categories (Figure 6). Of viable isolates, 69% (43/62) were susceptible to penicillin, 29% (18/62) had intermediate susceptibility (penicillin minimum inhibitory concentrations (MIC) between 0.094 and 0.25 µg/ml), and 2% (1/62) were penicillin resistant (MIC 0.38 µg/ml). All viable isolates were susceptible to third-generation cephalosporins, ciprofloxacin, rifampicin and nalidixic acid.

In 2024, 93% (41/44) of IMD episodes at enhanced surveillance sites had clinical data collected (Table 4). Median age was seven years (interquartile range (IQR) 1-31 years), and patients stayed a median of seven days (IQR 6-14 days) in hospital. Ninety per cent (37/41) were admitted with meningitis. The in-hospital case fatality was 12% (5/41), with a median time to death within 24 hours of admission (IQR 1-3 days). Eighteen per cent (7/39) of people with known HIV-infection status were people living with HIV (Table 4). Thirty-three per cent (12/36) of people who survived the IMD hospital admission were discharged with sequelae. Three people had two sequelae each (one had hearing loss and neurological deficit, one developed hydrocephalus and new-onset seizures, and one had visual loss and skin scarring). Of the other nine people with sequelae, five developed new-onset seizures and four had a neurological deficit (limb weakness).

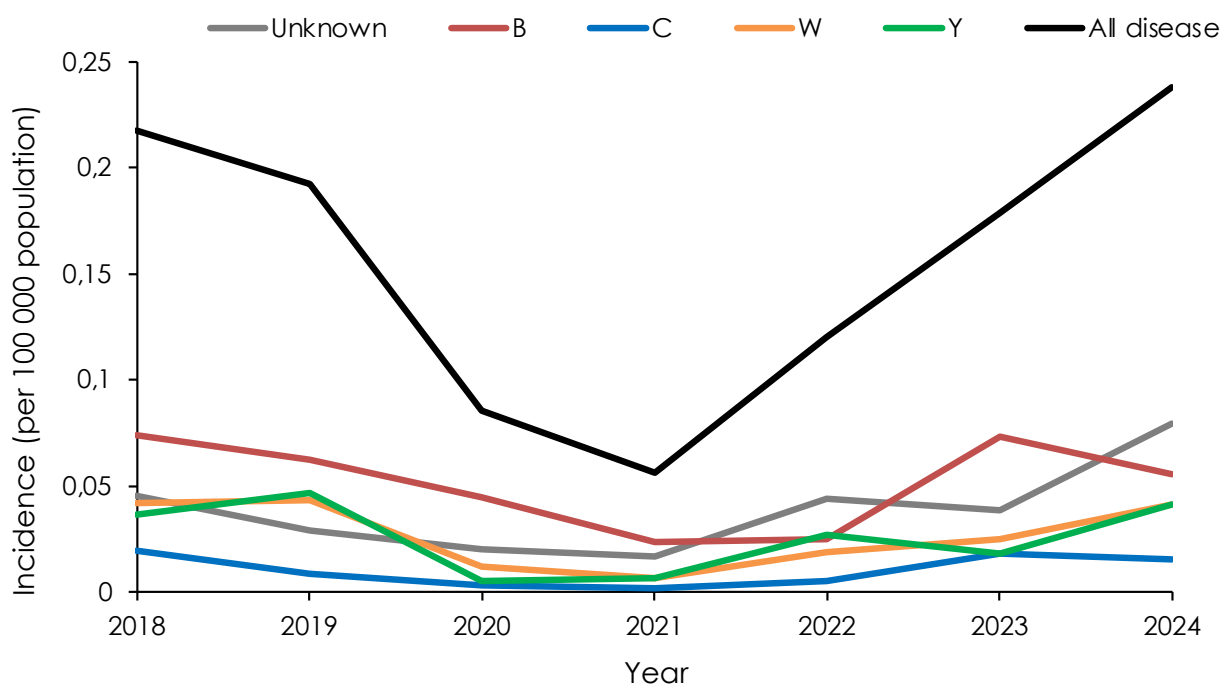
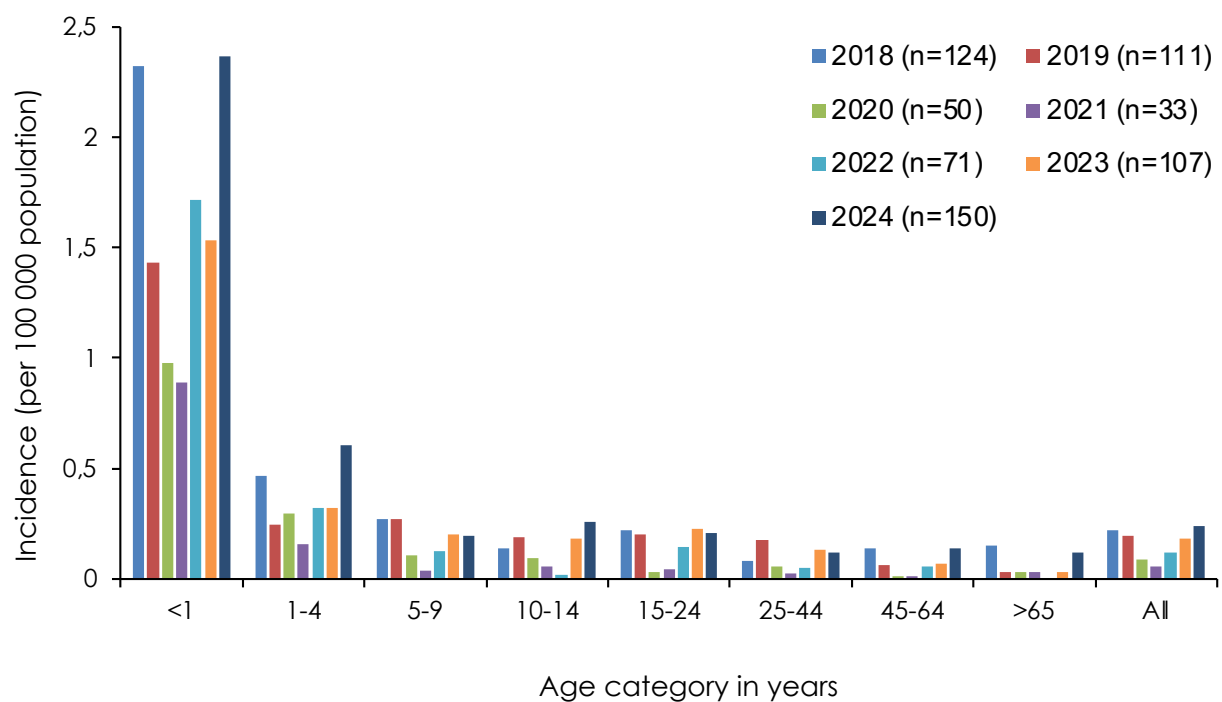


Figure 3. Incidence of invasive meningococcal disease by serogroup, South Africa, 2018-2024 (N=646)

Table 8: Number of cases and incidence of meningococcal disease reported to GERMS-SA by province, South Africa, 2019-2024, N=522 (including audit cases)

Site of specimen	2019		2020		2021		2022		2023		2024	
	n	Incidence	n	Incidence	n	Incidence	n	Incidence	n	Incidence	n	Incidence
Eastern Cape	12	0.18	6	0.09	5	0.07	5	0.07	12	0.15	25	0.35
Free State	3	0.10	0	0.00	0	0.00	3	0.10	4	0.13	5	0.16
Gauteng	37	0.24	10	0.06	8	0.05	23	0.14	32	0.21	39	0.24
KwaZulu-Natal	13	0.12	4	0.03	3	0.03	6	0.05	9	0.08	8	0.06
Limpopo	2	0.03	1	0.02	0	0.00	3	0.05	2	0.03	3	0.05
Mpumalanga	1	0.02	1	0.02	1	0.02	2	0.04	0	0.00	0	0.0
Northern Cape	1	0.08	0	0.00	0	0.00	1	0.08	3	0.22	7	0.51
North West	4	0.10	1	0.02	1	0.02	2	0.05	2	0.05	2	0.05
Western Cape	38	0.56	27	0.39	15	0.20	26	0.35	43	0.56	61	0.81
South Africa	111	0.19	50	0.08	33	0.05	71	0.12	107	0.18	150	0.24

* Incidence were calculated based on population denominators provided by the Stats-SA, and are expressed as cases per 100 000 population.

**Figure 4. Incidence of invasive meningococcal disease by age-category, South Africa, 2018-2024 (N=646)**

(Age unknown for 2 episodes: 2018 n=1 and 2024 n=1)

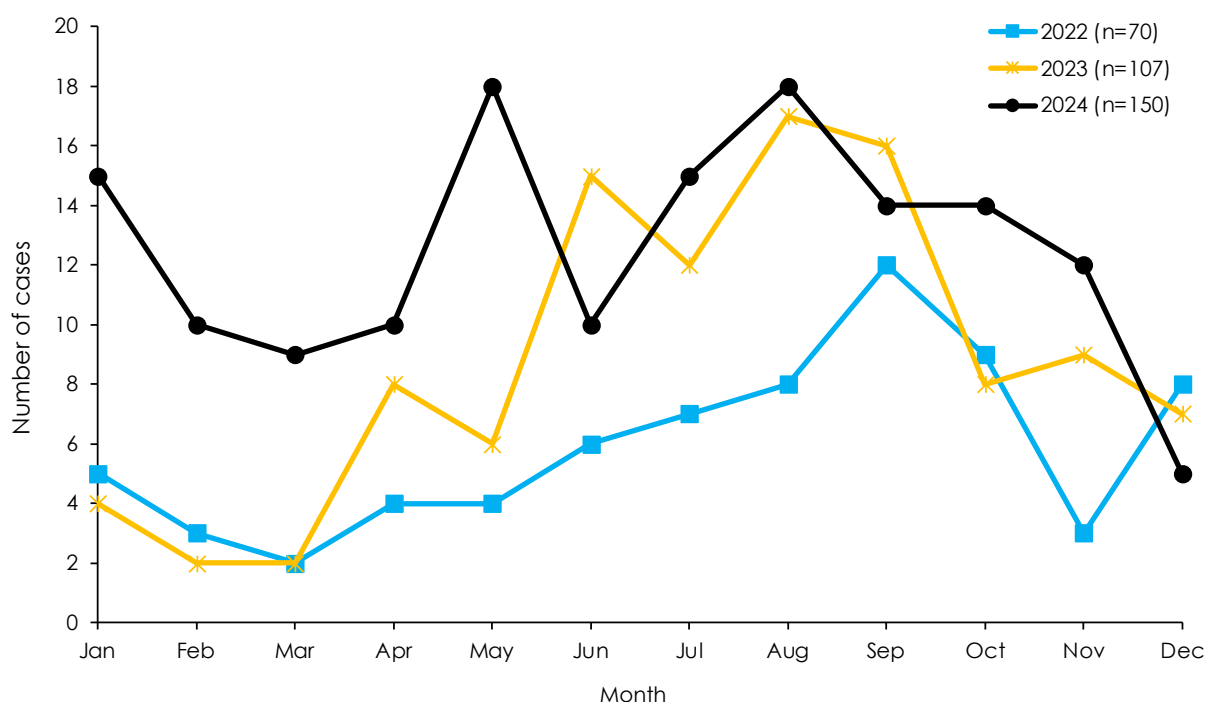


Figure 5. Number of laboratory-confirmed, invasive, meningococcal cases, reported to GERMS-SA, by month and year, South Africa, 2022-2024 (N=328)

Table 9: Number and percentage of cases of meningococcal disease reported to GERMS-SA by specimen type, South Africa, 2019-2024, N=522

Site of specimen	2019		2020		2021		2022		2023		2024	
	n	%	n	%	n	%	n	%	n	%	n	%
Cerebrospinal fluid	70	63	24	48	20	61	46	65	73	68	85	57
Blood	41	37	26	52	13	39	25	35	34	32	63	42
Other	0	0	0	0	0	0	0	0	0	0	2	1
Total	111		50		33		71		107		150	

Table 10: Number of cases of invasive meningococcal disease reported to GERMS-SA by serogroup and province, South Africa, 2024, N=150*

Province	Serogroup							
	Serogroup not available	A	B	C	W	Y	NG	Total
Eastern Cape	6	0	6	4	2	6	1	25
Free State	2	0	1	0	1	1	0	5
Gauteng	16	0	8	3	7	3	2	39
KwaZulu-Natal	3	0	3	0	1	1	0	8
Limpopo	0	0	1	0	1	1	0	3
Mpumalanga	0	0	0	0	0	0	0	0
Northern Cape	5	0	2	0	0	0	0	7
North West	0	0	1	0	0	1	0	2
Western Cape	18	0	13	3	14	13	0	61
South Africa	50	0	35	10	26	26	3	150

*100/150 (75%) had viable isolates or specimens available for serogrouping/genogrouping; NG: Non-groupable unencapsulated meningococcal isolates

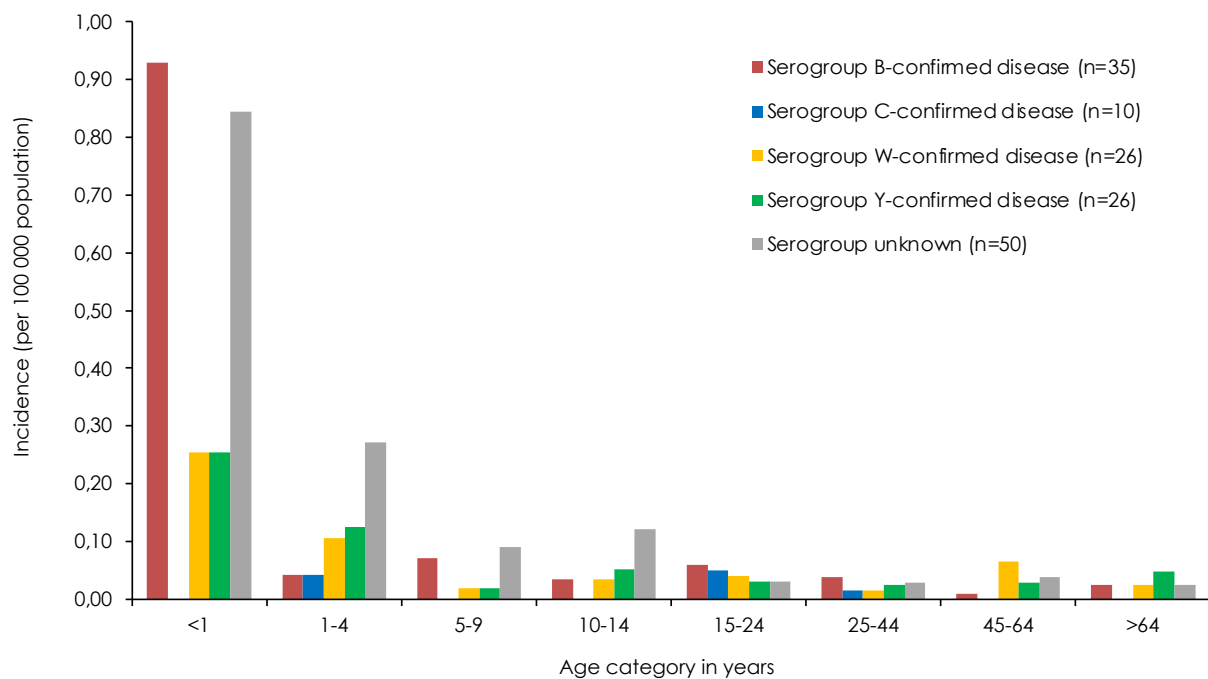


Figure 6. Age-specific incidence* for laboratory-confirmed, invasive, meningococcal cases, by serogroup B, C, W and Y, South Africa, 2024, N=150 (**specimens or viable isolates unavailable for serogrouping n=50, non-groupable disease n=0).**

*Incidence were calculated based on population denominators provided by Stats-SA, and are expressed as cases per 100 000 population.

Discussion

IMD incidence in South Africa has been steadily increasing since 2021 and has now exceeded that of 2019 (whereafter many respiratory-transmitted infections decreased as a result of various COVID-19 containment measures). A variety of serogroups, including serogroups B, C, W, and Y, are causing sporadic episodes of IMD across all age categories in all provinces of South Africa, with no particular pattern emerging. However, serogroup B continues to dominate amongst infants where IMD incidence is highest. Fortunately, the proportion of penicillin-susceptible isolates has increased since 2023 (from 50% to 69%), and all tested isolates were fully susceptible to antibiotics used for empiric antibiotic treatment of meningitis and for chemoprophylaxis in close contacts of cases.

Although still occurring infrequently, meningococcal disease has a poor outcome in those affected even when adequate antibiotic cover is provided. Clinicians are urged to consider the diagnosis in any person presenting with fever and/or headache with rapid clinical deterioration. On suspicion of IMD, immediate initiation of third-generation cephalosporin or high-dose intravenous penicillin is recommended.

Two meningococcal vaccines are available in South Africa (a quadrivalent conjugate vaccine against serogroups A, C, W, and Y and a recombinant vaccine against serogroup B); however, neither are available through the routine infant immunisation programme and individuals wishing to prevent meningococcal disease are required to pay for the vaccine out of pocket. People in whom meningococcal vaccination should be considered include young infants, children and adolescents; people living and working in close communities (military, mining, student hostels), laboratory workers routinely exposed to *Neisseria meningitidis* cultures, travellers to hyperendemic areas (African meningitis belt countries and Saudi Arabia), and those with underlying medical conditions affecting complement mediated immunity.

Haemophilus influenzae

Results

In 2024, 225 episodes of invasive *Haemophilus influenzae* (HI) disease were identified through the GERMS-SA surveillance programme. Of these, 79 (35%) viable isolates were received by the NICD for further characterisation, 51 (23%) episodes were diagnosed through molecular methods only, and 95 (42%) episodes were detected through an audit of the NHLS laboratory information system (Table 2). Eight people were co-infected with another bacterial pathogen: six with *Streptococcus pneumoniae*, one with *Neisseria meningitidis*, and one with *Streptococcus pyogenes*. In South Africa, the incidence of invasive HI was 0.36 per 100 000 population (lower than 2023: 0.50 per 100 000 and 2022: 0.58 per 100 000) (Figure 7). Incidence was highest in the Western Cape province (1.03 per 100 000 population) (Table 11). In 2024, the incidence of HI dropped in almost all age categories, with infants (3.63 per 100 000) and children aged 1-4 years (0.75 per 100 000) having the highest incidence of HI disease (Figure 8). Of the 49% (110/225) of episodes with known serotypes, the majority of invasive HI episodes were caused by non-typeable (HNT, 57/110), followed by serotype b (Hib, 25/110) disease (Table 11). Serotypes a, d, e, and f were also detected in 11, 3, 5, and 9 episodes, respectively. The incidence of HNT disease was highest in all age groups, besides children aged 5-9 years, where Hib was slightly more common (Figures 9 and 10). For all HI serotypes, most invasive episodes were detected from blood specimens (64%, 144/225); however, significantly more Hib episodes (32%, 8/25) were identified from CSF than HNT episodes (7%, 4/57) ($p < 0.001$) (Table 12). Thirteen per cent (10/79) of HI cases were non-susceptible to ampicillin (MICs $> 1 \mu\text{g/ml}$), compared to 20% (30/148) in 2023 and 8% (12/156) in 2022. Isolates non-susceptible to ampicillin in 2024 by serotype included 33% (6/18) of Hib, 7% (3/45) of HNT and 6% (1/16) of serotype f episodes.

At enhanced surveillance sites, 94% (90/96) of HI episodes had clinical information collected (Table 4). Median admission duration was 9 days (interquartile range (IQR) 5-18 days). Twenty-three per cent (21/90) of patients died in hospital, with a median time to death of one day (IQR 0-9 days) from the specimen collection date. Deaths occurred with all serotypes and in all age categories. Of those tested for HIV, 37% (31/84) were living with HIV. (Table 4) Other conditions predisposing to HI disease were reported in 71% (64/90) of patients – the most common conditions included prematurity (born < 37 weeks gestation) in infants (64%, 7/11), ever having tuberculosis (19%, 17/90), chronic lung disease (excluding TB) (10%, 9/90), malignancy (7%, 6/90), diabetes (4%, 4/90), and chronic renal disease (4%, 4/90).

Of patients from ESS with meningitis, 21% (3/14) died, and 27% (4/11) who were discharged from hospital suffered long-term sequelae. One developed new-onset seizures, one developed hearing loss, one had limb weakness, and one developed new-onset seizures plus hydrocephalus.

Hib conjugate vaccination history was available for four of the five children aged < 15 years admitted to ESS with Hib infection. One child was too young (< 8 weeks) to have received any Hib vaccine, and two HIV-unexposed, uninfected children < 18 months of age had received three doses each. The fourth child, aged 8 years, had received three doses of Hib vaccine plus the 18-month booster dose; however, they were living with HIV infection, severely immunocompromised, and had concurrently been diagnosed with tuberculosis.

