GERMS-SA | Centre for Respiratory Diseases and Meningitis

Quarterly report on laboratory-based surveillance for invasive bacterial disease caused by vaccine-preventable or epidemic-prone pathogens

NATIONAL INSTITUTE FOR COMMUNICABLE DISEASES
Division of the National Health Laboratory Service

Report quarter: Quarter 4 of 2024

Reporting period: 01 January 2024 to 31 December 2024

Data are provisional as on date data extracted. Episodes of disease are reported by date of specimen collection. Data cleaning is ongoing and this may result in some changes in subsequent reports. Refer to end of report for methodology and case definitions.

Highlights

- In the current reporting period, 1907 episodes of invasive *Streptococcus pneumoniae*, 219 episodes of invasive *Haemophilus influenzae*, 147 cases of invasive *Neisseria meningitidis*, 826 cases of invasive *Streptococcus agalactiae* and 682 cases of *Streptococcus pyogenes* were reported to GERMS-SA.
- Proportion of cases detected by audit (identified through Surveillance Data Warehouse but no specimen/isolate submitted) ranged from 16% (24/147) for *N. meningitidis* to 55% (454/826) for *S. agalactiae*.
- Case trends returned to pre-pandemic levels in 2024, with no concerning patterns based on patient age or serotypes/groups detected. Where serotype/serogroup could be determined, *S. pneumoniae* episodes were predominantly caused by non-PCV10/PCV13 serotypes (853/1247, 68%), serotype 8 being most commonly identified. *H. influenzae* episodes were predominantly caused by non-typeable isolates (52/102, 51%) and *N. meningitidis* by serogroup B (33/94, 35%).
- Laboratory processing delays resulted in minimum data being available for the second half of 2024 for *S. agalactiae* and *S. pyogenes*, and trends should be interpreted with caution.
- All microbiology laboratories are encouraged to submit isolates for serotyping.

Table of contents

Number of cases detected, proportion identified on audit and organism viability by pathogen