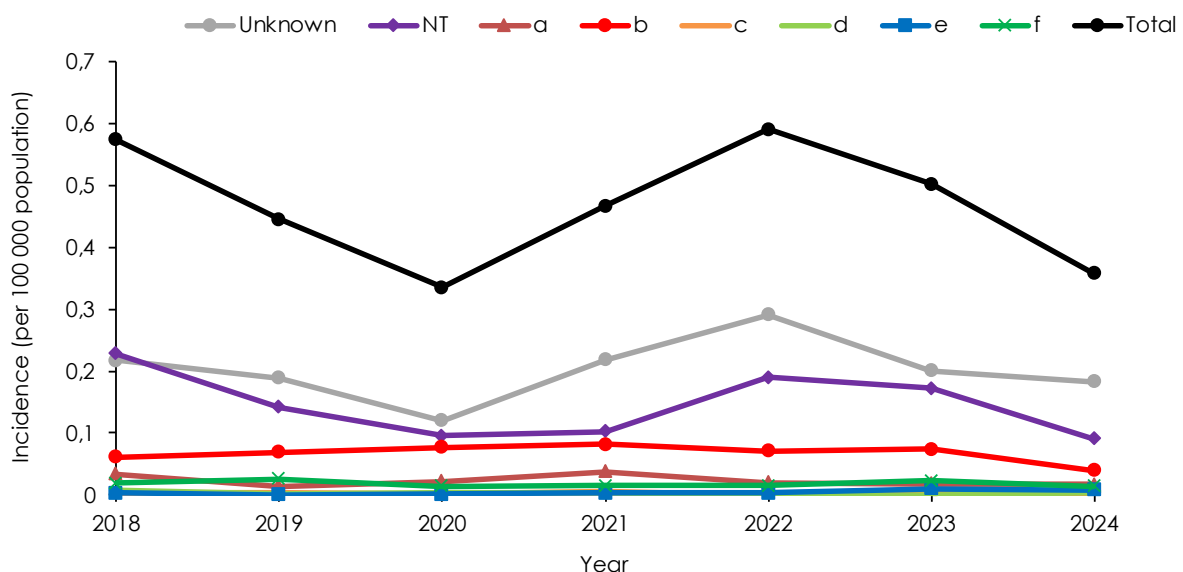


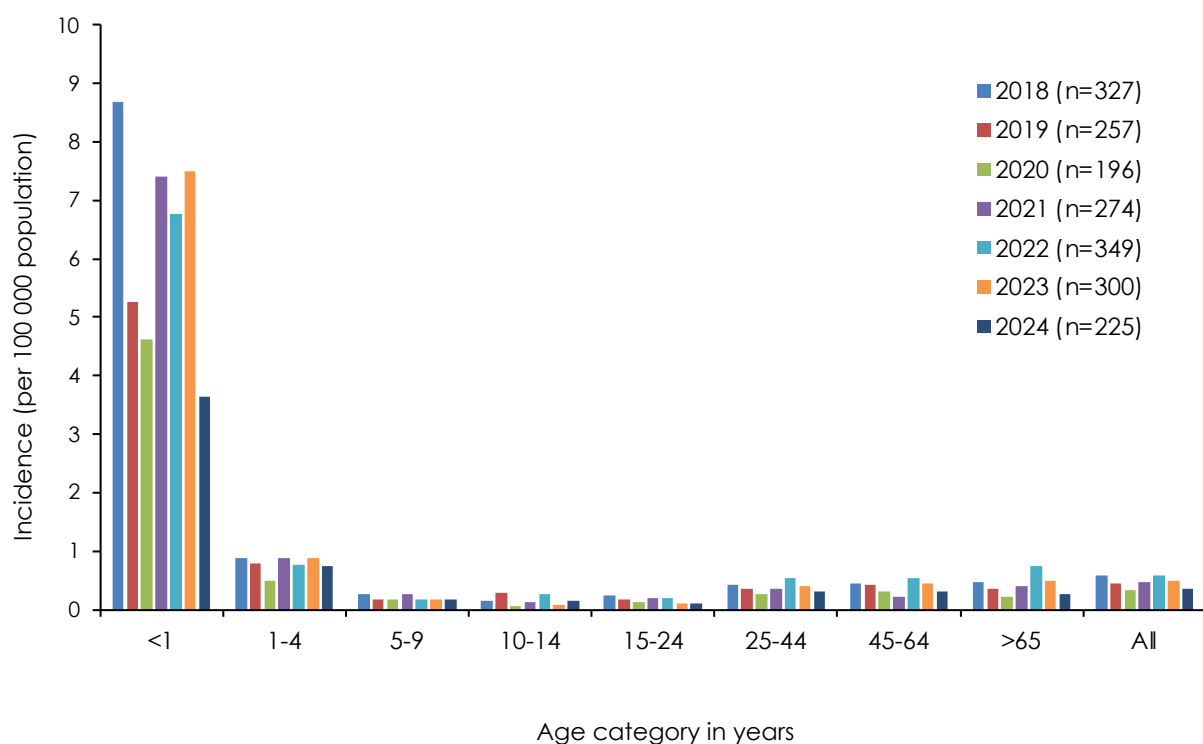
Figure 7. Incidence of invasive *Haemophilus influenzae* disease by serogroup, South Africa, 2018-2024 (N=1 928)

Table 11: Number of cases and incidence of invasive *Haemophilus influenzae* disease reported to GERMS-SA by serotype and province, South Africa, 2024, N=225*

Province	Serotype								Total	Incidence per 100 000 population†
	Serotype not available	A	B	C	D	E	F	Non-typeable		
Eastern Cape	11	1	4	0	0	0	1	7	24	0.33
Free State	6	0	1	0	0	1	2	1	11	0.36
Gauteng	34	2	11	0	1	1	3	14	66	0.41
KwaZulu-Natal	14	1	1	0	0	0	0	5	21	0.17
Limpopo	4	0	1	0	1	0	0	0	6	0.09
Mpumalanga	7	0	0	0	0	0	0	2	9	0.18
Northern Cape	4	0	0	0	0	0	0	1	5	0.36
North West	2	1	1	0	0	0	0	1	5	0.12
Western Cape	33	6	6	0	1	3	3	26	78	1.03
South Africa	115	11	25	0	3	5	9	57	225	0.36

*110 (49%) with specimens or viable isolates available for serotyping.

†Incidence were calculated based on population denominators provided by Stats-SA, and are expressed as cases per 100 000 population.

**Figure 8. Incidence of invasive *Haemophilus influenzae* disease by age-category, South Africa, 2018-2024 (N=1 928)**

(Age unknown for 65 episodes: 2018 n=9, 2019 n=2, 2020 n=8, 2021 n=9, 2022 n=14, 2023 n=12 and 2024 n=11)

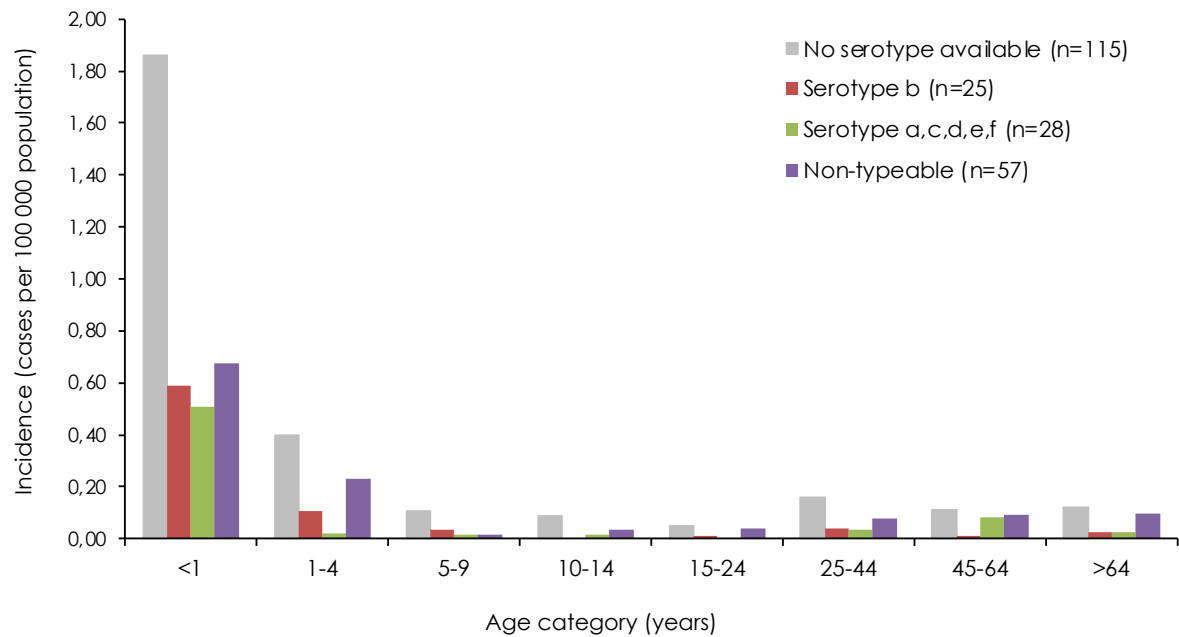


Figure 9. Age-specific incidence* for laboratory-confirmed, invasive *Haemophilus influenzae* disease, reported to GERMS-SA, by serotype, South Africa, 2024, N=225 (age unknown, n=11; isolates unavailable for serotyping, n=121).

*Incidence rates were calculated based on population denominators provided by Stats-SA, and are expressed as cases per 100 000 population.

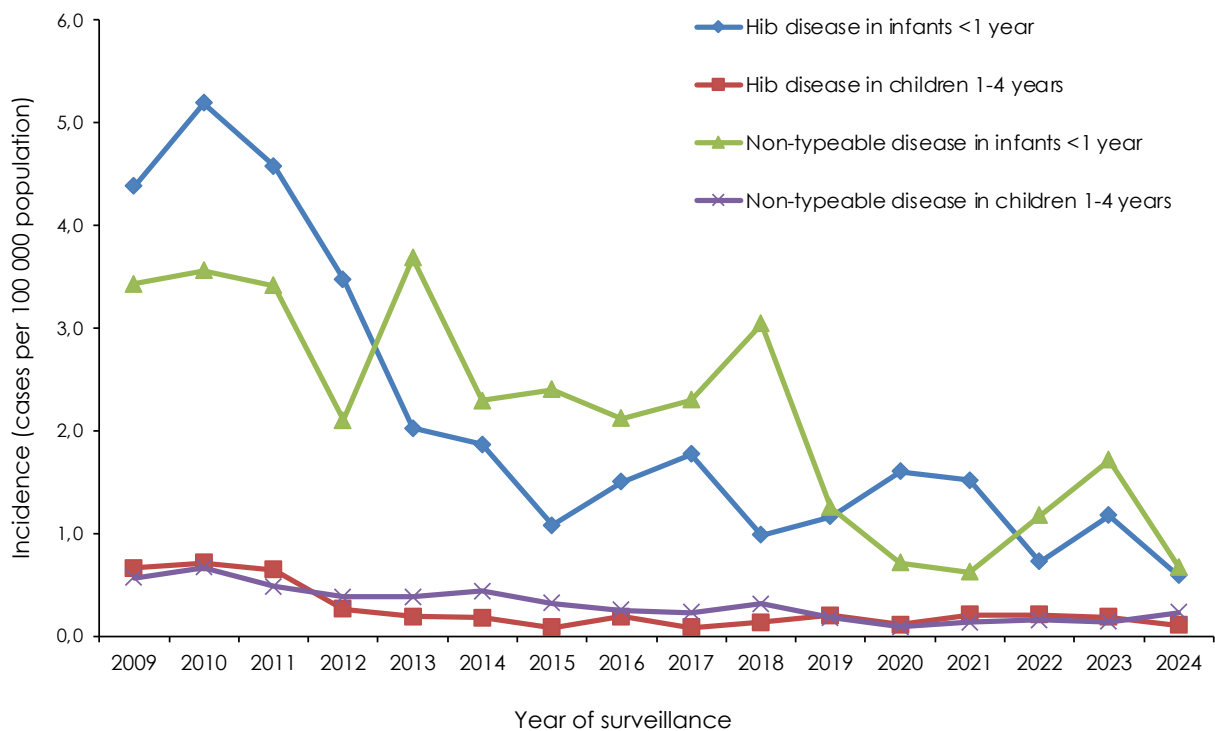


Figure 10. Incidence* of laboratory-confirmed, *Haemophilus influenzae* serotype b and non-typeable disease, reported to GERMS-SA, in children <5 years old, South Africa, 2009-2024.

*Incidence rates were calculated based on population denominators provided by Thembisa model, and are expressed as cases per 100 000 population.

Table 12: Number and percentage of cases of invasive *Haemophilus influenzae* disease reported to GERMS-SA by specimen type, South Africa, 2024, N=225

Site of specimen	No serotype available		Serotype b		Serotypes a, c, d, e, f		Non-typeable	
	n	%	n	%	n	%	n	%
Cerebrospinal fluid	23	20	8	32	6	21	4	7
Blood	62	54	16	64	18	64	48	84
Other	30	26	1	4	4	14	5	9
Total	115		25		28		57	

Discussion

HI incidence has steadily decreased since 2022, with declines noted in both HNT and Hib disease. Infants and children aged 1-4 years have the highest burden of disease for all serotypes. The Western Cape province continues to report a higher incidence of HI disease than all other provinces. In 2023, an increase in ampicillin-resistant HI isolates had been noted. In 2024, the overall ampicillin susceptibility increased from that of 2023; however, susceptibility of Hib isolates to ampicillin remained

similar to 2023 (see 2023 GERMS-SA Annual Report). In-hospital case fatality following HI infection was high, and over one in four people surviving hospital admission were discharged with significant complications of HI infection. All children with Hib disease and vaccination histories available were appropriately vaccinated for age; therefore, close monitoring is needed to detect any patterns of vaccine failures.

Streptococcus pneumoniae

Results

In 2024, 1 927 episodes of laboratory-confirmed invasive pneumococcal disease (IPD) were reported to the GERMS-SA surveillance programme. This included 1 129 viable isolates (59%) sent to the NICD for further characterisation, 191 (10%) episodes identified through molecular testing, and 607 (31%) detected through the NHLS laboratory information system (Table 2). Nine people were co-infected with another bacterial pathogen: 6 with *Haemophilus influenzae*, two with *Streptococcus pyogenes*, and one with *Streptococcus agalactiae*. The incidence of IPD in South Africa for 2024 was 3.06 per 100 000 population, similar to that of 2023 (3.02 per 100 000), yet remaining lower than 2019 (4.07 per 100 000) prior to the COVID-19 pandemic. Incidence in the Western Cape (8.45 per 100 000) remained significantly higher than other provinces ($p < 0.001$), which ranged between 0.85 and 3.75 per 100 000 (Table 13). Incidence peaked in infants (14.02 per 100 000), dropping to less than one episode per 100 000 population in age categories spanning 5 through 24 years and then increasing to a second peak in adults 45-64 years (4.76 per 100 000) (Figure 11). Where sex was known, 52% (948/1,823) of IPD episodes occurred in males. Most episodes were diagnosed from blood (1,307/1,927, 68%) and cerebrospinal fluid (492/1,927, 26%) specimens (Table 14). Penicillin non-susceptibility (minimum inhibitory concentration (MIC) $> 0.06 \mu\text{g/ml}$) was demonstrated in 32% (355/1,125) of cultured isolates, and children 5-9 years had the highest proportion of non-susceptible isolates (11/24, 46%) (Table 15 and Figure 12). Ceftriaxone non-susceptibility (MIC $> 0.5 \mu\text{g/ml}$) was detected amongst 7% (80/1,125) of isolates. In 2024, the top three serotypes (in order) occurring in children < 5 years

included serotypes 8, 10A, and 19F, whilst in people > 5 years, serotypes 8, 4, and 3 dominated. (Figures 13a and 13b). Overall, potential coverage of serotypes in the 10-valent Serum Institute of India pneumococcal conjugate vaccine (PCV) was 16% (203/1,287), 32% (413/1,287) for PCV13, and 63% (813/1,287) for the 23-valent polysaccharide vaccine. (Figure 14 and Table 16).

At enhanced surveillance sites, 89% (735/828) of people with IPD had clinical data collected. Patients were admitted for a median of 7 days (interquartile range (IQR) 2-13 days). In-hospital case fatality was 33% (247/735), increasing from 30% (19/63) in infants to 50% (33/66) in people > 64 years. Most deaths occurred within two days of specimen collection (IQR 1-5 days).

Of those tested for HIV, 51% (366/711) were living with HIV. Thirty-nine per cent (22/56) of infants with maternal HIV status available were HIV-exposed (six babies were HIV-infected and 16 were HIV-uninfected). Sixty-seven per cent (493/735) of patients had a condition/risk factor (excluding HIV infection) predisposing them to IPD. The top five factors included a history of tuberculosis (10%, 71/735), diabetes (7%, 53/735), chronic lung disease (7%, 53/735), chronic renal disease (5%, 37/735), or malignancy (5%, 36/735, each). Among infants, 19% (12/63) were premature, and among people > 15 years, 31% (178/577) were current smokers and 17% (97/577) reported excessive alcohol use.

Of 162 people at ESS with pneumococcus detected in CSF, 44% (71/162) died during their hospitalisation, and 25% (23/91) who survived to discharge suffered at least one sequela upon discharge, with two people having three sequelae each. Sequelae included new-onset seizures (16), limb weakness/paralysis (four), amputation (three), hearing loss (two), and vision loss (two).

Of 125 children <10 years of age with IPD at ESS, 86% (108/125) had non-PCV13 serotype disease, and 14% (17/125) had IPD caused by serotypes present in PCV13, including five serotype 19F, five serotype 19A, three serotype 14, two serotype 3, and

one each for serotypes 18C and 7F. Vaccination history was available for 13 of 17 children with PCV13 serotype disease: two children were too young to have received the 6-week dose, one child (age three years) had never received any PCV13 doses, two had received appropriate doses for their age, two had received at least one dose but missed others appropriate for age, and six had received all three doses. The serotypes responsible for disease in children who had been fully vaccinated included serotypes 19A (four children), 19F, and 3 (one child each). Half (3/6) of the fully vaccinated children had an underlying risk factor predisposing them to IPD.

Table 13: Number of cases and incidence of invasive pneumococcal disease reported to GERMS-SA by province, South Africa, 2019-2024, N=10 747 (including audit cases)

Site of specimen	2019		2020		2021		2022		2023		2024	
	n	Incidence rate*	n	Incidence rate*	n	Incidence rate*	n	Incidence rate*	n	Incidence rate*	n	Incidence rate*
Eastern Cape	274	4.23	136	2.10	201	3.10	223	3.45	233	3.60	269	3.75
Free State	83	2.90	62	2.16	70	2.43	62	2.16	62	2.16	77	2.53
Gauteng	774	5.08	377	2.42	466	2.98	511	3.22	538	3.33	580	3.64
KwaZulu-Natal	237	2.14	101	0.90	119	1.03	165	1.46	163	1.43	165	1.34
Limpopo	96	1.65	52	0.88	45	0.76	69	1.15	67	1.11	57	0.89
Mpumalanga	102	2.20	41	0.87	56	1.18	52	1.09	40	0.83	43	0.85
Northern Cape	89	8.02	26	2.33	25	2.23	27	2.42	25	2.23	33	2.40
North West	66	1.67	36	0.90	31	0.79	48	1.18	57	1.38	64	1.54
Western Cape	631	9.34	417	6.07	538	7.80	704	10.08	622	8.77	639	8.45
South Africa	2 352	4.07	1 249	2.14	1 551	2.64	1 861	3.15	1 807	3.02	1 927	3.06

*Incidence was calculated based on population denominators provided by Stats-SA, and are expressed as cases per 100 000 population.

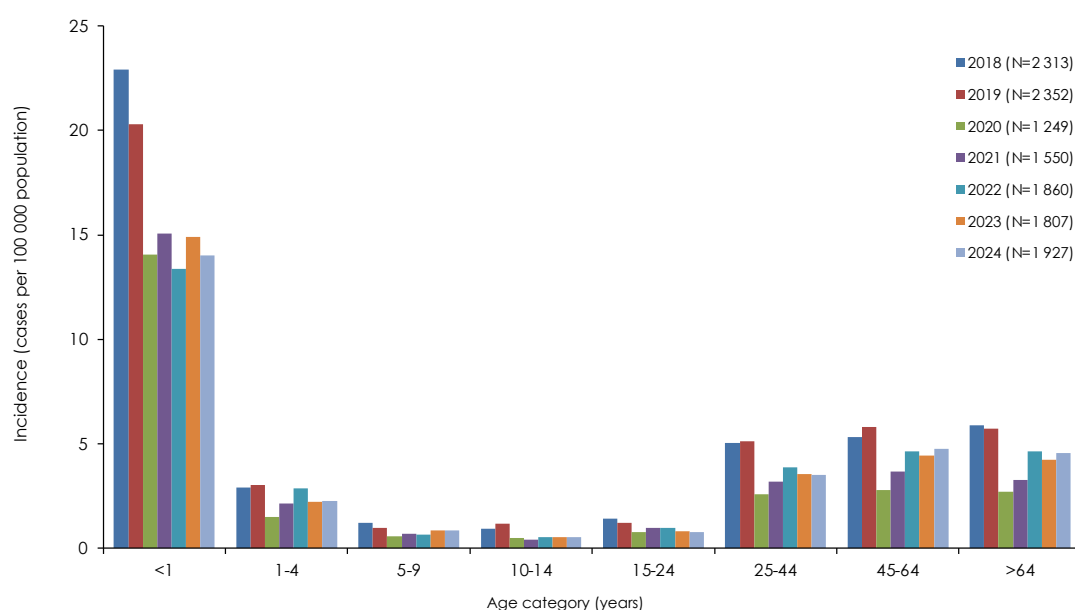


Figure 11. Age-specific incidence* for laboratory-confirmed, invasive pneumococcal disease, reported to GERMS-SA, South Africa, 2018-2024, N=13 058

2018: N=2 313, age unknown for n=42; 2019: N=2 352, age unknown for n=38; 2020: N=1 249, age unknown for n=31; 2021: N=1 550, age unknown for n=38; 2022: N=1 860, age unknown for n=42; 2023: N=1 807, age unknown for n=81; 2024: N=1 927, age unknown for n=72).

*Incidence were calculated based on population denominators provided by Stats-SA, and are expressed as cases per 100 000 population.

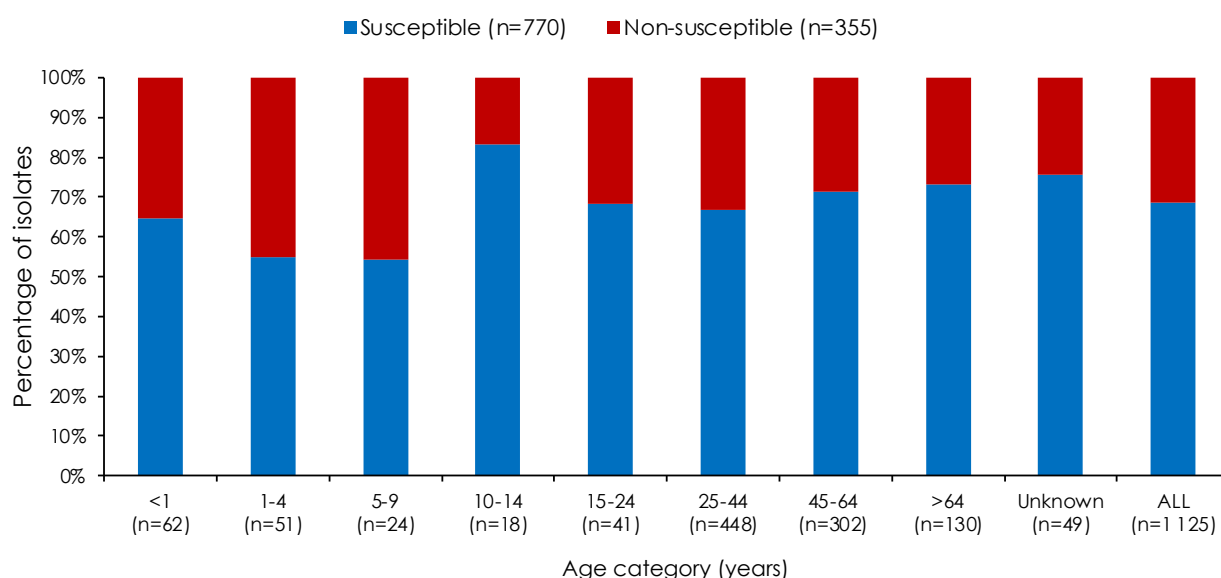
Table 14. Number and percentage of cases of invasive pneumococcal disease reported to GERMS-SA by specimen type, South Africa, 2019-2024, N=10 747

Site of specimen	2019		2020		2021		2022		2023		2024	
	n	%	n	%	n	%	n	%	n	%	n	%
Cerebrospinal fluid	701	30	340	27	386	25	425	23	514	28	492	26
Blood	1 484	63	813	65	1 068	69	1 313	71	1 149	64	1 307	68
Other	167	7	96	8	97	6	123	7	144	8	128	7
Total	2 352		1 249		1 551		1 861		1 807		1 927	

Table 15. Number and percentage of penicillin susceptible and non-susceptible isolates from invasive pneumococcal disease cases reported to GERMS-SA by province, South Africa, 2024, N=1 927

Province	Isolate not available	Susceptible*		Non-susceptible*	
	n	n	%	n	%
Eastern Cape	104	114	69	51	31
Free State	40	27	73	10	27
Gauteng	324	169	66	87	34
KwaZulu-Natal	93	46	64	26	36
Limpopo	27	19	63	11	37
Mpumalanga	32	8	73	3	27
Northern Cape	19	10	71	4	29
North West	29	22	63	13	37
Western Cape	134	355	70	150	30
South Africa	802	770	68	355	32

* 2024 CLSI meningitis breakpoints for penicillin were used: susceptible, $\leq 0.06\mu\text{g/ml}$; non-susceptible, $\geq 0.12\mu\text{g/ml}$.

**Figure 12. Number of laboratory-confirmed, invasive pneumococcal disease cases, reported to GERMS-SA, by age group and penicillin susceptibility, South Africa, 2024, N=1 927 (n=1 125 with viable isolates).**

2024 CLSI meningitis breakpoints for penicillin were used: susceptible, MIC $\leq 0.06\mu\text{g/ml}$; non-susceptible $> 0.12\mu\text{g/ml}$

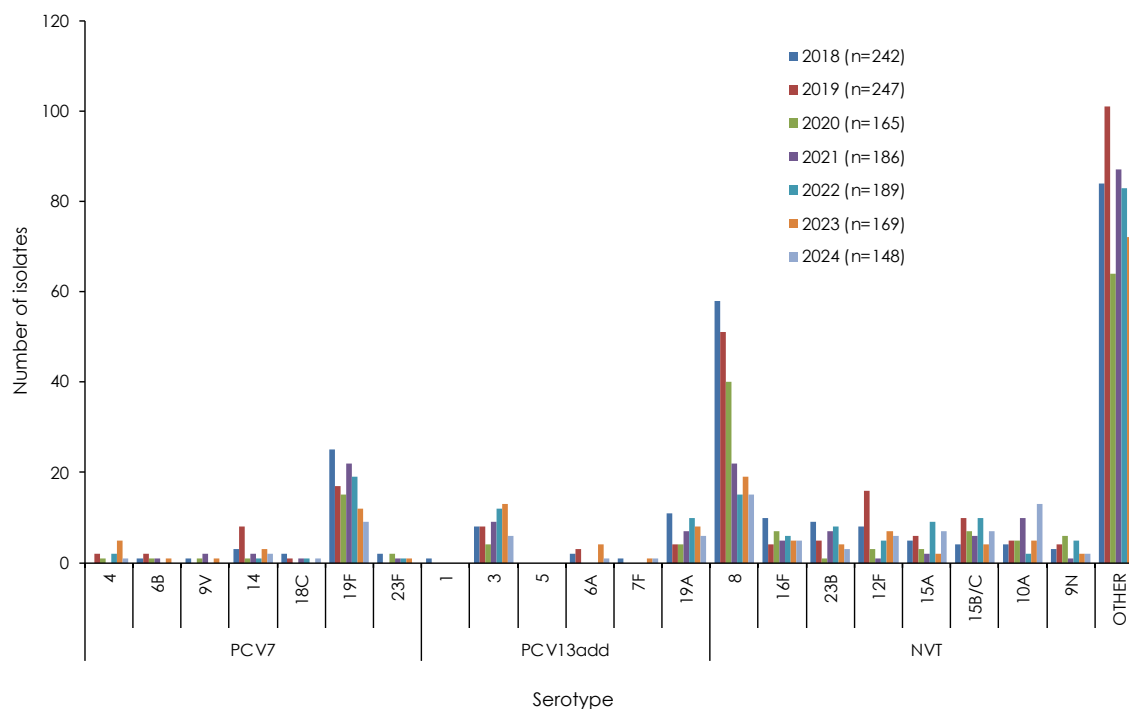


Figure 13a. Most common pneumococcal serotypes causing laboratory-confirmed, invasive pneumococcal disease, reported to GERMS-SA, in children <5 years, South Africa, 2018-2023 (N=2 028)

(2018: N=386, n=144 without serotype determined; 2019: N=361, n=114 without serotype; 2020: N=224, n=59 without serotype; 2021: N=264, n=78 without serotype; 2022: N=275, n=86 without serotype; 2023: N=245, n=76 without serotype; 2024: N=273, n=125 without serotype).

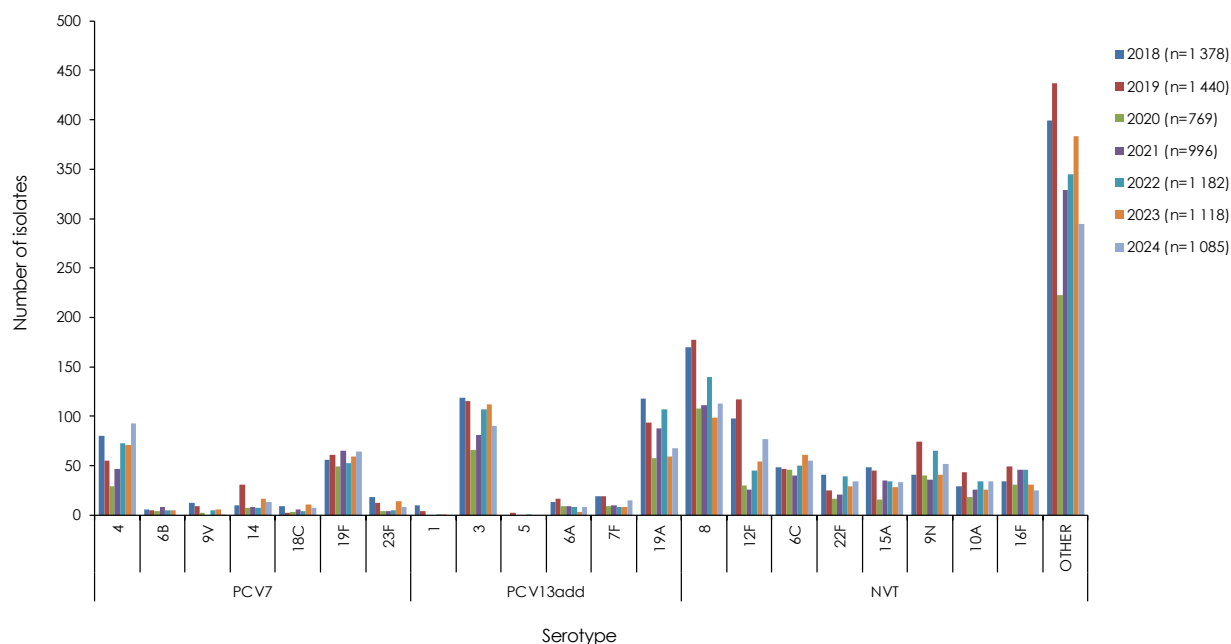


Figure 13b. Most common pneumococcal serotypes causing laboratory-confirmed, invasive pneumococcal disease, reported to GERMS-SA, in adults and children >5 years, South Africa, 2018-2024 (N=10 641).

(2018: N=1 885, n=507 without serotype determined; 2019: N=1 952, n=512 without serotype; 2020: N=993, n=224 without serotype; 2021: N=1 249, n=253 without serotype; 2022: N=1 544, n=362 without serotype; 2023: N=1 436, n=318 without serotype; 2024: N=1 582, n=497 without serotype).

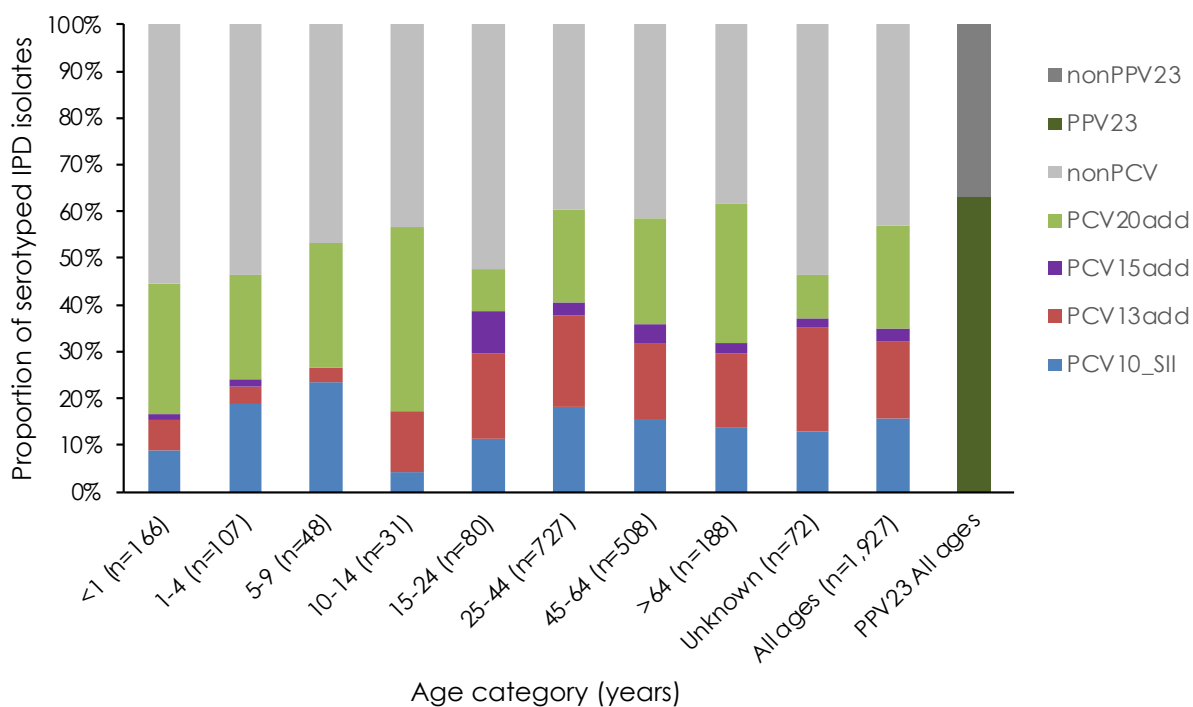


Figure 14. Potential pneumococcal serotype coverage of laboratory-confirmed, invasive pneumococcal disease, reported to GERMS-SA, by various pneumococcal conjugate vaccines and age categories, South Africa, 2024 (N=1 927, n=640 episodes not serotyped)

PCV10_SII: 10-valent pneumococcal conjugate vaccine from Serum Institute India contains serotypes 1, 5, 6A, 6B, 7F, 9V, 14, 19A, 19F and 23F; PCV13add: 13-valent vaccine contains PCV10_SII serotypes plus serotypes 3, 4 and 18C; PCV15add: 15-valent vaccine contains PCV13 serotypes plus 22F and 33F; PCV20add: 20-valent vaccine contains PCV15 serotypes plus 8, 10A, 11A, 12F and 15B; PPV23: serotypes in PCV13 less 6A, plus 2, 8, 9N, 10A, 11A, 12F, 15B, 17F, 20, 22F, 33F.

Table 16. Number and percentage of invasive pneumococcal cases reported by the serotypes contained in the 10-, 13- 15- and 20-valent pneumococcal conjugate vaccine candidates and the 23-valent pneumococcal polysaccharide vaccine by age category, South Africa, 2024, N=1 927 (n=1 287 with isolates/specimens available for serotyping)

Age category (years)	Total isolates available for serotyping	SII 10-valent serotypes		GSK 10-valent serotypes		Pfizer 13-valent serotypes		Merck 15-valent serotypes		Pfizer 20-valent serotypes		23-valent serotypes	
		n	%	n	%	n	%	n	%	n	%	n	%
<1	90	8	9	8	9	14	16	15	17	40	44	41	46
1-4	58	11	19	6	10	13	22	14	24	27	47	28	48
5-9	30	7	23	5	17	8	27	8	27	16	53	17	57
10-14	23	1	4	1	4	4	17	4	17	13	57	14	61
15-24	44	5	11	5	11	13	30	17	39	21	48	24	55
25-44	503	91	18	108	21	190	38	204	41	303	60	342	68
45-64	347	54	16	61	18	111	32	124	36	203	59	225	65
>64	138	19	14	21	15	41	30	44	32	85	62	93	67
unk	54	7	13	11	20	19	35	20	37	25	46	29	54
	1 287	203	16	226	18	413	32	450	35	733	57	813	63

Serotypes included in each of the pneumococcal vaccine categories:

Serum Institute India 10-valent serotypes:

1, 5, 6A, 6B, 7F, 9V, 14, 19A, 19F, 23F

GlaxoSmithKline 10-valent serotypes:

1, 4, 5, 6B, 7F, 9V, 14, 18C, 19F, 23F

Pfizer 13-valent serotypes:

1, 4, 5, 6B, 7F, 9V, 14, 18C, 19F, 23F, 3, 6A, 19A

*Merck 15-valent serotypes:

1, 4, 5, 6B, 7F, 9V, 14, 18C, 19F, 23F, 3, 6A, 19A, 22F, 33F

*Pfizer 20-valent serotypes:

1, 4, 5, 6B, 7F, 9V, 14, 18C, 19F, 23F, 3, 6A, 19A, 22F, 33F, 8, 10A, 11A, 12F, 15B

23-valent serotypes:

1, 4, 5, 6B, 7F, 9V, 14, 18C, 19F, 23F, 3, 19A, 22F, 33F, 8, 10A, 11A, 12F, 15B, 2, 9N, 17F, 20

* Merck PCV15 and Pfizer PCV20 are not yet licenced for use in South Africa

Discussion

IPD incidence in South Africa has remained unchanged from 2022 through 2024, with incidence across provinces varying widely. Although infants have the highest incidence of IPD, a bimodal disease pattern is seen with the second peak extending throughout adulthood. The high incidence across adulthood reflects the continuum of an ageing HIV-infected population and the high rate of comorbidities and lifestyle factors associated with increased IPD risk. IPD infection is devastating, with one in three people dying and one in four people with pneumococcal meningitis having long-term complications. Overall, serotypes 8, 4, and 3 were the most common, causing 26% of all IPD in South Africa. Serotype 8

remained the top disease-causing serotype in both children and adults. An unexpected increase in serotype 10A was noted in children, with no obvious clusters seen, and episodes occurring in five different provinces. The rise in serotype 4 IPD has continued amongst adults but not in children. In April 2024, South Africa moved to a 10-valent PCV formulation in the Expanded Programme on Immunisation, which excludes serotypes 3, 4, and 18C contained in the previously used PCV13. Ongoing surveillance is extremely important to monitor changes in serotype-specific IPD trends in both children and adults.

Group A Streptococcus (*Streptococcus pyogenes*)

Results

In 2024, 708 episodes of invasive group A streptococcus (group A strep) were reported through the GERMS-SA surveillance programme, of which 367 (52%) were sent to the reference laboratory for further characterisation, 14 (2%) were detected through molecular testing alone, and 327 (46%) were detected through audit of the NHLS laboratory information system (Table 2). In 2024, the case definition for invasive group A strep infection changed to only include specimens from invasive specimen sites (previously, non-invasive sites were included if accompanied by a diagnosis of necrotising fasciitis or streptococcal toxic shock syndrome). Overall incidence was 1.12 episodes per 100 000 people, lower than that in 2023 (1.54 per 100 000 people). The Western Cape reported the highest incidence of invasive group A strep (3.13 per 100 000), followed by Gauteng (1.49 per 100 000) and Free State (1.08 per 100 000) (Table 17). Incidence was highest in infants (4.14 per 100 000), dropping to a low of 0.28 per 100 000 in 10-14 year-olds and then increasing with increasing age to another peak in people >64 years (1.67 per 100 000 population) (Figure 15). Where sex was known, infections occurred more often in males (56%, 389/692) than females. From all age categories, most episodes were diagnosed from blood cultures (68%, 483/708) (Figure 16, Table 18). Two isolates (1%, 2/367) were resistant to penicillin (MIC<2µg/ml), and one isolate (<1%, 1/333) showed intermediate resistance to erythromycin (MIC<0.25µg/ml) (Table 19).

At enhanced surveillance sites, 88% (323/369) of people with invasive group A strep had clinical data collected (Table 4). Of these, 22% (72/323) presented with streptococcal toxic shock syndrome, 10% (31/323) with necrotising fasciitis, and 4% (13/323) had pregnancy/postpartum-associated disease. The remainder had invasive group A strep associated with underlying wound infection (17%, 56/323), cellulitis (6%, 19/323), septic arthritis (4%, 12/323), osteomyelitis (2%, 8/323), bacteraemia without focus (27%, 88/323), meningitis (2%, 6/323), or deep abscess (6%, 18/323). Most infections were community-acquired (73%, 237/314), whilst 24% (77/323) were healthcare-associated (occurring >48 hours post hospital admission) (admission date was unknown for nine episodes). People with invasive group A strep infection spent a median of nine days in hospital (IQR 2-18 days). In-hospital mortality was 25% (79/323), ranging from 10% (3/31) among those with necrotising fasciitis to 43% (31/72) among those with streptococcal toxic shock syndrome. Common risk factors for developing invasive group A strep included having burn wounds (11%, 35/323), a penetrating wound following trauma (10%, 32/323), blunt trauma (9%, 29/323), or surgery in the past two weeks (6%, 20/323). Other factors associated with infection included having diabetes (10%, 33/323), being homeless (4%, 13/323), or obese (3%, 11/323). Of those with known HIV status, 27% (83/304) were people living with HIV.

Table 17: Number of cases and incidence of invasive group A streptococcal disease reported to GERMS-SA by province, South Africa, 2019-2024, N=4 795 (including audit cases)

Province	2019		2020		2021		2022		2023		2024 **	
	n	Incidence rate*	n	Incidence rate*	n	Incidence rate*	n	Incidence rate*	n	Incidence rate*	n	Incidence rate*
Eastern Cape	143	2.19	71	1.10	150	2.32	120	1.85	75	1.16	74	1.03
Free State	22	0.77	11	0.38	21	0.73	35	1.22	26	0.90	33	1.08
Gauteng	200	1.31	95	0.61	174	1.11	259	1.63	327	2.03	238	1.49
KwaZulu-Natal	162	1.47	49	0.44	93	0.83	96	0.85	74	0.65	84	0.68
Limpopo	7	0.12	5	0.09	10	0.17	19	0.32	25	0.41	13	0.20
Mpumalanga	11	0.24	9	0.19	23	0.49	20	0.42	19	0.39	16	0.32
Northern Cape	7	0.63	7	0.63	3	0.27	2	0.18	6	0.54	3	0.22
North West	2	0.05	3	0.07	9	0.22	10	0.25	11	0.27	10	0.24
Western Cape	416	6.16	262	3.82	266	3.85	375	5.37	357	5.04	237	3.13
South Africa	970	1.68	512	0.88	749	1.28	936	1.58	920	1.54	708	1.12

* Incidence was calculated based on population denominators provided by Stats-SA, and are expressed as cases per 100 000 population.