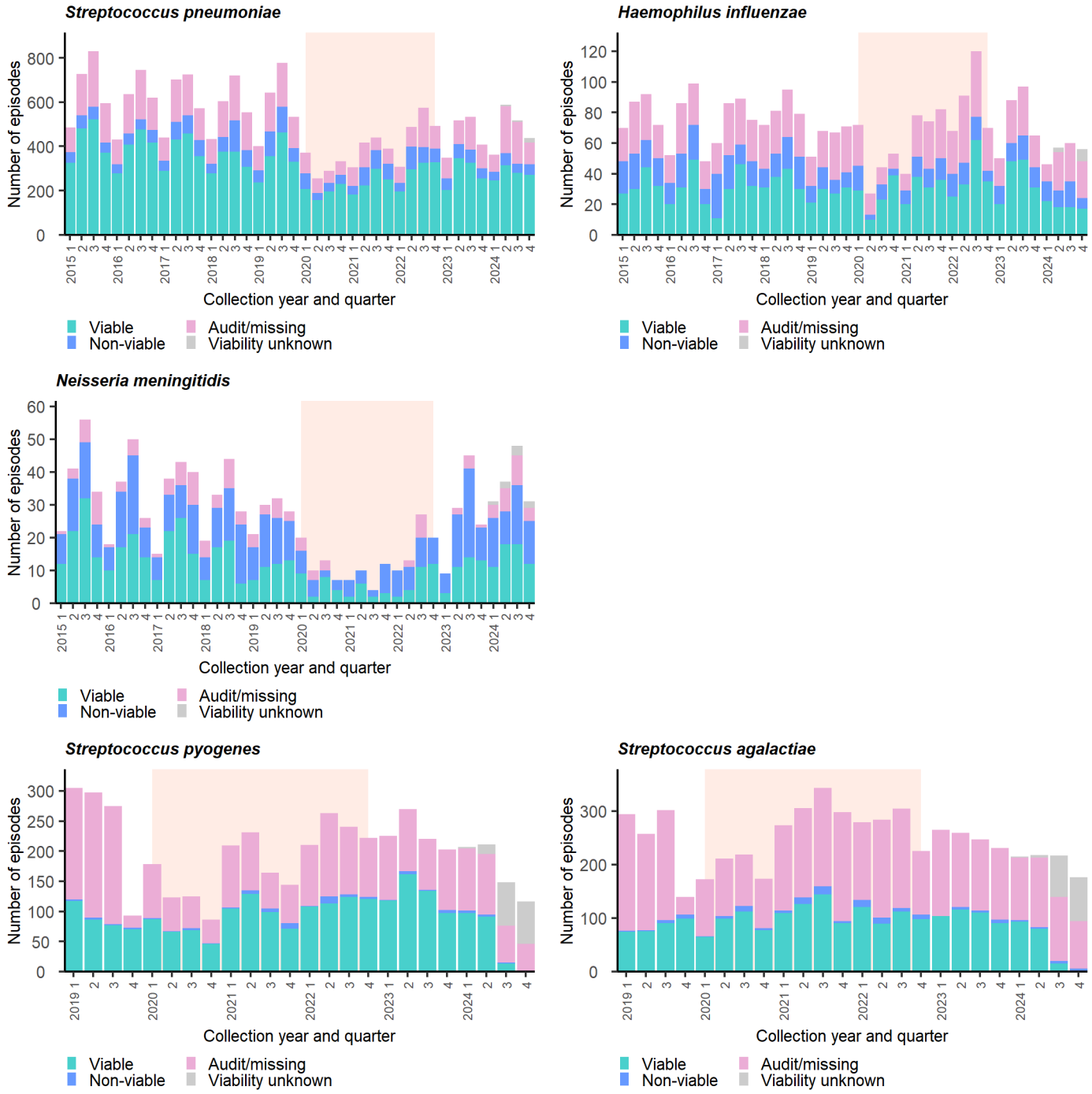

Figure 1: Number of cases detected, proportion identified on audit and organism viability by pathogen, GERMS-SA laboratory-based surveillance, South Africa, 01 January 2015 to 31 December 2024. Surveillance for *Streptococcus agalactiae* and *Streptococcus pyogenes* only started 01 January 2019. Viability unknown: Cases reported to CRDM, but viability unknown due to capturing delays. COVID-19 pandemic period shaded in light orange.

Data are provisional as on date data extracted. Episodes of disease are reported by date of specimen collection. Data cleaning is ongoing and this may result in some changes in subsequent reports.

Streptococcus pneumoniae

Table 1: Number of invasive *Streptococcus pneumoniae* disease episodes by viability, GERMS-SA laboratory-based surveillance, South Africa, 01 January 2015 to 31 December 2024.

	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024
Viable	1701 (64)	1577 (65)	1533 (63)	1335 (58)	1385 (59)	789 (63)	955 (62)	1146 (62)	1130 (63)	1113 (58)
Non-viable	208 (8)	198 (8)	282 (12)	328 (14)	346 (15)	184 (15)	274 (18)	273 (15)	222 (12)	182 (10)
Audit/missing	729 (28)	658 (27)	624 (26)	650 (28)	621 (26)	276 (22)	322 (21)	442 (24)	455 (25)	577 (30)
Viability unknown	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	35 (2)
Total	2638	2433	2439	2313	2352	1249	1551	1861	1807	1907

Viability unknown: Cases reported to CRDM, but viability unknown due to capturing delays.

Table 2: Number of invasive *Streptococcus pneumoniae* disease episodes by province, GERMS-SA laboratory-based surveillance, South Africa, 01 January 2015 to 31 December 2024.

	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024
Eastern Cape	232 (9)	208 (9)	208 (9)	259 (11)	274 (12)	136 (11)	201 (13)	224 (12)	236 (13)	267 (14)
Free State	131 (5)	147 (6)	109 (4)	106 (5)	83 (4)	62 (5)	70 (5)	62 (3)	62 (3)	74 (4)
Gauteng	970 (37)	855 (35)	891 (37)	757 (33)	774 (33)	377 (30)	467 (30)	516 (28)	539 (30)	568 (30)
KwaZulu-Natal	354 (13)	320 (13)	268 (11)	242 (10)	237 (10)	101 (8)	116 (7)	158 (8)	158 (9)	160 (8)
Limpopo	99 (4)	84 (3)	66 (3)	84 (4)	96 (4)	52 (4)	45 (3)	69 (4)	67 (4)	58 (3)
Mpumalanga	86 (3)	102 (4)	99 (4)	116 (5)	102 (4)	41 (3)	56 (4)	53 (3)	40 (2)	42 (2)
North West	108 (4)	73 (3)	70 (3)	71 (3)	66 (3)	37 (3)	32 (2)	48 (3)	57 (3)	65 (3)
Northern Cape	27 (1)	42 (2)	53 (2)	51 (2)	89 (4)	26 (2)	25 (2)	27 (1)	26 (1)	29 (2)
Western Cape	631 (24)	602 (25)	675 (28)	627 (27)	631 (27)	417 (33)	539 (35)	704 (38)	622 (34)	644 (34)
Total	2638	2433	2439	2313	2352	1249	1551	1861	1807	1907

Table 3: Number of invasive *Streptococcus pneumoniae* disease episodes by patient age, GERMS-SA laboratory-based surveillance, South Africa, 01 January 2015 to 31 December 2024.