** 2024 case definition changed to only include specimens from invasive specimen sites (previously non-invasive sites were included if accompanied by a diagnosis of necrotising fasciitis or streptococcus toxic shock syndrome)

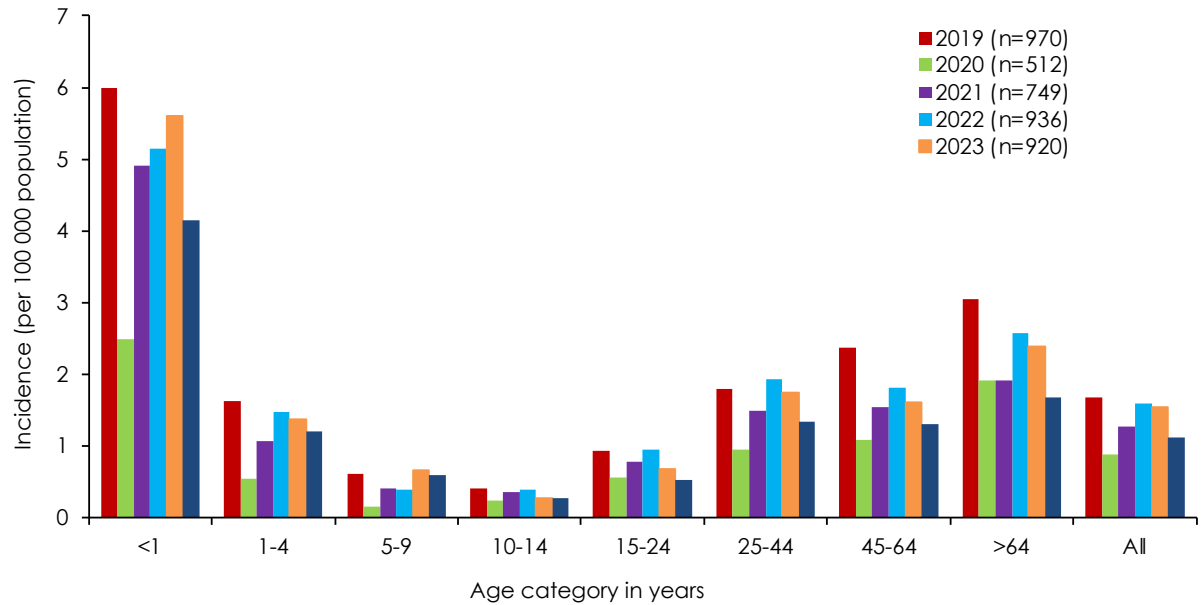


Figure 15. Incidence of invasive *Streptococcus pyogenes* by age-category, South Africa, 2019-2024 (N=4 795)

(Age unknown for 159: 2019 n=15; 2020 n=30; 2021 n=23; 2022 n=32; 2023 n=87; 2024=15)

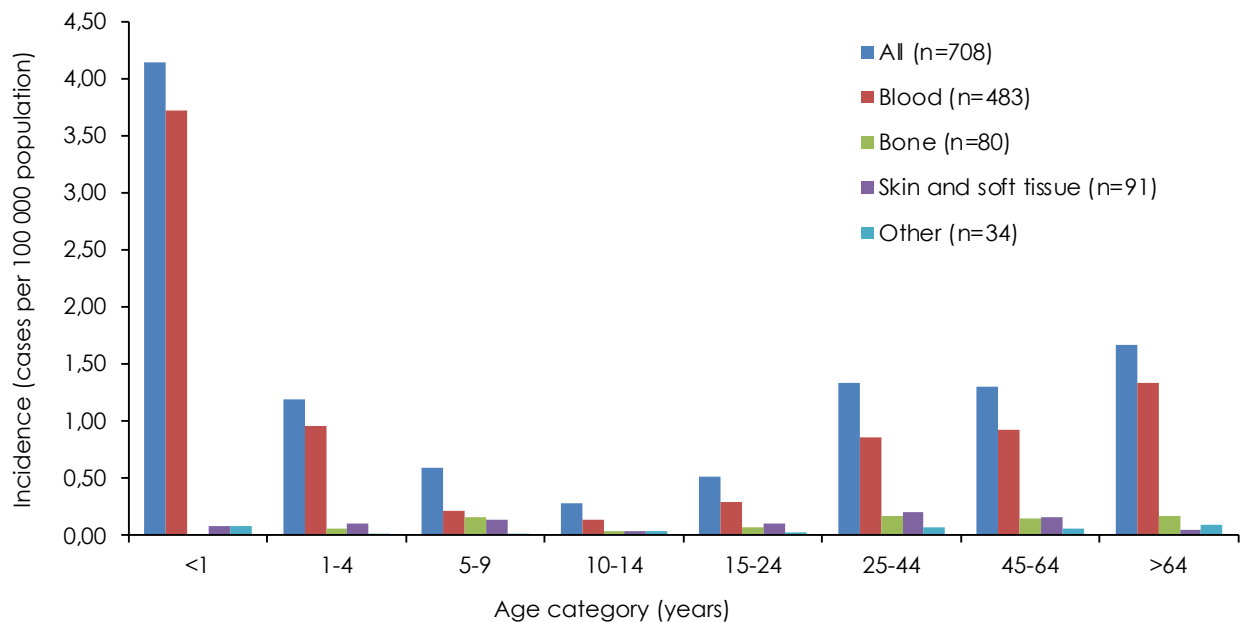


Figure 16. Age-specific incidence* for laboratory-confirmed, invasive group A streptococcal disease, reported to GERMS-SA, South Africa, 2024, n=708

*Incidence were calculated based on population denominators provided by Stats-SA, and are expressed as cases per 100 000 population.

Table 18: Number and percentage of cases of invasive group A streptococcal disease reported to GERMS-SA by specimen type and age category, South Africa, 2024, N=708 (age unknown for n=15)

Site of specimen	Age <5 years		Age >5 years		Age unknown		All ages	
	n	%	n	%	n	%	n	%
Cerebrospinal fluid/brain	5	5	15	3	0	0	20	3
Blood	90	85	382	65	11	73	483	68
Skin and soft tissue*	6	6	82	14	3	20	91	13
Bone	3	3	77	13	0	0	80	11
Other**	2	2	31	5	1	7	34	5
Total	106		587		15		708	

*Other includes invasive specimens from respiratory, genitourinary and gastrointestinal tracts.

Table 19. Number and percentage of penicillin and erythromycin susceptible and non-susceptible isolates from invasive group A streptococcal disease cases reported to GERMS-SA, South Africa, 2024, N=708 (isolate available for n=367)

Site of specimen	Isolate not available	Susceptible*		Intermediate*		Resistant*	
	n	n	%	n	%	n	%
Penicillin	341	365	99	0	0	2	1
Erythromycin	333	332	100	1	0	0	0

*2024 CLSI breakpoints for penicillin (oral penicillin V) were used: susceptible, $\leq 0.06\mu\text{g/ml}$; intermediately resistant, $0.12\text{--}1\mu\text{g/ml}$; resistant, $\geq 2\mu\text{g/ml}$.

Discussion

In 2024, the national incidence of invasive group A strep infection was slightly lower than in 2023. This reduction may partly reflect the revised case definition restricting inclusion to infections from normally sterile site specimens only. Age-specific incidence showed a bimodal pattern, indicating increased susceptibility in infants and the elderly. Most infections were

community-acquired and identified from blood cultures. Severe clinical presentations, such as streptococcal toxic shock syndrome, occurred frequently and were accompanied by a very high in-hospital mortality. Resistance to penicillin and erythromycin remained rare, supporting continued efficacy of first-line antibiotics.

Group B Streptococcus (*Streptococcus agalactiae*)

Results

In 2024, 862 laboratory-confirmed episodes of invasive group B streptococcus (group B strep) were reported through the GERMS-SA network: 352 (41%) viable isolates were sent to the NICD reference laboratory for further characterisation; 16 (2%) were identified through molecular testing alone; and 494 (57%) were detected through the NHLS laboratory information system (Table 2).

Nationally in 2024, incidence for invasive group B strep was 1.37 per 100 000 people and has remained lower than the post-COVID-19 spike in disease experienced in 2021 (incidence of 2.01 per 100 000) (Figures 17a and 17b). In 2024, infants had

the highest incidence (37.09 per 100 000 population or 0.37 per 1 000 live births), dropping to a low of 0.10 per 100 000 in 10–14 year olds and then increasing with increasing age to a second peak in people >64 years (1.09 per 100 000 population) (Table 20 and Figure 17a). Incidence per 1 000 live births in 2024 was 0.23 for early-onset (<7 days of life) and 0.12 for late-onset (7–90 days) invasive group B strep disease (Figure 17b). Incidence of laboratory-confirmed episodes varied by province, with the Western Cape, Gauteng, Free State, and KwaZulu-Natal provinces reporting the highest rates (Table 20). In infants, most cases were isolated from blood (387/439, 88%) or cerebrospinal fluid (48/439, 11%) (Table 21 and Figure 18a).

However, in people >1 year of age, blood (189/389, 49%) and genitourinary tract specimens (134/389, 34%) (particularly from females of reproductive age) were most frequent (Table 21, Figure 18b). Where sex was known, 57% (457/798) of diseases occurred amongst females. Of serotyped isolates, serotypes III (111/346, 32%), Ia (95/346, 27%), and V (42/346, 12%) were most common for all presentations (early-onset, late-onset, and disease in the >1-year age group) and most provinces (Table 22, Figure 19a). Isolates from blood specimens were mostly serotype Ia (71/270, 26%) or serotype III (87/270, 32%), while CSF isolates were mainly serotype III (16/28, 57%). Of the genitourinary isolates typed, serotype Ia was most common (Figure 19b). In addition, an increase in non-typeable isolates from previous years was noted in all presentations and specimen types. (Table 22, Figures 19a and 19b). Ninety-seven per cent (342/352) of invasive group B strep isolates tested were sensitive to penicillin (MIC<0.12µg/ml), 65% (229/352) to erythromycin (MIC<0.5µg/ml), and only 5% (19/352) to tetracycline (MIC<2µg/ml).

In 2024, 90% (369/412) of group B strep episodes at enhanced surveillance sites had clinical data collected (Table 4). These were classified as neonatal/infant disease (40%, 146/369), pregnancy-associated disease (26%, 97/369), and other presentations (34%, 126/369). The median length of hospital stay was 6 days (IQR 2-13 days). Overall, in-hospital mortality was 18% (65/369): 19% (27/146) in infants, 0% with pregnancy-associated disease in mothers, and 30% (38/126) in other presentations >1 year of

age. Most deaths occurred within one day of hospital admission (IQR 0-5 days). Of those tested for HIV, 19% (66/356) were HIV infected.

Among 146 infants with group B strep, 63% (92/146) had early-onset (<7 days of life) and 33% (49/146) had late-onset (7-90 days) disease. Underlying maternal risk factors in the infants included 24% (35/146) with premature rupture of membranes prior to birth and 5% (7/146) with pre-eclampsia. Infant risk factors included 36% (53/146) with prematurity (born before 37 weeks gestation), 13% (19/146) with very low birth weight (<1500g), and 18% (26/146) who required intubation.

Of the 97 women with pregnancy-associated disease, 44% (43/97) of the pregnancies resulted in death of the neonate/foetus, 3% (3/97) had neonates with clinical group B strep infection, 4% (4/97) were still pregnant at discharge from hospital, 13% (13/97) had neonates who appeared clinically well, and in 35% (33/97) the pregnancy outcome was unknown.

The median age of people with invasive group B strep not associated with infancy or pregnancy was 49 years (IQR 31-61 years). Among these, where sex was known, 56% (68/122) of diseases occurred in males. Underlying risk factors for disease included diabetes (26%, 33/126), a history of smoking (18%, 23/126), sleeping in an overcrowded room (13%, 17/126), excess alcohol consumption (10%, 13/126), and obesity (6%, 8/126).

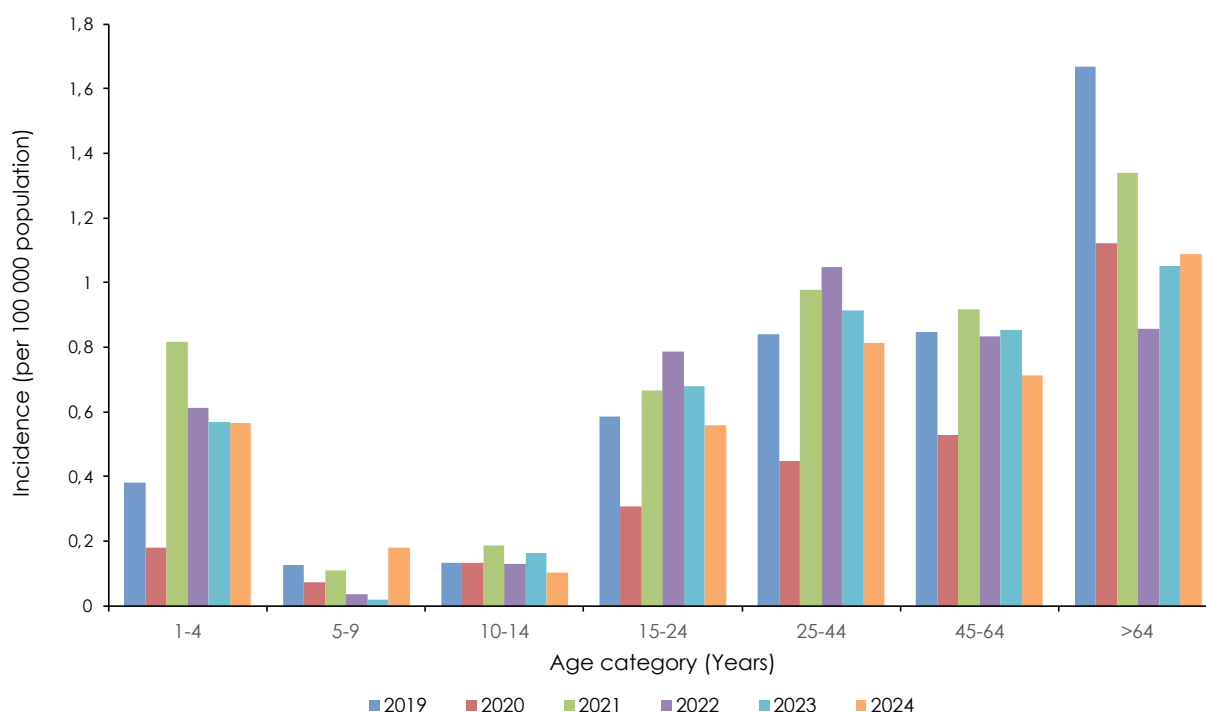


Figure 17a. Incidence of laboratory-confirmed invasive group B streptococcal disease by age category (>12 Months) and year reported to GERMS-SA, South Africa, 2019-2024 (N=5 949, n=312 with unknown age and n=3 360 <12 months)

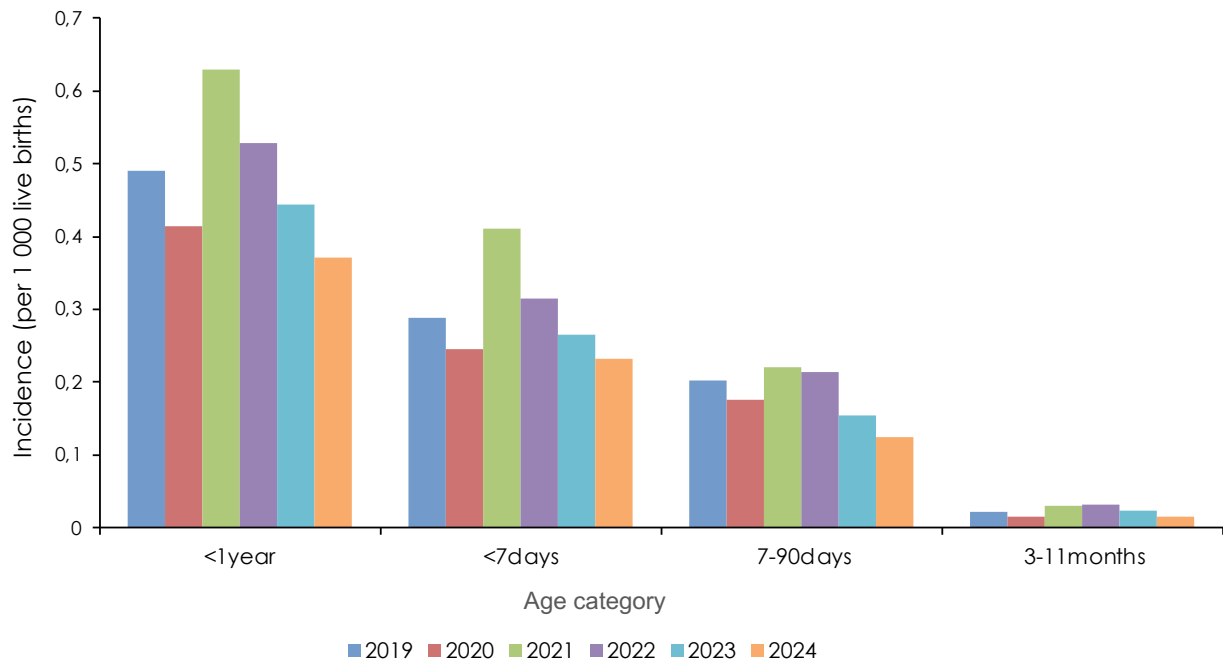


Figure 17b. Incidence of invasive group B streptococcus per 1 000 live births by age category (<12 months) and year reported to GERMS-SA, South Africa, 2019-2024 (N=3 360)

Table 20. Number of cases and incidence of invasive group B streptococcal disease reported to GERMS-SA by province and age category*, South Africa, 2024, N=862 (age unknown for n=34)

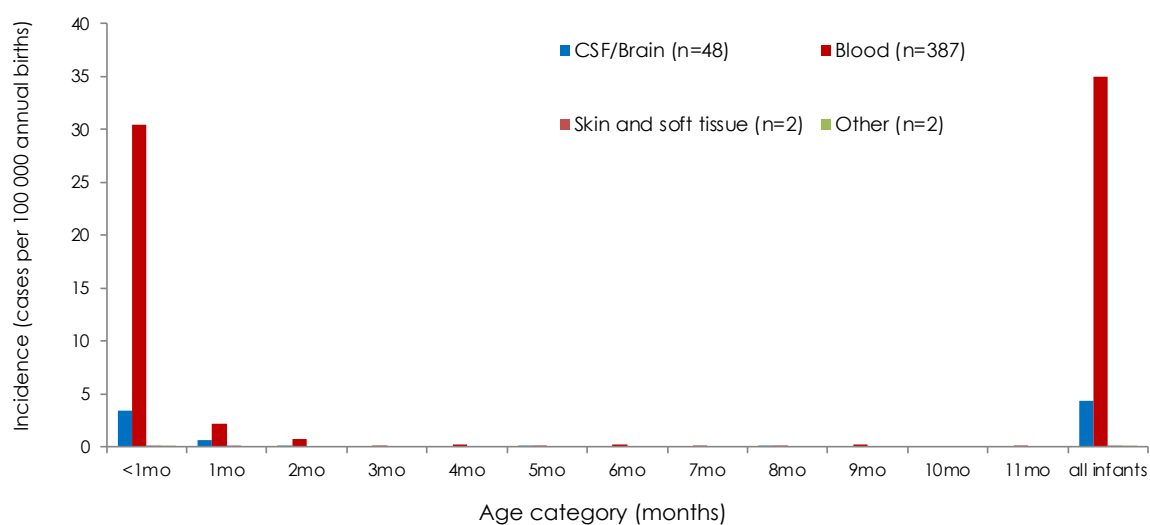
Province	Early onset (<7 days)		Late onset (7-90 days)		Age category >1 year		All ages	
	n	Incidence (per 1 000 live births*)	n	Incidence (per 1 000 live births*)	n	Incidence (per 100 000 population)	n	Incidence (per 100 000 population)
Eastern Cape	8	0.06	14	0.10	29	0.41	55	0.77
Free State	12	0.21	5	0.09	18	0.60	40	1.31
Gauteng	122	0.44	56	0.20	173	1.10	373	2.34
KwaZulu-Natal	64	0.26	21	0.08	63	0.52	157	1.28
Limpopo	8	0.05	10	0.06	20	0.32	38	0.59
Mpumalanga	14	0.13	1	0.01	7	0.14	23	0.45
Northern Cape	1	0.04	2	0.07	4	0.30	7	0.51
North West	12	0.16	3	0.04	8	0.20	24	0.58
Western Cape	33	0.25	35	0.27	67	0.90	145	1.92
South Africa	274	0.23	147	0.12	389	0.63	862	1.37

*N=18 episodes in infants aged >90 days and less than one year excluded from above. Denominators included mid-year population estimates from Stats-SA

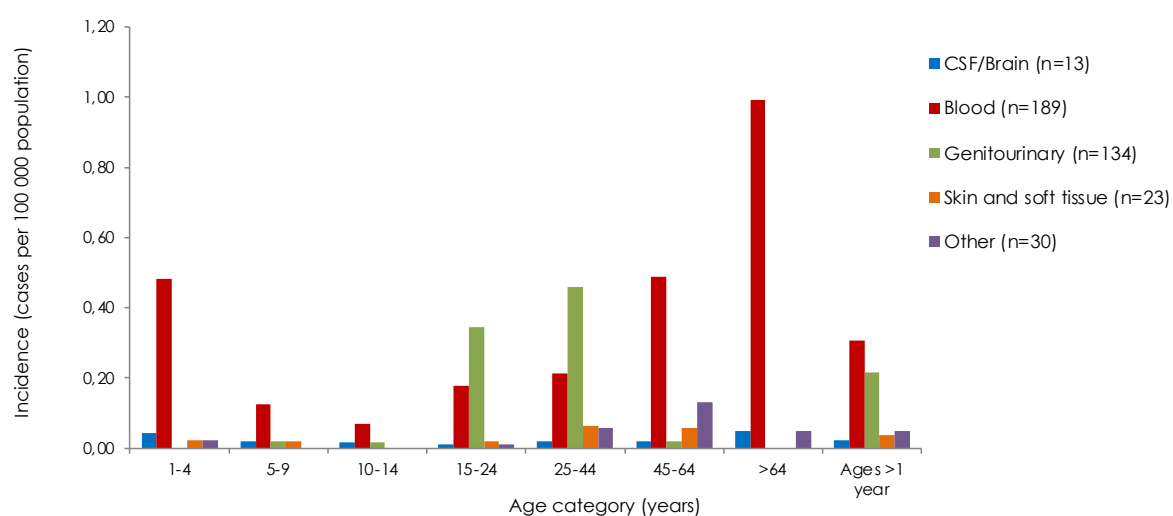
Table 21. Number and percentage of cases of invasive group B streptococcal disease reported to GERMS-SA by specimen type and age category*, South Africa, 2024, N=862

Site of specimen	Age <1 year		Age >1 years		Age unknown	
	n	%	n	%	n	%
Cerebrospinal fluid/brain	48	11	13	3	5	15
Blood	387	88	189	49	24	71
Skin and soft tissue	2	0	23	6	4	12
Genitourinary**	0	0	134	34	1	3
Other***	2	0	30	8	0	0
Total	439		389		34	

* Genitourinary specimens include uterine tissue, products of conception and placental tissue **Other includes invasive specimens from bone, respiratory and gastrointestinal tracts.