	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024
<5 years	382 (14)	400 (16)	387 (16)	386 (17)	361 (15)	224 (18)	265 (17)	275 (15)	263 (15)	264 (14)
5-17 years	164 (6)	177 (7)	136 (6)	143 (6)	139 (6)	69 (6)	75 (5)	75 (4)	96 (5)	87 (5)
18-64 years	1744 (66)	1627 (67)	1674 (69)	1525 (66)	1600 (68)	823 (66)	1046 (67)	1297 (70)	1202 (67)	1241 (65)
≥65 years	180 (7)	176 (7)	194 (8)	198 (9)	199 (8)	96 (8)	115 (7)	162 (9)	153 (8)	182 (10)
Unknown	168 (6)	53 (2)	48 (2)	61 (3)	53 (2)	37 (3)	50 (3)	52 (3)	93 (5)	133 (7)
Total	2638	2433	2439	2313	2352	1249	1551	1861	1807	1907

Table 4: Number of invasive *Streptococcus pneumoniae* disease episodes by serotype, GERMS-SA laboratory-based surveillance, South Africa, 01 January 2015 to 31 December 2024.

	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024
PCV10	400 (15)	357 (15)	348 (14)	314 (14)	290 (12)	166 (13)	229 (15)	233 (13)	210 (12)	194 (10)
PCV13add	173 (7)	216 (9)	179 (7)	220 (10)	183 (8)	106 (8)	146 (9)	201 (11)	221 (12)	200 (10)
Other	1300 (49)	1172 (48)	1243 (51)	1102 (48)	1233 (52)	685 (55)	826 (53)	958 (51)	908 (50)	853 (45)
Unknown	765 (29)	688 (28)	669 (27)	677 (29)	646 (27)	292 (23)	350 (23)	469 (25)	468 (26)	660 (35)
Total	2638	2433	2439	2313	2352	1249	1551	1861	1807	1907

PCV10: 1, 5, 6A, 6B, 7F, 9V, 14, 19A, 19F and 23F. PCV13 additional: 3, 4, 18C. Other: all serotypes not included in PCV10/13. Unknown: Characterisation pending, no isolate/specimen available, insufficient specimen for molecular assay or tested negative for all targets in molecular assay (cycle threshold too high / not included in assay).