**Figure 18a. Age-specific incidence* for laboratory-confirmed, invasive group B streptococcal disease in children <1 year of age, reported to GERMS-SA, South Africa, 2024, N=439**

*Incidence were calculated based on population denominators provided by Stats-SA, and are expressed as cases per 100 000 population.

**Figure 18b: Age-specific incidence* for laboratory-confirmed, invasive group B streptococcal disease in persons >1 year of age, reported to GERMS-SA, South Africa, 2024, N=389**

*Incidence were calculated based on population denominators provided by Stats-SA, and are expressed as cases per 100 000 population. N=439 episodes in children<1 year and n=34 episodes with age unknown)

Table 22. Serotype distribution of invasive group B streptococcal disease reported to GERMS-SA by province, South Africa, 2024, N=862

Province	Total	Isolates available for sero-typing	Ia		Ib		II		III		IV		V		IX		NT	
			n	%	n	%	n	%	n	%	n	%	n	%	n	%	n	%
Eastern Cape	55	30	13	43	5	17	0	0	8	27	0	0	2	7	1	3	1	3
Free State	40	7	2	29	1	14	1	14	2	29	0	0	1	14	0	0	0	0
Gauteng	373	151	43	28	8	5	15	10	47	31	2	1	21	14	0	0	15	10
KwaZulu-Natal	157	51	8	16	4	8	3	6	12	24	3	6	10	20	0	0	11	22
Limpopo	38	24	4	17	1	4	4	17	10	42	0	0	3	13	0	0	2	8
Mpumalanga	23	3	0	0	0	0	0	0	1	33	0	0	1	33	0	0	1	33
Northern Cape	7	2	0	0	0	0	1	50	1	50	0	0	0	0	0	0	0	0
North West	24	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	100
Western Cape	145	77	25	32	10	13	2	3	30	39	0	0	4	5	0	0	6	8
South Africa	862	346	95	27	29	8	26	8	111	32	5	1	42	12	1	0	37	11

Of 862 episodes, 346 had viable isolates and were serotyped

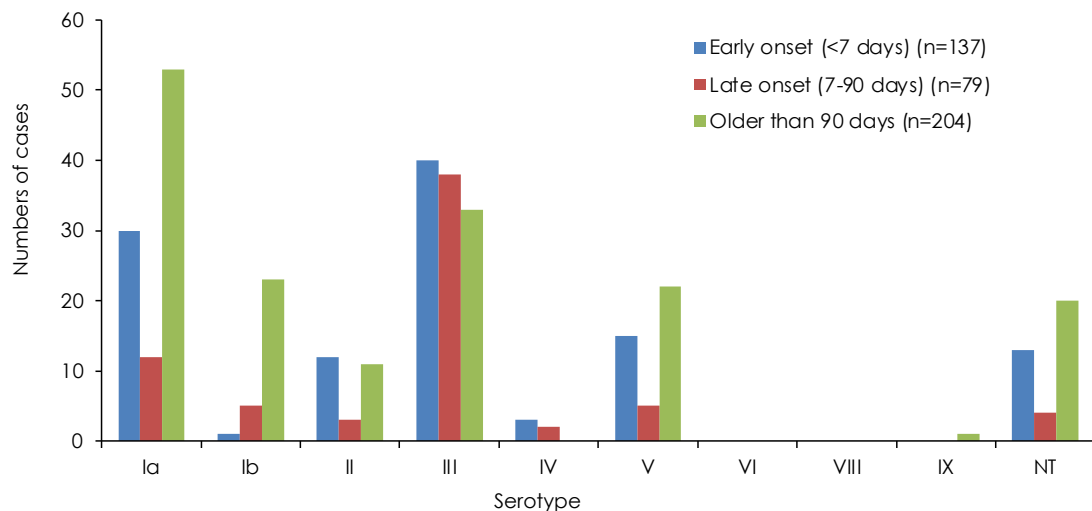


Figure 19a. Numbers of cases of laboratory-confirmed, invasive group B streptococcal disease by serotype and age-category, reported to GERMS-SA, South Africa, 2024, N=862 (typing done for n=346)

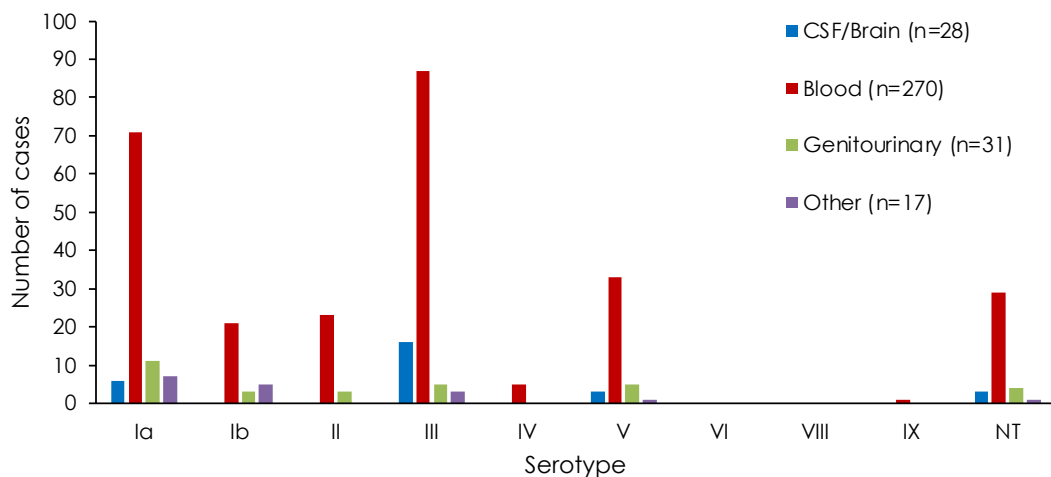


Figure 19b. Numbers of cases of laboratory-confirmed, invasive group B streptococcal disease by serotype and specimen type, reported to GERMS-SA, South Africa, 2023, N=862 (typing done for n=346)

Discussion

In 2024, invasive group B strep disease remained an important cause of morbidity and mortality in South Africa. Infants continued to experience the highest disease burden, particularly within the first week of life. A secondary peak among adults was also evident. Blood was the most common specimen type across all age groups, while genitourinary isolates predominated among reproductive-age females. Serotypes III and Ia accounted for most infections, consistent with global

trends, while an increase in non-typeable isolates warrants continued monitoring. Most isolates remained susceptible to penicillin, supporting its continued use for prophylaxis and treatment. Despite this, in-hospital mortality remained high, underscoring the need for strengthened perinatal screening, timely antibiotic prophylaxis, and surveillance to guide maternal vaccine implementation in the future.

Enteric fever (typhoid and paratyphoid fever): *Salmonella enterica* serovar Typhi and *Salmonella enterica* serovars Paratyphi A, Paratyphi B, and Paratyphi C

Results

A total of 139 cases of laboratory-confirmed enteric fever were identified through the enteric fever surveillance programme of the Centre for Enteric Diseases in 2024 (Table 23).

The cases include *Salmonella* Typhi and *Salmonella* Paratyphi isolated from all sample sites, of which 77% (107/139) were from blood cultures. There were 19 cases of enteric fever caused by *Salmonella enterica* serovar Paratyphi A (Table 24). Enteric fever cases were reported from eight provinces (Table 23), and the majority were reported from two provinces: Gauteng (75/139, 54%) and the Western Cape (23/139, 16.5%). Most cases (119/139, 82%) were identified in the public health sector (Table 23), and the majority of cases were reported in September (Figure 20). The highest number of cases was reported in children aged 5 to 14 years (60/139, 43%), followed by the 15–24-year age group (21/139; 15%) and then children aged 0–4 years (19/139, 14%), as shown in Table 25. A comparison of cases by month shows higher case numbers from July to September 2024 compared to earlier months, with a notable dip in cases during the month of May (Figure 20). A comparison of the distribution of *Salmonella* Typhi and Paratyphi cases by month for 2022–2024 is shown in Figure 21. Of the isolates received and tested at the centre, 90% (81/90) were susceptible to ciprofloxacin and 100% (90/90) were susceptible to azithromycin, according to CLSI breakpoints. The majority of ciprofloxacin-resistant isolates were from the Western Cape (4/21, 19%) (Table 26).

Thirty-three cases (33/139; 24%) were reported from ESS, and CIFs were received for 70% (23/33). Additional patient information was available, although completeness varied. Patients ranged in age from one to 61 years, with a median age of 15 years. HIV status was documented for 65% (15/23), of whom 7% (1/15) were HIV-infected. No deaths were reported.

Whole Genome Sequencing (WGS) results: Cluster analysis for *Salmonella* Typhi and *Salmonella* Paratyphi

From the total of 139 cases of enteric fever reported to the Centre for Enteric Diseases from eight provinces (with the Northern Cape being the only province to report no cases), isolates were received for 83% of cases (115/139), and WGS was completed for 91% of the isolates received (105/115). WGS results were further interrogated to identify potential clusters that were circulating in South Africa in 2024. For this report, a cluster is defined as three or more genetically related strains identified during 2024. Analysis of WGS results identified eight clusters of genetically related enteric fever cases, which were epidemiologically investigated. Findings of the *Salmonella* Typhi and *Salmonella* Paratyphi WGS cluster analyses are summarised below (Figure 22).

Outbreak of enteric fever cases caused by *Salmonella* Paratyphi (Paratyphoid fever): Gauteng - Hammanskraal

Between 24 April and 06 December 2024, 18 genetically related cases of paratyphoid fever were reported across two provinces and three districts. The majority were from Gauteng, with 15 cases in the City of Tshwane and two in the City of Johannesburg, while one case was detected in the Dr Kenneth Kaunda District of the North West. All of the 15 cases confirmed in the City of Tshwane resided in the Hammanskraal area. During investigation, no direct epidemiological links were identified among these cases; therefore, contaminated municipal water may be suspected as the most likely source of infection, similar to the cholera outbreak reported in 2023 (Figure 23).

Clusters of enteric fever cases caused by *Salmonella* Typhi (typhoid fever): Gauteng - Hammanskraal

In addition to the paratyphoid fever outbreak that occurred between April and December 2024, three distinct clusters of typhoid fever were identified during a similar period, with the Hammanskraal area in the City of Tshwane being the predominant area of residence for cases in each cluster. Contaminated municipal water is suspected as the most likely source of infection, supported by the concurrent identification of multiple clusters involving different *S. Typhi* strains in the same area during this period (Figure 22).

- **Cluster 1:** Between 13 February and 01 September 2024, 12 genetically related cases of typhoid fever were reported in Gauteng, affecting two districts. Eleven cases were from the City of Tshwane, all residing in the Hammanskraal area, and one case was reported from the City of Ekurhuleni. No direct epidemiological links were identified among the cases.
- **Cluster 2:** Between 24 January and 29 October 2024, nine genetically related cases were reported in Gauteng, also affecting two districts. Eight cases occurred in the City of Tshwane, all from the Hammanskraal area, and one case was reported from the City of Ekurhuleni. No direct epidemiological links were identified among the cases.
- **Cluster 3:** Between 27 February and 1 September 2024, five genetically related cases were reported across two provinces and three districts. Three cases were from Gauteng (City of Tshwane, all residing in Hammanskraal), and two cases were reported from the Western Cape (City of Cape Town and West Coast District). No direct epidemiological links were identified among the cases.

Clusters of enteric fever cases caused by *Salmonella* Typhi (typhoid fever) spanning multiple provinces (Figure 22):

- **Cluster 1:** Between 21 January and 9 November 2024, nine genetically related cases of typhoid fever were reported

across three provinces and six districts. The majority were from Gauteng (n = 7), with cases reported from the City of Tshwane (n = 3), City of Johannesburg (n = 2), City of Ekurhuleni (n = 1), and West Rand District (n = 1). One case was reported from the Dr Kenneth Kaunda District in the North West and one from the Nkangala District in Mpumalanga. This cluster represents a continuation of the outbreak strain responsible for a large outbreak that began in the North West in November 2020, affecting over 100 cases reported across six provinces. The outbreak has been associated with illegal mining activities.

- **Cluster 2:** Between 18 January and 23 December 2024, four genetically related cases of typhoid fever were reported across three provinces, affecting three districts. Two cases were reported from the City of Cape Town in the Western Cape, while one case each was reported from the Chris Hani District in the Eastern Cape and eThekweni Metro in KwaZulu-Natal. No direct epidemiological links were identified among the cases.

Cluster of enteric fever cases caused by *Salmonella* Typhi (typhoid fever): the Western Cape

Between 23 April and 18 November 2024, four genetically related cases of typhoid fever were reported from the Western Cape, affecting two districts. Two cases in April 2024 were reported from the City of Cape Town, and two cases in November were reported from the Garden Route District. No direct epidemiological links were identified among the cases (Figure 22).

Cluster of enteric fever cases caused by *Salmonella* Typhi (typhoid fever): North West

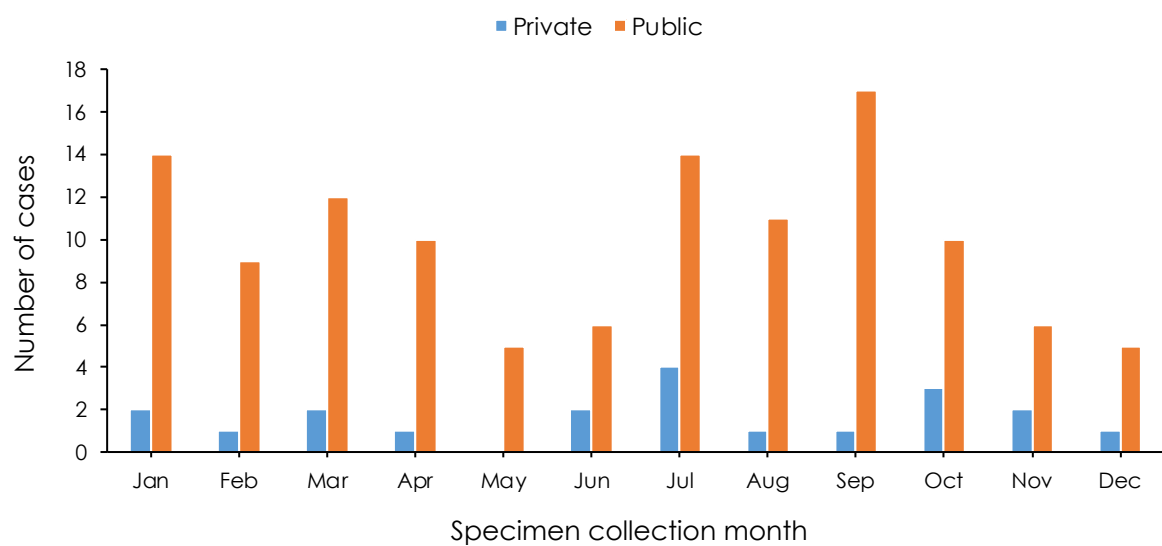
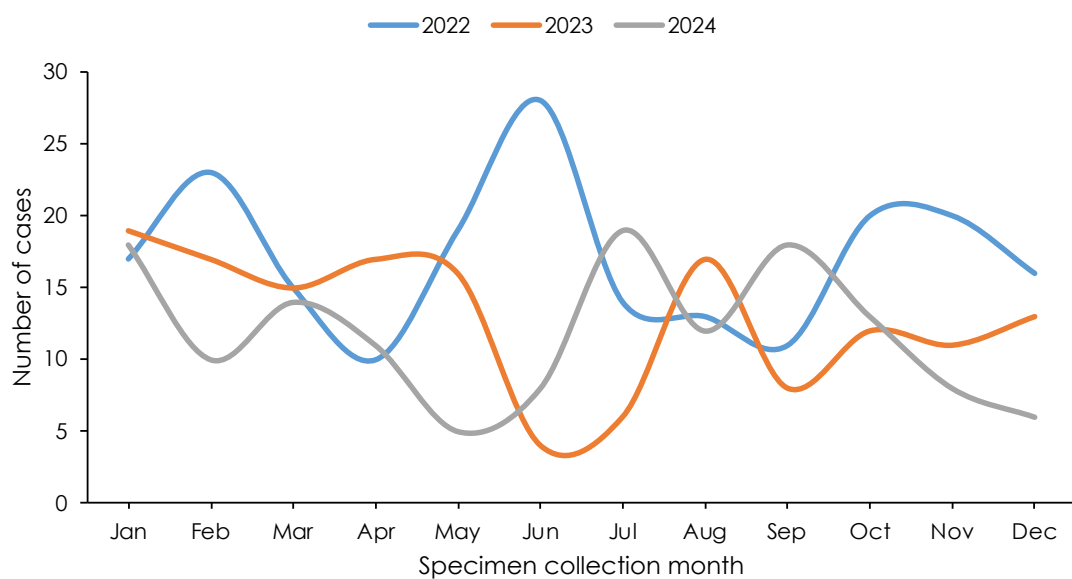
Three genetically related cases of typhoid fever were reported from the Dr Kenneth Kaunda District in the North West. The first case had a specimen collection date of 13 April, the second on 29 July, and the third on 18 October 2024. No direct epidemiological links were identified among the cases (Figure 22).

Table 23. Number of cases of *Salmonella* Typhi and Paratyphi by health sector and province, South Africa, 2024, n = 139 (including audit reports, missing isolates, mixed and contaminated cultures)

Province	Private sector	Public sector	Total
Eastern Cape	1	2	3
Free State	0	3	3
Gauteng	13	62	75
KwaZulu-Natal	0	14	14
Limpopo	1	1	2
Mpumalanga	2	6	8
Northern Cape	0	0	0
North West	1	10	11
Western Cape	2	21	23
South Africa	20	119	139

Table 24. Number of cases of *typhoidal salmonella* by serovar and province, South Africa, 2024, n = 139 (including audit reports, missing isolates, mixed and contaminated cultures)

Province	Paratyphi A	Typhi	Total
Eastern Cape	0	3	3
Free State	0	3	3
Gauteng	18	57	75
KwaZulu-Natal	0	14	14
Limpopo	0	2	2
Mpumalanga	0	8	8
Northern Cape	0	0	0
North West	1	10	11
Western Cape	0	23	23
South Africa	19	120	139

**Figure 20. Number of cases of *Salmonella* Typhi and Paratyphi by month of sample collection and health sector, South Africa, 2024 (N=139)****Figure 21. Trends of cases of *Salmonella* Typhi and Paratyphi reported by month and year of sample collection, South Africa, 2022 – 2024 (N=498)**

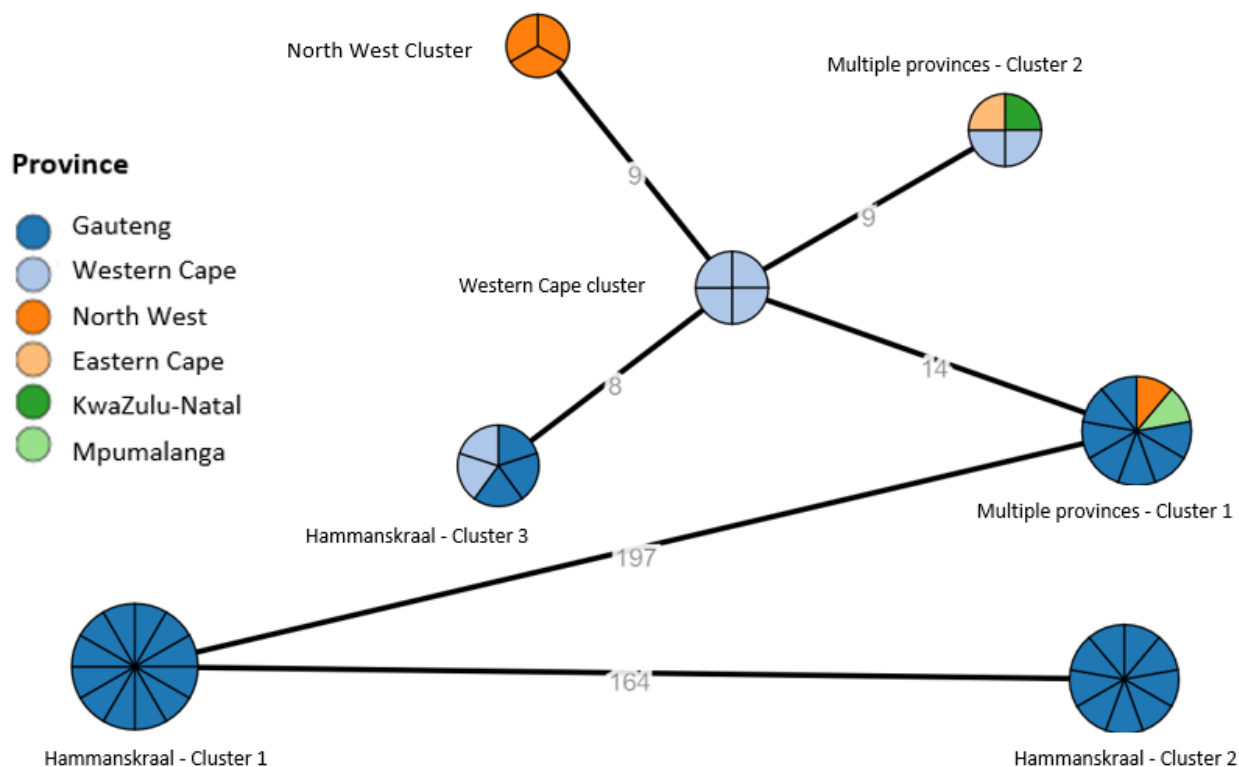


Figure 22: Minimum spanning tree drawn using cgMLST data from *Salmonella* Typhi isolates sourced from South Africa, 2024.

The circular nodes represent isolate(s). Isolates showing ≤ 5 allelic differences, are collapsed together into a single circular node. The larger the circular node, the more isolates which are reflected. The number values between adjacent nodes indicate the number of allele differences between connecting nodes (isolates).

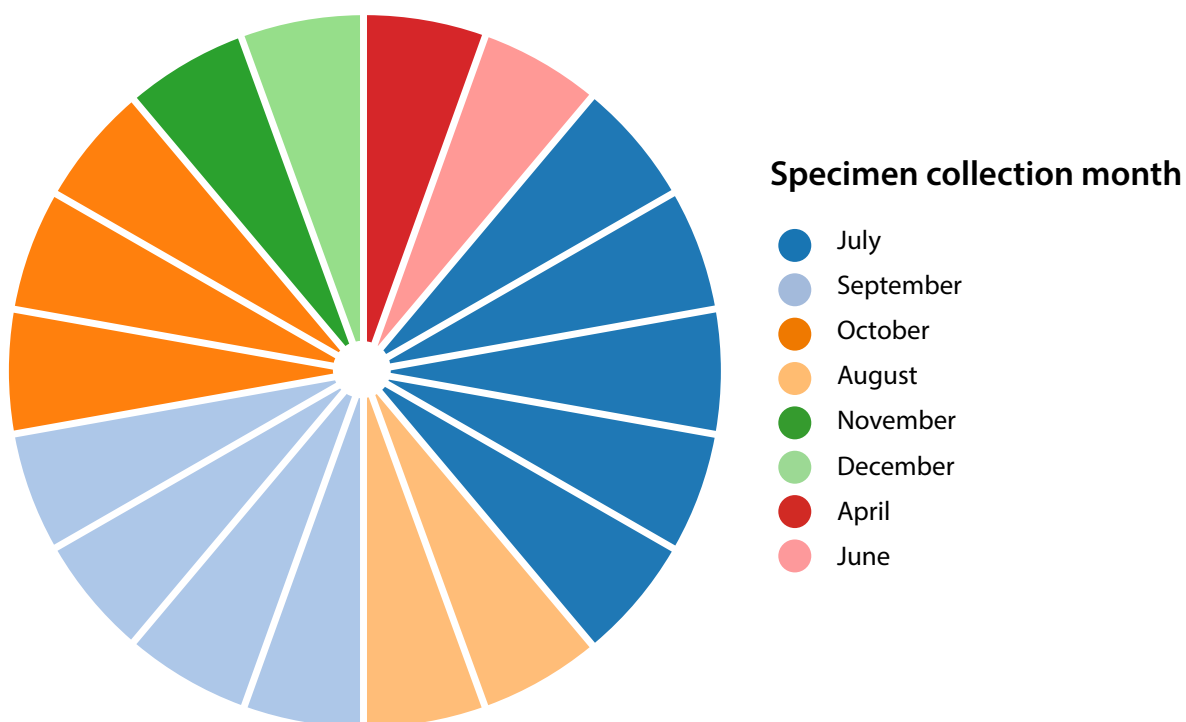
Table 25. Number of cases of *Salmonella* Typhi and Paratyphi by age category, South Africa, 2024, n=139 (including audit reports)

Age category (years)	n	%
0 - 4	19	14
5 - 14	60	43
15 - 24	21	15
25 - 34	14	10
35 - 44	8	6
45 - 54	6	4
55 - 64	4	3
≥ 65	1	1
Unknown	6	4
Total	139	100

Table 26. Ciprofloxacin and azithromycin susceptibility* of viable *Salmonella* Typhi and Paratyphi isolates received and tested at the Centre for Enteric Diseases by province, South Africa, 2024 (n = 90)

Province	Ciprofloxacin		Azithromycin	
	Susceptible, n (%)	Non-Susceptible, n (%)	Susceptible, n (%)	Non-Susceptible, n (%)
Eastern Cape	0	2 (100)	2 (100)	0
Free State	0	0	0	0
Gauteng	47 (96)	2 (4)	49 (100)	0
KwaZulu-Natal	5 (100)	0	5 (100)	0
Limpopo	2 (100)	0	2 (100)	0
Mpumalanga	3 (75)	1 (25)	4 (100)	0
Northern Cape	0	0	0	0
North West	7 (100)	0	7 (100)	0
Western Cape	17 (89)	4 (19)	21 (100)	0
South Africa	81 (90)	9 (10)	90 (100)	0 (0)

*According to CLSI breakpoints

**Figure 23: Minimum spanning tree drawn using cgMLST data from *Salmonella* Paratyphi A isolates sourced from South Africa, 2024.**The circular nodes represent isolate(s). Isolates showing ≤ 5 allelic differences, are collapsed together into a single circular node.

Discussion

Enteric fever caused by *Salmonella* Typhi remains endemic in South Africa. Following the outbreaks in 2005–2006, the number of culture-confirmed cases annually remained stable at <150 cases per year from 2006 through 2021. In 2021, the highest annual total number of cases since 2006 was reported (n=133). In 2022, this increased to a total of 204 cases, then decreased to 155 cases in 2023. The decline in cases persists in 2024, with only 139 cases being reported. In keeping with previous years, the highest number of cases were reported in the 5–14-year age group.

Although small, localised outbreaks of enteric fever were identified in 2024, most cases were sporadic. The increase in the number of cases observed between July and September was mainly driven by cases reported from the City of Tshwane Metro in Gauteng.

Salmonella Typhi isolates from both invasive and non-invasive sites were included in these analyses, as both added to the burden of infection in South Africa and represent a public health risk. The diagnosis of enteric fever remains challenging, and reported cases significantly underrepresent the true number of cases. Heightened clinical awareness and appropriate laboratory tests are critical in identifying cases. Culture remains the gold standard for confirming enteric fever, so prevailing clinician-testing behaviour heavily influences the likelihood of detecting cases. Greater numbers of cases reported from Gauteng and the Western Cape could, in part, reflect healthcare-seeking behaviour and prevailing clinician-testing practices.

Cases of enteric fever caused by *Salmonella* enterica serovars Paratyphi A, Paratyphi B, or Paratyphi C generally remain uncommon in South Africa, with only two cases reported in 2023: one Paratyphi B var Java from the Northern Cape and one Paratyphi A from the Western Cape. However, in 2024, the highest number of *Salmonella* Paratyphi A cases since 2003 was recorded, with 19 cases reported: 18 from the City of Tshwane in Gauteng and one from Dr Kenneth Kaunda District in the North West.

The proportion of isolates showing resistance to ciprofloxacin (10%) is significantly higher than in 2023 (2%), which indicates that growing resistance in *Salmonella* isolates remains a concern. *Salmonella* Typhi isolates should routinely be tested against azithromycin, which is an alternative oral antibiotic option for treating disease caused by ciprofloxacin-resistant strains. Ceftriaxone may also be used as an alternative therapy, but needs to be administered parenterally.

Cluster analysis of all *S. Paratyphi* and *S. Typhi* isolates that underwent WGS in 2024 revealed eight clusters of enteric fever that were either contained within a province or spanned multiple provinces. These clusters were investigated further to identify possible epidemiological links; however, no epidemiological links were identified among the cases within each cluster. Hence, contaminated municipal water supply is suspected as the most likely source of infection, specifically in the Hammanskraal area. This is supported by the concurrent identification of multiple clusters involving different *S. Typhi* strains in the same area during 2024.

Nontyphoidal *Salmonella enterica* (NTS)

Results

A total of 3 294 cases of non-typhoidal salmonellosis, from all sample sites, were reported through the surveillance programme in 2024 when marginally higher numbers were reported than in 2023 (n=3 162) and 2022 (n=3 185). In 2024, 30% (986/3 294) were indicative of invasive disease (Table 27). Of the 986 invasive non-typhoidal salmonellosis cases reported, the majority (85%, 840/986) were from the public sector; the majority (57%, 1 318/2 308) of non-invasive non-typhoidal salmonellosis cases were reported by the private sector. Invasive cases were mostly isolated from blood culture 89% (873/986). All CSF isolates were reported by the public sector (Table 28). This could be due in part to differences in health-seeking behaviour and diagnostic practices among clinicians in the respective health sectors.

The highest numbers of cases of invasive disease were reported from Gauteng (392/986; 40%), followed by the Western Cape (239/986; 24%) and Eastern Cape (95/986; 10%) provinces (Table 27). Gauteng also reported the highest number of cases of non-invasive disease (1 031/2 308; 45%), followed by the Western Cape (478/2 308; 21%). In keeping with previous years, a seasonal prevalence was noted for non-invasive disease, with lower numbers of cases identified in the winter months. No overt seasonal pattern was noted with invasive disease (Figure 24). As in previous years, although seasonal prevalence was noted for non-invasive disease (increased numbers in the earlier months

of the year and low numbers in the winter months), invasive disease showed no seasonality (Figure 25).

Non-invasive disease was highest in children younger than five years (521/2 308; 23%), followed by people ≥65 (337/2 308; 15%) and people aged 35–44 (281/2 308; 12%). In contrast, invasive disease was most common in people aged 35 to 44 years (195/986; 20%), followed by children younger than five years (161/986; 16%) and people aged 25 to 34 years (157/986; 16%) (Table 29). Overall, stool specimens accounted for 61% (2 022/3 294) of the total cases.

A total of 1 311 viable isolates were received and serotyped; this included isolates submitted as part of routine laboratory-based surveillance as well as isolates submitted for outbreak investigation purposes. A total of 67 distinct serovars were identified, but two serovars accounted for the majority of the cases: *Salmonella* Enteritidis (1 003/1 311; 77%) and *Salmonella* Typhimurium (176/1 311; 13%). Proportions of common serovars differed among provinces, but *Salmonella* Enteritidis was the most common serovar in all provinces (Figure 26). Antimicrobial susceptibility testing was not routinely performed, but was offered on request. Of the two isolates tested, both were non-susceptible to ciprofloxacin but remained susceptible to azithromycin, based on CLSI breakpoints.

Identification of Non-typhoidal *Salmonella* clusters linked to foodborne disease outbreaks identified through routine whole genome sequencing, 2024

Cluster 1: This cluster was associated with a suspected foodborne disease outbreak that affected six people residing in different communities in Gauteng and North West between January and April 2024. The most common food item reported by cases prior to illness onset was crumbed chicken products (e.g., nuggets, schnitzel, strips). Six *Salmonella* Muenchen isolates were identified through routine NTS surveillance and confirmed by WGS, which showed that all were highly genetically related. Further analysis using EnteroBase revealed six additional genetically related isolates from the UK (n = 5) and Scotland (n = 1) that occurred during the same period. Travel history was available for three of these international cases, all of whom had travelled to South Africa prior to illness onset, suggesting that infection was most likely acquired in South Africa (Figure 27).

Cluster 2: This cluster was associated with an outbreak of salmonellosis that affected 61 community members who had purchased and consumed shawarmas from two related fast-food outlets in Mkhondo, Mpumalanga, during August–September 2024. Ten stool specimens were collected during the outbreak investigation, all of which tested positive for *Salmonella* Enteritidis. WGS confirmed that the isolates were highly genetically related (Figure 28).

Cluster 3: This cluster was associated with a foodborne disease outbreak of *Salmonella* Enteritidis that affected residents/patients at a mental health clinic in the City of Tshwane during July 2024. A total of 18 samples were collected during the outbreak investigation, including 16 clinical specimens (15 from patients and one from a food handler) and two food samples (roasted beef and roasted vegetables). All samples tested positive for *Salmonella* Enteritidis. WGS confirmed that the human and non-human isolates were highly genetically related (Figure 28).

Cluster 4: This cluster was associated with a foodborne disease outbreak that affected more than 10 patrons at a restaurant on the West Coast, the Western Cape, in December 2024. A total of 10 clinical specimens were collected, all of which tested positive for *Salmonella* Enteritidis. WGS confirmed that the isolates were highly genetically related (Figure 28).

Cluster 5: This cluster was associated with a foodborne disease outbreak in which six family members became ill after consuming goat meat and a partially consumed cool drink received from a neighbour's house. A two-year-old child died as a result of the illness. Six stool specimens were collected, and all tested positive for *Salmonella* Typhimurium. WGS confirmed that the isolates were highly genetically related (Figure 29).

Table 27. Number of cases of invasive and non-invasive nontyphoidal salmonellosis by province, South Africa, 2024, n = 3 294 (including audit reports)

Province	Non-invasive nontyphoidal salmonellosis (%)	Invasive nontyphoidal salmonellosis (%)	Total (%)
Eastern Cape	189 (8)	95 (10)	284 (9)
Free State	105 (5)	41 (4)	146 (4)
Gauteng	1031 (45)	392 (40)	1423 (43)
KwaZulu-Natal	189 (8)	85 (9)	274 (8)
Limpopo	42 (2)	39 (4)	81 (2)
Mpumalanga	98 (4)	26 (3)	124 (4)
Northern Cape	50 (2)	17 (2)	67 (2)
North West	126 (5)	52 (5)	178 (5)
Western Cape	478 (21)	239 (24)	717 (22)
South Africa	2 308	986	3 294

Table 28. Number of cases of invasive and non-invasive nontyphoidal salmonellosis by healthcare sector and primary anatomical site of isolation, South Africa, 2024, n = 3 294 (including audit reports)

Sector & Specimen	Public	Private	Total
Non invasive	991	1 318	2 308
Stool	731	1 291	2 022
Urine	156	20	176
Other	104	6	110
Invasive	840	146	986
Blood culture	743	130	873
CSF	14	0	14
Urine	0	1	1
Other	83	15	98
South Africa	1 831	986	3 294

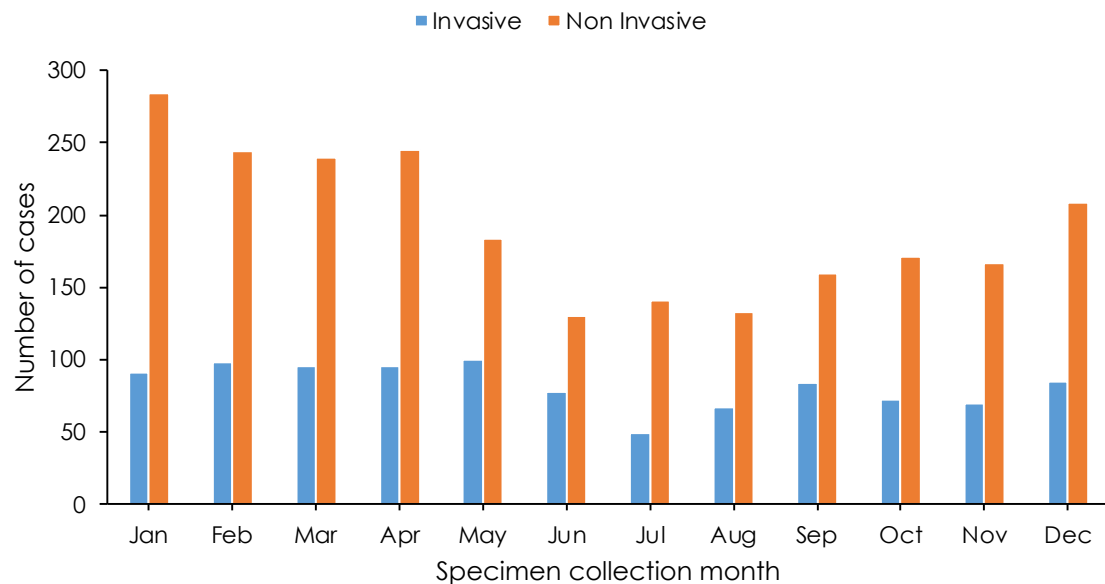


Figure 24. Number of cases of non-invasive (n=2 308) and invasive (n=986) nontyphoidal salmonellosis by month, South Africa, 2024

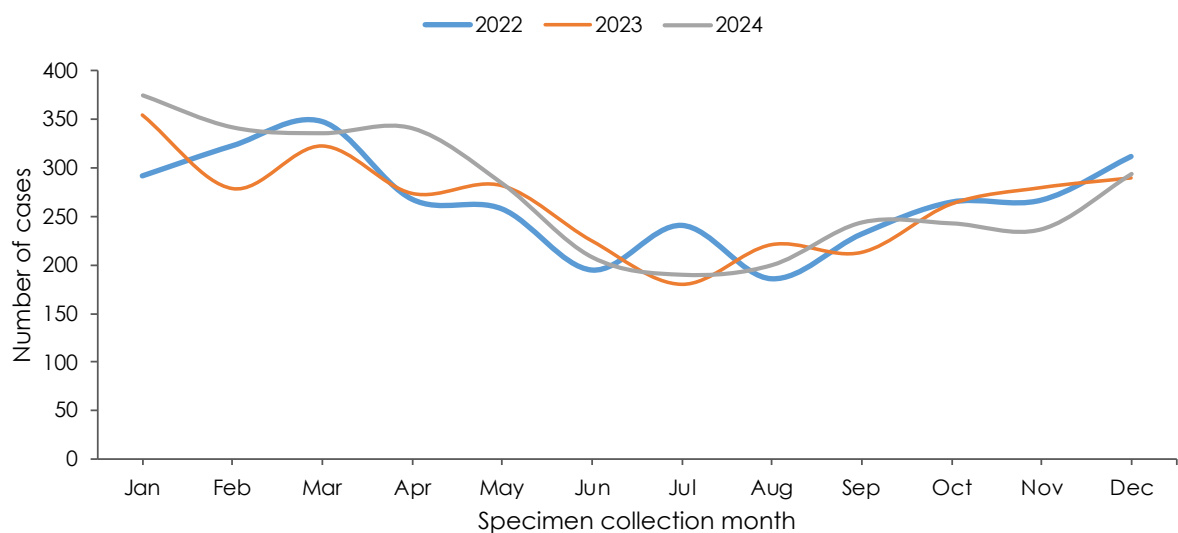


Figure 25. Number of cases of nontyphoidal *Salmonella* by month and year, South Africa, 2022 – 2024 (N=9 641)

Table 29. Number of cases of invasive and non-invasive nontyphoidal salmonellosis by age category, South Africa, 2024, n=3 294 (including audit reports)

Age category (years)	Non-Invasive	Invasive	Total (%)
0 - 4	521 (23)	161 (16)	682 (21)
5 - 14	198 (9)	20 (2)	218 (7)
15 - 24	154 (7)	40 (4)	194 (6)
25 - 34	234 (10)	157 (16)	391 (12)
35 - 44	281 (12)	195 (20)	476 (14)
45 - 54	242 (10)	134 (14)	376 (11)
55 - 64	264 (11)	100 (10)	364 (11)
≥ 65	337 (15)	120 (12)	457 (14)
Unknown age	77 (3)	59 (6)	136 (4)
Total	2 308	986	3 294