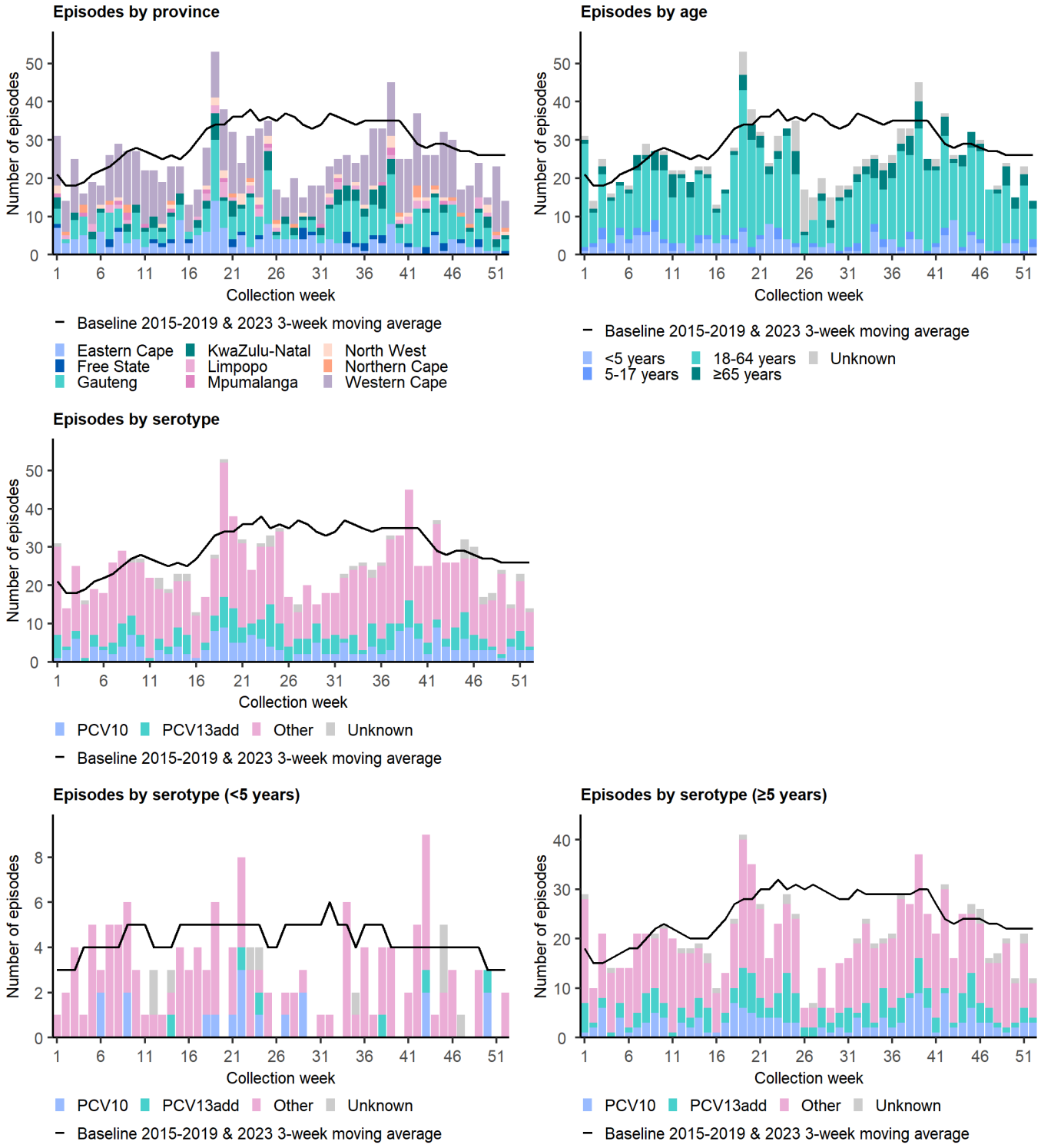

Figure 2: Disease episodes of invasive *Streptococcus pneumoniae* with viable isolates and those serotyped using molecular techniques, GERMS-SA laboratory-based surveillance, South Africa, 01 January 2024 to 31 December 2024. PCV10: 1, 5, 6A, 6B, 7F, 9V, 14, 19A, 19F and 23F. PCV13 additional: 3, 4, 18C. Other: all serotypes not included in PCV10/13. Unknown: Characterisation pending, insufficient specimen for molecular assay or tested negative for all targets in molecular assay (cycle threshold too high / not included in assay).

Data are provisional as on date data extracted. Episodes of disease are reported by date of specimen collection. Data cleaning is ongoing and this may result in some changes in subsequent reports.