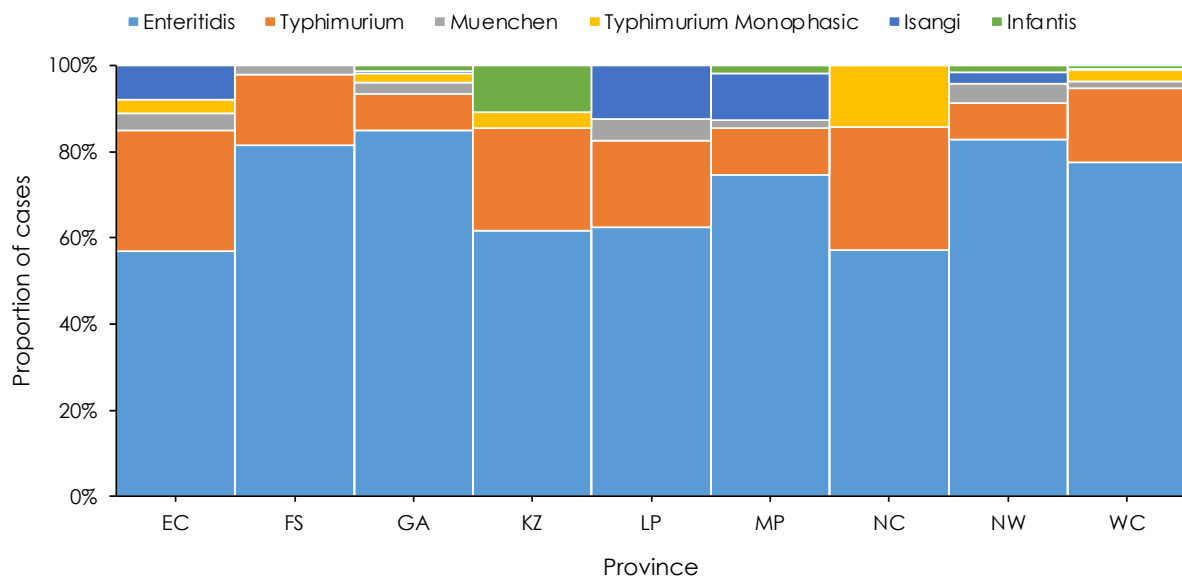


Figure 26. Proportions of the six most common *Salmonella enterica* serovars causing nontyphoidal salmonellosis by province, South Africa, 2024 (N=1 311)

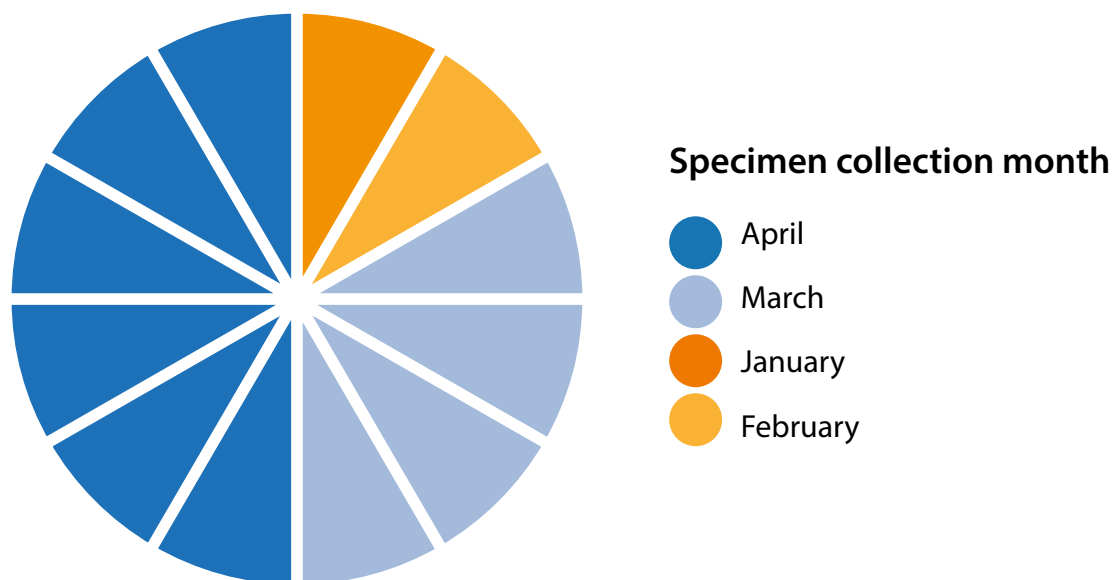


Figure 27. Minimum spanning tree drawn using cgMLST data from *Salmonella Muenchen* isolates sourced from South Africa, 2024.

The circular nodes represent isolate(s). Isolates showing ≤ 5 allelic differences, are collapsed together into a single circular node.

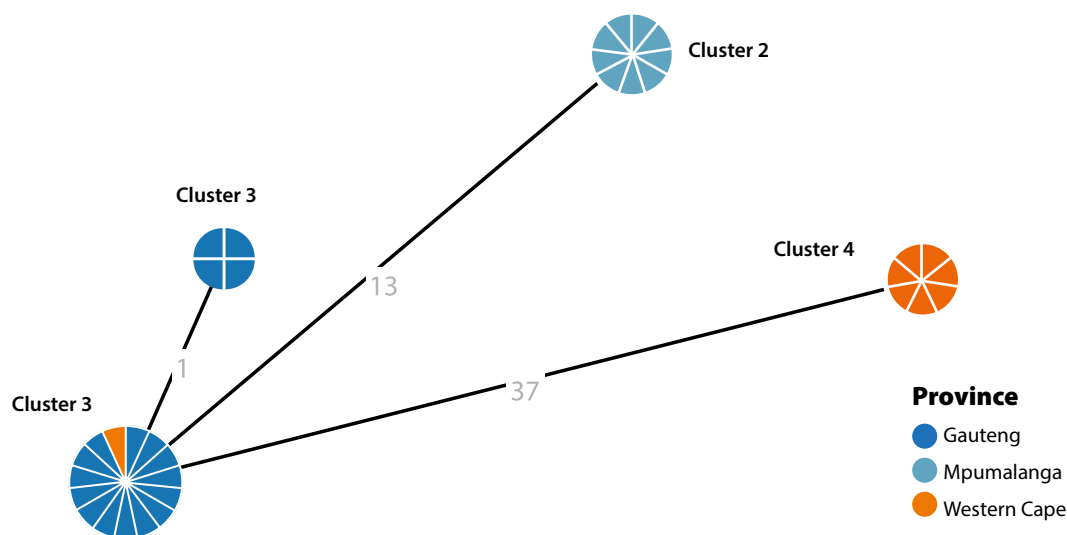


Figure 28. Minimum spanning tree drawn using cgMLST data from *Salmonella Enteritidis* isolates sourced from South Africa, 2024.

The circular nodes represent isolate(s). Isolates showing zero allelic differences, are collapsed together into a single circular node. The larger the circular node, the more isolates which are reflected. The number values between adjacent nodes indicate the number of allele differences between connecting nodes (isolates).

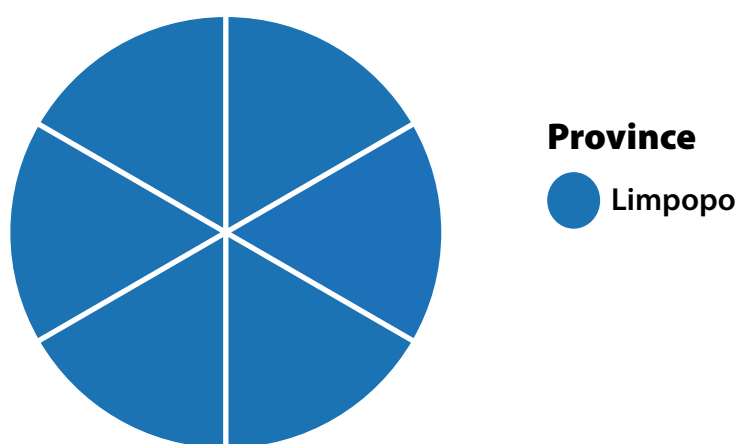


Figure 29. Minimum spanning tree drawn using cgMLST data from *Salmonella Typhimurium* isolates sourced from South Africa, 2024.

The circular nodes represent isolate(s). Isolates showing ≤ 5 allelic differences, are collapsed together into a single circular node.

Discussion

Non-typhoidal salmonellosis is usually foodborne and typically manifests as acute gastroenteritis. Invasive disease is usually associated with HIV infection or the presence of other co-morbid conditions.

Greater numbers of invasive diseases reported from Gauteng and the Western Cape may reflect healthcare-seeking behaviour and clinician-testing practices. Children younger than 5 years bear the highest burden of non-invasive disease, but invasive disease was reported more commonly in adults aged 35-44 years; as in previous years, this is likely the effect of a high proportion of HIV-infected cases in this age group.

Salmonella Enteritidis was the predominant serovar, followed by *Salmonella Typhimurium*, a pattern observed since 2012. Provincial differences in serovar proportions might reflect local transmission dynamics or undetected outbreaks and require further investigation. By assisting to establish clusters of NTS and the source of outbreaks in different settings, the use of WGS serves as a useful tool specifically to investigate suspected foodborne disease outbreaks (often caused by NTS) that occur within the country.

Shigella species

Results

A total of 921 culture-confirmed cases of shigellosis were reported through the surveillance programme in 2024, similar to the numbers reported in previous years: 2022 (n = 948) and 2023 (n=952). In 2024, most cases (670/921; 73%) were identified in the public health sector. Thirty-nine per cent of cases were reported from the Western Cape (358/921), with Gauteng and Eastern Cape contributing to 24% (217/921) and 13% (120/921) of the total cases, respectively (Table 30). The total includes *Shigella* spp. isolated from all sample sites, but in 90% (829/921) of the cases, the isolate was recovered from stool or rectal swab samples, reflecting non-invasive dysentery or diarrhoea. In the remaining 10% of cases, the isolate was recovered from blood culture (48/921; 5%) or other extra-intestinal sample sites (44/921; 5%) (Table 31). The highest number of shigellosis cases occurred in January, March, and April (Figure 30). As in 2022 and 2023, increased numbers of cases were identified in the earlier months of the year. No typical pattern of seasonality was noted in Figure 31. The highest numbers of cases of shigellosis were reported in children younger than five years (288/921; 31%), followed by children 5-14 years of age (124/921; 13%). The proportion of invasive shigellosis cases remains low (49/921; 5%), and as in previous years invasive disease was highest in children younger than five years (12/49; 24%) (Table 32).

A total of 572 viable isolates were received and serotyped, including isolates submitted as part of routine laboratory-based surveillance as well as isolates submitted for outbreak

investigation purposes. Twenty-eight different serotypes were identified. The most common serovar was *S. flexneri* type 2a (254/572; 44%), followed by *S. sonnei* (109/572; 19%), *S. flexneri* type 3a (68/572; 12%), and *S. flexneri* type 1b (50/572; 9%). The proportion of the serotypes differed among provinces, with *S. flexneri* type 2a predominating in three provinces (the Northern Cape, Mpumalanga, and Eastern Cape). In Limpopo, Free State, and Gauteng, *S. sonnei* dominated (Figure 32). Antimicrobial susceptibility testing was performed on 684 isolates. Of those isolates where susceptibility testing was performed, 98% (669/684) were susceptible to ciprofloxacin and 99% (675/684) were susceptible to azithromycin.

A total of 263 shigellosis cases were reported from enhanced surveillance sites (ESS), accounting for 29% (263/921) of all cases captured through the surveillance programme. Case reports were completed for 74% (195/263) of these patients. Children aged ≤15 years constituted 52% (102/195) of cases. HIV status was recorded for 75% (147/195) of patients with completed case reports, of whom 25% (37/147) were HIV-infected. HIV seropositivity was highest among patients aged 35–44 years (n=13) and lowest in children <5 years. A CD4 cell count measured close to diagnosis was available for 86% (32/37) of HIV-infected patients, with a median of 256 cells/μl (interquartile range: 1–1 019 cells/μl). Nearly half (47%) had CD4 counts <200 cells/μl. The in-hospital case-fatality ratio among patients at ESS was 3% (6/183).

Table 30. Number of cases of shigellosis by health sector and province, South Africa, 2024, n=921 (including audit reports)

Province	Private sector	Public sector	Total
Eastern Cape	7	113	120 (13)
Free State	31	25	56 (6)
Gauteng	153	64	217 (24)
KwaZulu-Natal	19	81	100 (11)
Limpopo	4	2	6 (1)
Mpumalanga	12	10	22 (2)
Northern Cape	9	11	20 (2)
North West	11	11	22 (2)
Western Cape	5	353	358 (39)
South Africa	251	670	921

Table 31. Number of cases of invasive and non-invasive shigellosis by healthcare sector and primary anatomical site of isolation, South Africa, 2024, n = 921 (including audit reports)

Sector & Specimen	Public	Private	Total
Non invasive	638	234	872
Stool	596	233	829
Other	42	1	43
Invasive	47	2	49
Blood culture	46	2	48
Other	1	0	1
South Africa	685	236	921

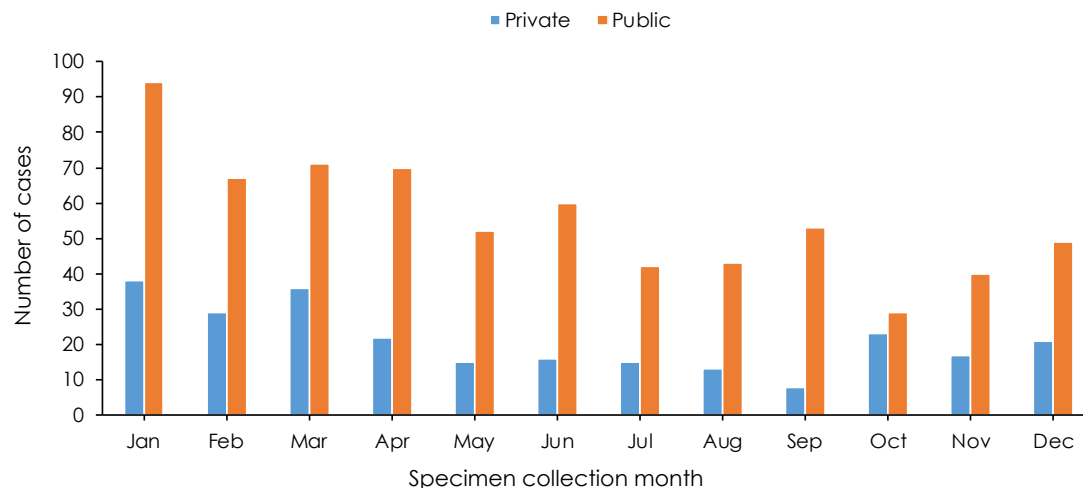


Figure 30. Number of cases of shigellosis by month and health sector, South Africa, 2024, n = 921 (including audit reports)

*Includes *Shigella* isolates from invasive and non-invasive cases. Twenty-eight different serovars of *Shigella* were identified with the six most common serovars in the figure above accounting for 62% (572/921) of the total.

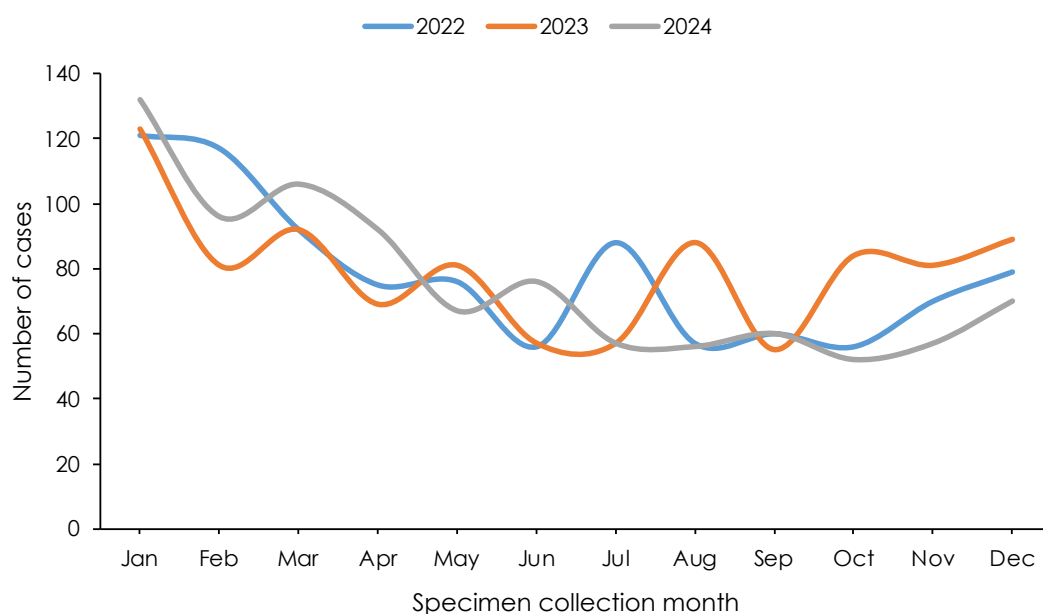


Figure 31. Trends of cases of shigellosis by month and year, South Africa, 2022 - 2024 (including audit reports), (N=2 821)

Table 32. Number of non-invasive and invasive cases of shigellosis reported by age category, South Africa, 2024, n=921 (including audit reports)

Age category (years)	Non-invasive (%)	Invasive (%)	Total (%)
0 - 4	276 (31)	12 (24)	288 (31)
5 - 14	121 (14)	3 (6)	124 (13)
15 - 24	46 (5)	2 (4)	48 (5)
25 - 34	108 (12)	4 (8)	112 (12)
35 - 44	108 (12)	9 (18)	117 (13)
45 - 54	70 (8)	3 (6)	73 (8)
55 - 64	61 (7)	4 (8)	65 (7)
≥ 65	73 (8)	11 (22)	84 (9)
Unknown age	9 (1)	1 (2)	10 (1)
Total	872 (95)	49 (5)	921

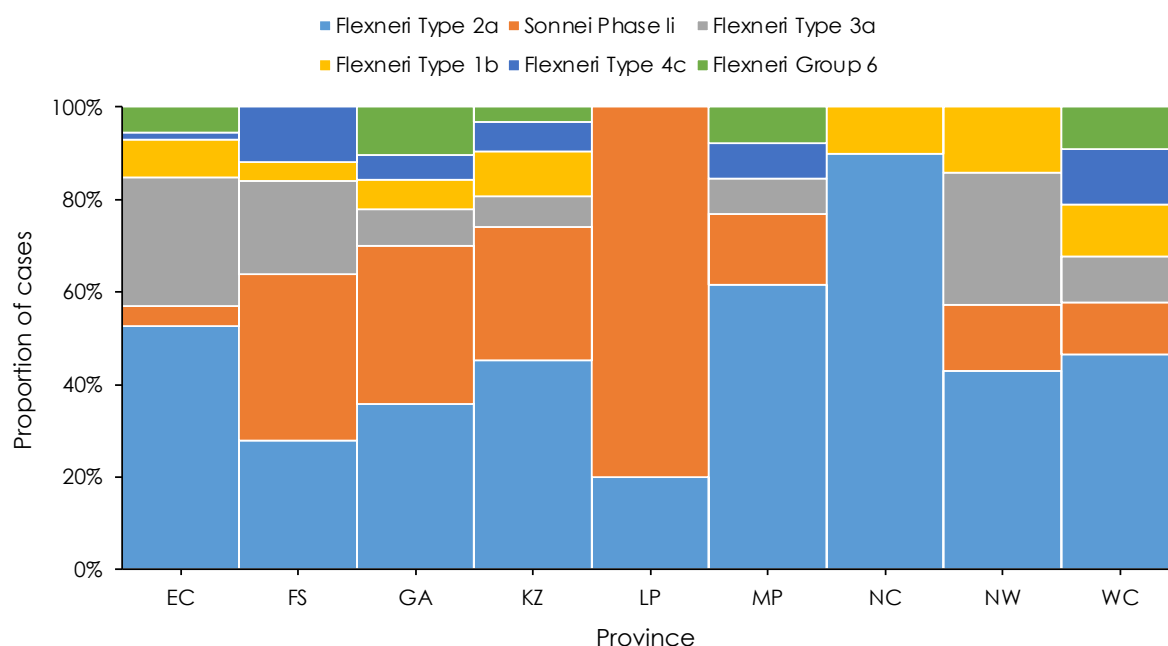


Figure 32. Proportions of the most common *Shigella* species and serotypes by province, South Africa, 2024, (572/921) *

*Includes *Shigella* isolates from invasive and non-invasive cases. Twenty-eight different serovars of *Shigella* were identified with the six most common serovars in the figure above accounting for 62% (572/921) of the total.

Discussion

Although *Shigella* infection has been associated with waterborne outbreaks in South Africa, person-to-person transmission plays an important role. Children younger than five years continue to bear the highest burden of shigellosis. The primary manifestation of disease due to *Shigella* is non-invasive dysentery or diarrhoea, and invasive disease is uncommon.

Although proportions differ, as in previous years, *S. flexneri* type 2a and *S. sonnei* were two of the three commonest serotypes. Provincial differences in serotype proportions might reflect local transmission dynamics or undetected outbreaks.

Listeriosis

Results

In 2024, a total of 73 cases of listeriosis were reported to the Centre for Enteric Diseases through the NMC surveillance system. Cases were reported from all nine provinces, with the majority reported from Gauteng (24/73; 33%), the Western Cape (18/73; 25%), and KwaZulu-Natal (14/73; 19%) (Table 33). Patients ranged in age from 0 to 90 years, with a median age of 35 years. Where sex was known, 51% (36/71) were female. Most cases occurred in adults aged 15–49 years (21/73; 29%), followed by neonates aged ≤28 days (17/73; 23%) and the elderly aged ≥65

years (Table 34). The most common specimen types were blood culture (51/73; 70%) and CSF (17/73; 23%).

Twenty-seven cases (37%) were detected at ESS; however, listeriosis CIFs were completed for only 19 of these cases (70%) (Table 33). HIV status was reported for five cases, with one HIV-exposed neonate and four HIV-positive adults. Three deaths were recorded.

Table 33. Number and percentage of cases of listeriosis reported from ESS by province, South Africa, 2024 (n = 27)

Province	Total cases	Cases reported from ESS		Completed case reports	
		n	%	n	%
Eastern Cape	5	0	0	0	0
Free State	4	0	0	0	0
Gauteng	24	14	58	12	86
KwaZulu-Natal	14	5	36	3	60
Limpopo	2	0	0	0	0
Mpumalanga	1	0	0	0	0
Northern Cape	2	0	0	0	0
North West	3	1	33	1	100
Western Cape	18	7	33	1	100
South Africa	73	27	37	19	70

Discussion

The number of listeriosis cases for 2024 is lower than 2023 (n=83). It is below the expected range of annual cases (119–298) based on the estimated incidence of sporadic cases (2–5 cases

per million population per year). The distribution of cases by province and age group is similar to that reported in 2023.

Vibrio cholerae

Results

In 2024, a total of 13 laboratory-confirmed cholera cases were reported from three provinces: Limpopo (n=11), Gauteng, and Mpumalanga each reported one case (Table 35). All cases were confirmed at the Centre for Enteric Diseases using culture, serotyping, and PCR. All isolates were identified as *Vibrio cholerae* toxigenic serogroup O1, with 12 classified as serogroup Ogawa and one as serogroup Inaba (from Limpopo). WGS identified two sequence types: ST69 (n=6) and ST75 (n=7) (Figure 33).

The age groups 25–34 years and 35–44 years each accounted for three cases, followed by two cases in the 5–14 years age group (Table 36). Antimicrobial susceptibility testing was performed on 12 *Vibrio cholerae* O1 isolates, all of which were susceptible to azithromycin and ciprofloxacin (Table 37).

Overall, 162 cholera cases were notified through the NMC system, including 13 laboratory-confirmed cases, 5 suspected deaths, and 144 suspected cases. In addition, 68 stool specimens

were received and tested using PCR, of which 55 were negative for the cholera-toxin ctxA gene (do not meet the case definition for cholera), while 13 were positive for the cholera-toxin ctxA gene (considered to be cholera cases).

Discussion

In February 2023, a cholera outbreak was declared in South Africa; since then, the number of cases has significantly subsided. Earlier South African surveillance data from 2018–2021 established the emergence and dominance of non-epidemic, *V. cholerae* ST75 in the country. The presence of this sequence type continues to be closely monitored.

Only isolates/stool specimens tested at the centre are included in this report. Cases of nontoxigenic non-O1/non-O139 *V. cholerae* are not considered to be cholera and do not warrant a public health response.

Table 34. Number and percentage of cases of listeriosis reported from ESS by age group, South Africa, 2024 (n=27)

Province	Total number of cases	Cases reported from ES sites	
		n	%
Neonate (≤28 days)	17	5	29
Children (1 month-14 years)	10	5	50
Adults (15-49 years)	21	10	48
Adults (50-64 years)	11	4	36
Elderly (≥65 years)	13	2	15
Unknown age	1	1	100
Total	73	27	37

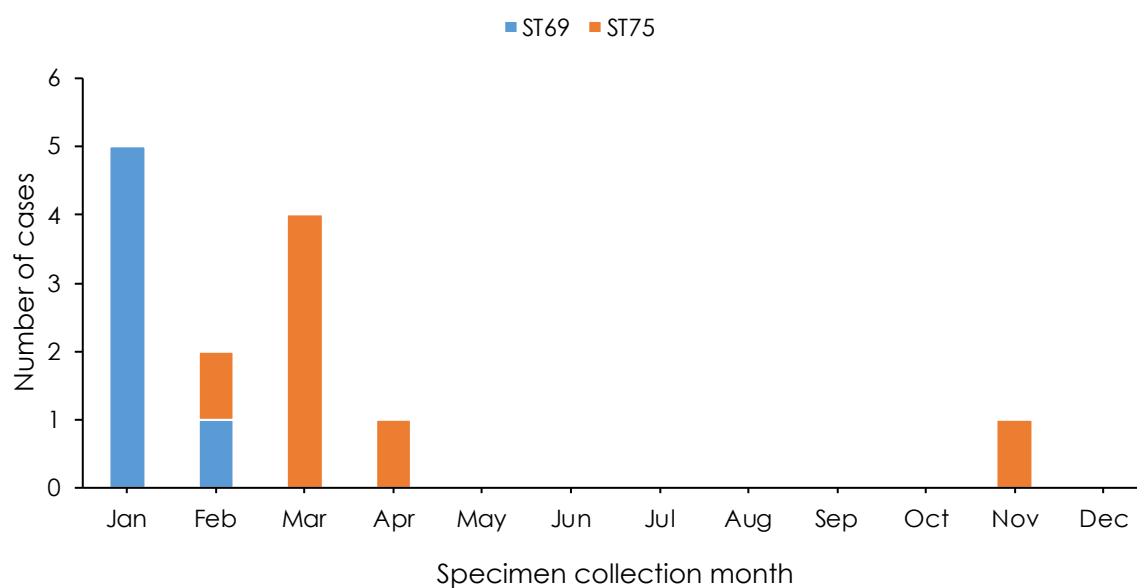


Figure 33. Number of cases of laboratory-confirmed cholera by month and sequence type, South Africa, 2024, n=12

Table 35. Number of cases of laboratory-confirmed cholera by sequence type and province, South Africa, 2024, n=13

Province	ST69	ST75	Total
Gauteng	1	0	1
Limpopo	5	6	11
Mpumalanga	0	1	1
South Africa	6	7	13

Table 36. Number of laboratory-confirmed cholera cases reported by age category, South Africa, 2024, n=13

Age category (years)	Private sector	Public sector	Total
0 - 4	1	0	1
5 - 14	0	2	2
15 - 24	2	1	1
25 - 34	0	3	3
35 - 44	0	3	3
45 - 54	0	1	1
55 - 64	0	1	1
≥ 65	0	0	0
Unknown age	0	1	1
Total	1	12	13

Table 37. Ciprofloxacin and azithromycin susceptibility* of viable *vibrio cholerae* isolates received and tested at the Centre for Enteric Diseases, South Africa, 2024 (n=12)

Antimicrobial agent	Susceptible, n (%)	Non-susceptible, n (%)
Ciprofloxacin	12 (100%)	0 (0%)
Azithromycin	12 (100%)	0 (0%)

*According to CLSI breakpoints

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Schistosomiasis And Soil-Transmitted Helminthiasis (STH) In Limpopo And Mpumalanga Provinces, 2024

INTRODUCTION

Neglected tropical diseases (NTDs) are a diverse group of conditions predominantly affecting populations in tropical regions, especially impoverished communities, women, and children. NTDs such as schistosomiasis and STH remain major public health concerns in South Africa. Accurate concentration and microscopy techniques are essential for diagnosis and for generating reliable surveillance data.

In January 2024, the GERMS-SA surveillance platform launched a pilot project for laboratory-based surveillance of schistosomiasis and STH to evaluate diagnostic quality at routine microbiology laboratories and to assess the viability and molecular characteristics of *Schistosoma* eggs. The pilot was implemented

in Limpopo and Mpumalanga. Participating NHLS microbiology laboratories submitted residual urine and stool specimens – previously tested positive for *Schistosoma* species or STHs (*Ascaris lumbricoides*, *Trichuris trichiura*, and hookworm species, *Necator americanus*, and *Ancylostoma duodenale*) – to the NICD Parasitology Reference Laboratory (PRL) for confirmatory testing.

This project contributes to improved national monitoring of NTDs, which have been NMC in South Africa since 2017. The pilot covered January–December 2024, with plans to expand into additional provinces in 2025, subject to funding and logistical feasibility.

METHODS

Participating laboratories submitted microscopy-confirmed positive samples to PRL. Upon arrival, all samples underwent repeat microscopy, and PCR was performed where results were discordant or unclear, or where specimen volume was inadequate. Throughout the year, PRL collaborated with the

SDW to compare submissions with data from the national NHLS database, enabling an audit to evaluate submission completeness. Data were stratified by province, laboratory, and quarter to identify trends.

RESULTS

Between January and December 2024, 741 samples were received by PRL: 576 (78%) from Mpumalanga and 165 (22%) from Limpopo. Submission volumes fluctuated across quarters – 281 (Q1), 202 (Q2), 108 (Q3), and 150 (Q4). Limpopo submitted no samples during Q3, while Mpumalanga maintained steady submissions throughout the year (Table 38; Figure 34).

Of the total specimens, 629 (84.9%) were reported by sending laboratories as positive for *Schistosoma haematobium* and one for *S. mansoni*. Six samples were submitted in error, testing positive for other parasites (*Cryptosporidium* spp., *Giardia duodenalis*, and *Entamoeba coli*). Upon retesting, PRL confirmed 569/629 (90.5%) positives by microscopy, while 13 samples were reclassified as mixed infections involving *S. haematobium*, *S. mansoni*, or *S. intercalatum* (morphology-based). Fifty-five samples were negative on retesting; PCR confirmed 46/55 (83.6%) as

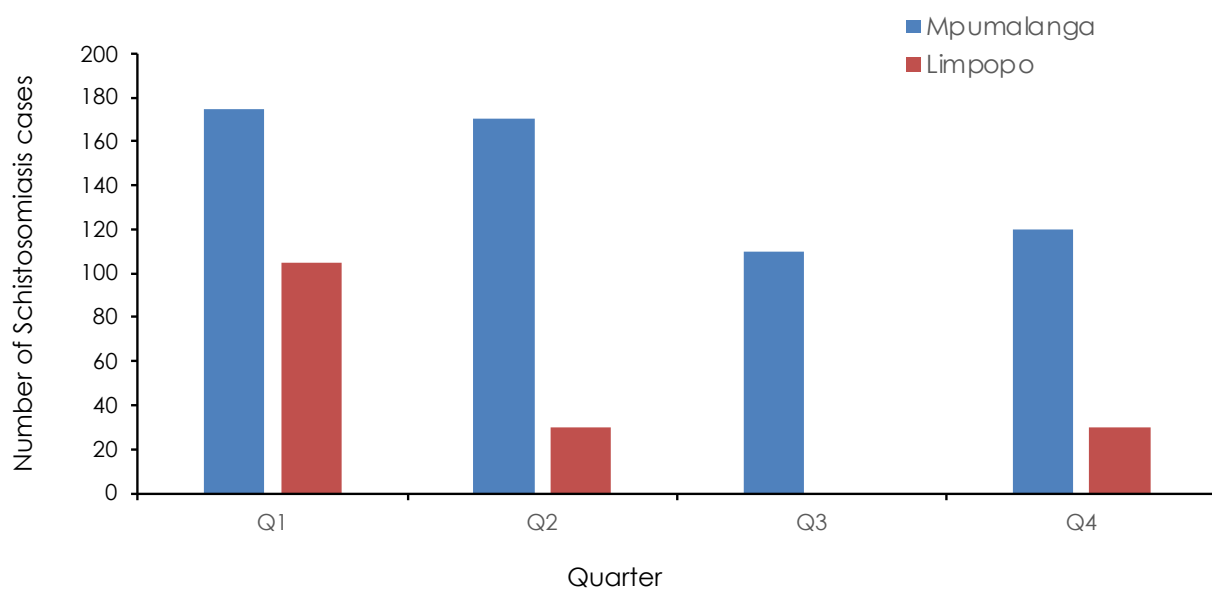
S. haematobium positive, likely reflecting ova degradation or transport delays. Five additional specimens with insufficient volume were processed via PCR; two yielded positive or mixed-species results (Table 39).

In January (Q1), a request was made for submission of both positive and negative samples to establish a diagnostic baseline. One hundred and two negative samples were received; 93% remained negative, and 6% were reclassified as positive by PRL. No further negatives were submitted in subsequent quarters.

Despite the inclusion of STHs in the pilot scope, no STH-positive samples were submitted during 2024. However, SDW audit data recorded five STH-positive results (three hookworm, one *Ascaris*, and one *Trichuris*) from NHLS laboratories in Mpumalanga and Limpopo, none of which were submitted for verification.

Table 38. Sample submissions by province and quarter

Quarter	Mpumalanga	Limpopo
Q1	177	104
Q2	171	31
Q3	108	0
Q4	120	30

**Figure 34. Sample Submissions by province and quarter (N=740)****Table 39. Confirmation results at PRL**

Category	<i>Schistosoma</i> cases
Positive by Sending Lab	629
Confirmed by PRL (Microscopy)	569
Confirmed by PRL (PCR)	46
Mixed Infections	13
Negative	55

AUDIT FINDINGS

An audit of NHLS SDW data identified 6 943 *Schistosoma*-positive specimens in Mpumalanga and Limpopo during 2024. Excluding non-participating sites, 6 918 valid positives remained – 5 462 from Limpopo and 1 456 from Mpumalanga. Only 629 (9%) were submitted to PRL for confirmatory testing, indicating substantial under-submission and highlighting the need for strengthened laboratory compliance.

For STHs, five positive cases were reported nationally from Limpopo and Mpumalanga, but none were submitted to NICD, revealing major surveillance gaps.

INCIDENCE ESTIMATES

Using the 2024 population denominator:

- Limpopo: 86.2 cases per 100 000 population
- Mpumalanga: 29.2 cases per 100 000 population

STH incidence remained below 0.1 per 100 000 population in both provinces. The markedly higher schistosomiasis burden underscores the public-health significance of this NTD and suggests that STH surveillance likely under-represents the true case load due to low sample submission.

OPERATIONS AND CAPACITY BUILDING

Throughout 2024, PRL and GERMS-SA provincial teams implemented several support activities to strengthen surveillance. These included co-ordination meetings, targeted microscopy training, and feedback sessions with NHLS staff to improve specimen quality and submission compliance.

Stakeholder engagement and awareness activities were also conducted through NICD communications to sustain participation and alignment with national NTD surveillance goals.

CONCLUSION

The 2024 pilot successfully established a framework for national-scale laboratory-based surveillance of schistosomiasis and STHs. Continuous submissions from Mpumalanga demonstrated feasibility, but inconsistent reporting from Limpopo and low overall submission of specimens (9%) compared with SDW audit data highlight areas requiring improvement.

The absence of STH sample submissions, despite positive records in NHLS databases, points to a need for enhanced laboratory engagement and improved submission compliance. Moving

forward, priorities include strengthening specimen transport and data integration, expanding coverage to additional provinces, and maintaining capacity-building through training and site visits.

Estimated incidence data confirm a high schistosomiasis burden in both provinces. With continued collaboration, this programme can substantially enhance South Africa's public-health response to parasitic NTDs.

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SUMMARY

In 2024, GERMS-SA marked 21 years of national laboratory-based surveillance, continuing to generate high-quality data on infectious diseases of public health importance despite major operational challenges such as the NHLS cyberattack and logistical delays. The integration of data through the SDW and NMC system improved completeness and timeliness of reporting, while routine audits and staff retraining helped maintain data accuracy. The expansion of surveillance to include NTDs strengthened monitoring of conditions that disproportionately affect underserved populations.

Audit findings highlighted ongoing underreporting from some laboratories, with a significant proportion of cases detected retrospectively. This limits confirmatory testing and genomic analysis, reducing opportunities for early outbreak detection. Strengthening isolate submission, improving transport logistics, and sustaining regular feedback and training will be essential to address these gaps. Continued investment in data systems, partnerships, and capacity building will ensure GERMS-SA remains a cornerstone of South Africa's infectious disease surveillance and a reliable source of evidence to guide public health action and policy.

Opportunistic infections: In 2024, laboratory-confirmed **cryptococcal** disease showed a slight decline from 2023, though this may reflect temporary data disruptions. The infection remains a major cause of illness and death among people living with HIV, particularly men aged 40–44 years with advanced immunosuppression. Access to flucytosine-based treatment improved, yet in-hospital mortality stayed high, underscoring the need for a consistent drug supply and earlier HIV care. Invasive **non-typhoidal *Salmonella* (iNTS)** disease remains closely linked to HIV infection, most commonly affecting adults aged 35–44 years. Slightly higher case numbers were observed compared to 2023, with *S. Enteritidis* and *S. Typhimurium* remaining the predominant serovars. Provincial variation likely reflects healthcare-seeking behaviour and clinician testing practices rather than true differences in disease incidence. WGS continued to identify sporadic clusters, underscoring its value for outbreak investigation.

Vaccine-preventable diseases: In 2024, GERMS-SA continued its critical role in tracking trends in invasive pneumococcal disease (IPD), *Haemophilus influenzae* (HI), and Group B Streptococcus (GBS), contributing valuable insights into vaccine impact and resistance patterns. **IPD** incidence remained stable compared to 2023, although still below pre-pandemic levels. The highest burden persisted among infants and adults aged 45–64 years, with serotypes 8, 4, and 3 most frequently detected. The national transition from PCV13 to PCV10 (SII) in April 2024 underscores the importance of continued serotype-specific monitoring to assess potential shifts in disease burden and vaccine effectiveness. ***H. influenzae*** incidence showed a slight decline across all provinces, with non-typeable strains predominating, followed

by type b (Hib), particularly in young children. Despite high vaccine coverage, severe outcomes and fatalities continued to be observed among infants and older adults. Approximately one-third of HI cases were associated with ampicillin resistance, reinforcing the need for ongoing antimicrobial resistance surveillance.

Invasive **GBS** disease continued to pose a significant threat, especially among neonates and older adults with underlying conditions. Serotypes III, Ia, and V remained dominant, consistent with recent trends. While most isolates remained susceptible to penicillin and ampicillin, overall mortality remained high, approaching one in five cases. The persistence of invasive disease despite preventive measures highlights the importance of perinatal screening and the future potential of maternal vaccination to reduce neonatal morbidity and mortality.

Epidemic-prone diseases (notifiable medical conditions):

The incidence of **invasive meningococcal disease (IMD)** increased notably in 2024, surpassing levels observed before the COVID-19 pandemic. Infants and young children were most affected, with serogroup B continuing to dominate nationally, while sporadic cases of serogroups Y and W were also detected. The Western Cape again reported the highest incidence, reflecting both improved case detection and regional clustering. Although most isolates remained penicillin-susceptible, the rapid clinical progression and high fatality rate of IMD underscore the importance of early diagnosis and prompt initiation of treatment. The number of **enteric fever** (typhoid and paratyphoid fever) cases continued to decline, from 155 in 2023 to 139 in 2024, maintaining South Africa's historically low incidence. Most cases occurred among children aged 5–14 years. While most were sporadic, a localised outbreak was recorded in the City of Tshwane, Gauteng. Notably, 2024 recorded the highest number of *Salmonella* Paratyphi A cases since 2003 (n=19), with 18 cases from Tshwane. Ciprofloxacin resistance rose markedly to 10% (from 2% in 2023), signalling the need for routine azithromycin and ceftriaxone susceptibility testing. WGS identified eight *Salmonella* Typhi and Paratyphi clusters, largely confined to specific provinces, with contaminated municipal water suspected in Hammanskraal. A total of 921 ***Shigella*** cases were reported in 2024, similar to previous years, with the highest burden in children under five years. Most infections were non-invasive, and person-to-person transmission remains the primary route. *S. flexneri* type 2a and *S. sonnei* continued as dominant serotypes, with >95% of isolates remaining susceptible to azithromycin and ciprofloxacin. Seventy-three cases of **listeriosis** were reported nationwide, below the expected annual range and fewer than in 2023 (n=83). Most were from Gauteng, the Western Cape, and KwaZulu-Natal, affecting mainly adults aged 15–49 years and neonates. The case distribution mirrored previous years, and no major outbreaks were detected.

Cholera cases declined sharply in 2024, with 13 laboratory-confirmed infections reported from Limpopo, Gauteng, and Mpumalanga. All isolates were toxigenic *Vibrio cholerae* O1 (Ogawa or Inaba) and remained fully susceptible to azithromycin and ciprofloxacin. WGS identified sequence types ST69 and ST75, both previously detected during the 2023 outbreak. Ongoing genomic monitoring supports early detection and response to potential re-emergence. **Invasive group A strep** showed a modest decline compared to 2023, yet it remained associated with severe clinical manifestations such as necrotising fasciitis and streptococcal toxic shock syndrome. The majority of cases occurred in infants, the elderly, and individuals with chronic illnesses. Despite universal susceptibility to first-line antimicrobials, the case fatality rate remained high, often within 24 hours of admission.

Neglected tropical diseases (NTDs): A total of 741 samples were received by the NICD Parasitology Reference Laboratory, with most originating from Mpumalanga. Quarterly submissions varied, partly due to transport delays and logistical constraints, particularly in Limpopo. Among the samples submitted as positive for *Schistosoma* species, 90% were confirmed by microscopy or PCR, demonstrating strong diagnostic concordance. PCR testing further identified several mixed *Schistosoma* species infections, highlighting the added value of molecular methods in confirming species and detecting degraded samples. The 2024 pilot established the feasibility of national-scale NTD surveillance and provides a solid foundation for future expansion to additional provinces, supporting broader efforts toward elimination of NTDs in South Africa.

PUBLICATIONS

Peer-reviewed GERMS-SA and GERMS-SA-related publications 2024:

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