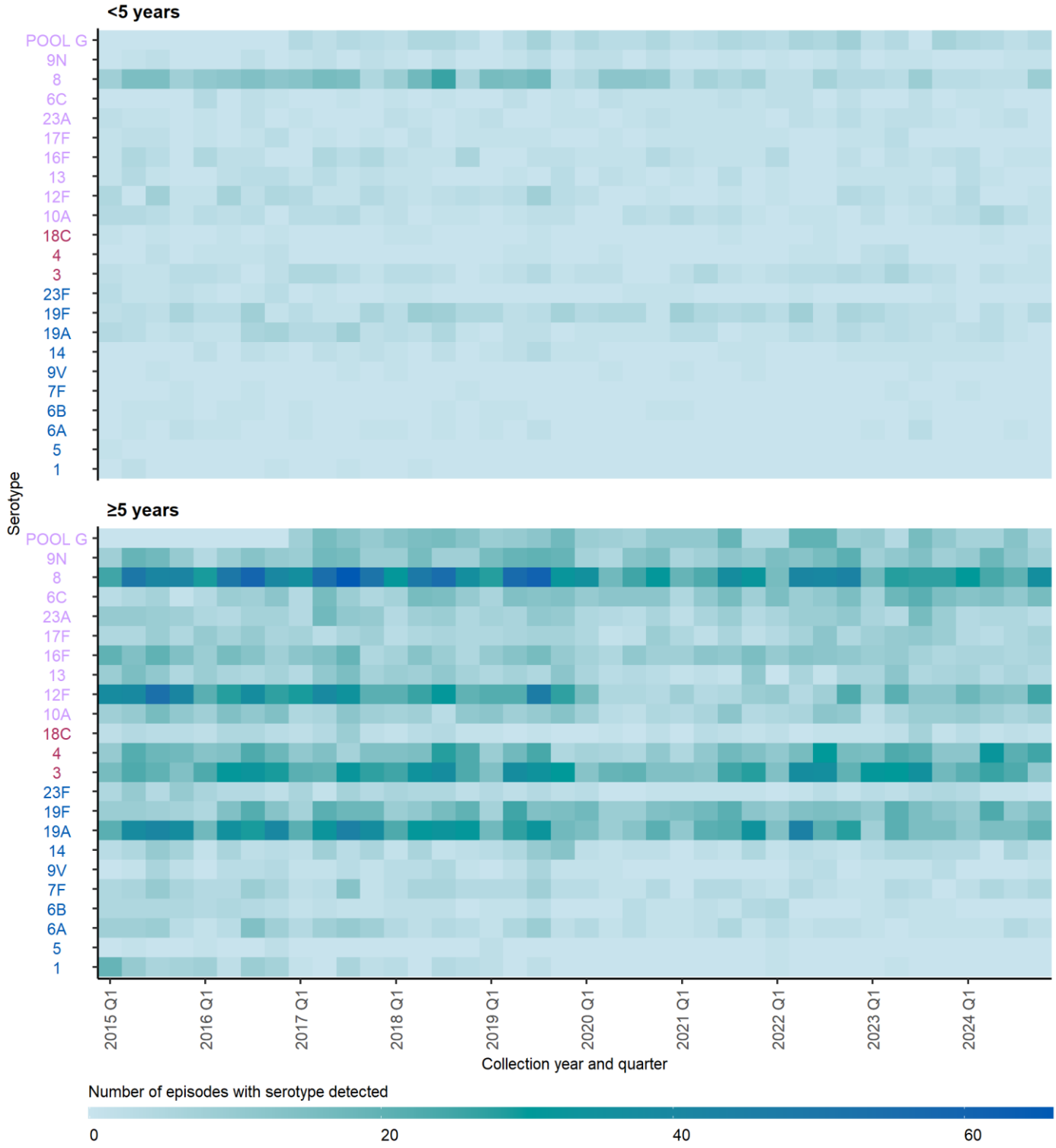

Figure 3: Serotypes identified in disease episodes of invasive *Streptococcus pneumoniae* with viable isolates and those serotyped using molecular techniques, GERMS-SA laboratory-based surveillance, South Africa, 01 January 2024 to 31 December 2024. Serotypes included in PCV 10 shown in blue, those included in PCV13 but not PCV10 in maroon, and the top 10 serotypes identified in the previous year that are not included in PCV13 in purple. Pool G: Due to cross-reactions we group serotypes 29, 34, and 42, and serogroups 35 and 47.

Data are provisional as on date data extracted. Episodes of disease are reported by date of specimen collection. Data cleaning is ongoing and this may result in some changes in subsequent reports.

Haemophilus influenzae

Table 5: Number of invasive *Haemophilus influenzae* disease episodes by viability, GERMS-SA laboratory-based surveillance, South Africa, 01 January 2015 to 31 December 2024.

	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024
Viable	133 (41)	120 (42)	119 (38)	142 (43)	109 (42)	101 (52)	125 (46)	155 (44)	148 (49)	75 (34)
Non-viable	80 (25)	69 (24)	80 (26)	69 (21)	44 (17)	33 (17)	48 (18)	51 (15)	53 (18)	48 (22)
Audit/missing	108 (34)	96 (34)	111 (36)	116 (35)	104 (40)	62 (32)	101 (37)	143 (41)	99 (33)	85 (39)
Viability unknown	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	11 (5)
Total	321	285	310	327	257	196	274	349	300	219

Viability unknown: Cases reported to CRDM, but viability unknown due to capturing delays.

Table 6: Number of invasive *Haemophilus influenzae* disease episodes by province, GERMS-SA laboratory-based surveillance, South Africa, 01 January 2015 to 31 December 2024.

	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024
Eastern Cape	26 (8)	23 (8)	33 (11)	45 (14)	25 (10)	19 (10)	27 (10)	41 (12)	22 (7)	24 (11)
Free State	9 (3)	12 (4)	12 (4)	7 (2)	8 (3)	12 (6)	10 (4)	15 (4)	7 (2)	11 (5)
Gauteng	111 (35)	101 (35)	86 (28)	93 (28)	88 (34)	57 (29)	86 (31)	108 (31)	89 (30)	66 (30)
KwaZulu-Natal	37 (12)	34 (12)	40 (13)	48 (15)	41 (16)	24 (12)	41 (15)	43 (12)	38 (13)	20 (9)
Limpopo	7 (2)	6 (2)	9 (3)	5 (2)	5 (2)	13 (7)	9 (3)	10 (3)	11 (4)	6 (3)
Mpumalanga	10 (3)	8 (3)	8 (3)	14 (4)	6 (2)	7 (4)	10 (4)	5 (1)	6 (2)	9 (4)
North West	3 (1)	6 (2)	8 (3)	10 (3)	5 (2)	5 (3)	6 (2)	7 (2)	4 (1)	5 (2)
Northern Cape	1 (0)	6 (2)	5 (2)	4 (1)	2 (1)	5 (3)	2 (1)	5 (1)	6 (2)	4 (2)
Western Cape	117 (36)	89 (31)	109 (35)	101 (31)	77 (30)	54 (28)	83 (30)	115 (33)	117 (39)	74 (34)
Total	321	285	310	327	257	196	274	349	300	219

Table 7: Number of invasive *Haemophilus influenzae* disease episodes by patient age, GERMS-SA laboratory-based surveillance, South Africa, 01 January 2015 to 31 December 2024.

	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024
<5 years	124 (39)	122 (43)	121 (39)	137 (42)	94 (37)	74 (38)	122 (45)	109 (31)	122 (41)	78 (36)
5-17 years	30 (9)	25 (9)	24 (8)	28 (9)	28 (11)	16 (8)	27 (10)	27 (8)	16 (5)	16 (7)
18-64 years	133 (41)	112 (39)	144 (46)	134 (41)	120 (47)	90 (46)	98 (36)	170 (49)	130 (43)	96 (44)
≥65 years	19 (6)	18 (6)	15 (5)	16 (5)	12 (5)	8 (4)	14 (5)	26 (7)	18 (6)	10 (5)
Unknown	15 (5)	8 (3)	6 (2)	12 (4)	3 (1)	8 (4)	13 (5)	17 (5)	14 (5)	19 (9)
Total	321	285	310	327	257	196	274	349	300	219

Table 8: Number of invasive *Haemophilus influenzae* disease episodes by serotype, GERMS-SA laboratory-based surveillance, South Africa, 01 January 2015 to 31 December 2024.

	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024
a	14 (4)	14 (5)	9 (3)	19 (6)	8 (3)	13 (7)	22 (8)	12 (3)	11 (4)	11 (5)
b	36 (11)	44 (15)	41 (13)	35 (11)	40 (16)	45 (23)	48 (18)	42 (12)	44 (15)	22 (10)
c	2 (1)	2 (1)	4 (1)	2 (1)	2 (1)	1 (1)	3 (1)	0 (0)	2 (1)	0 (0)
d	1 (0)	2 (1)	1 (0)	4 (1)	1 (0)	2 (1)	2 (1)	0 (0)	0 (0)	3 (1)
e	3 (1)	5 (2)	1 (0)	2 (1)	0 (0)	1 (1)	2 (1)	2 (1)	6 (2)	5 (2)
f	13 (4)	8 (3)	10 (3)	11 (3)	15 (6)	8 (4)	9 (3)	9 (3)	14 (5)	9 (4)
Non-typeable	133 (41)	104 (36)	118 (38)	130 (40)	82 (32)	56 (29)	60 (22)	112 (32)	103 (34)	52 (24)
Unknown	119 (37)	106 (37)	126 (41)	124 (38)	109 (42)	70 (36)	128 (47)	172 (49)	120 (40)	117 (53)
Total	321	285	310	327	257	196	274	349	300	219

Unknown: Characterisation pending, no isolate/specimen available, insufficient specimen for molecular assay or tested negative for all targets in molecular assay (cycle threshold too high).

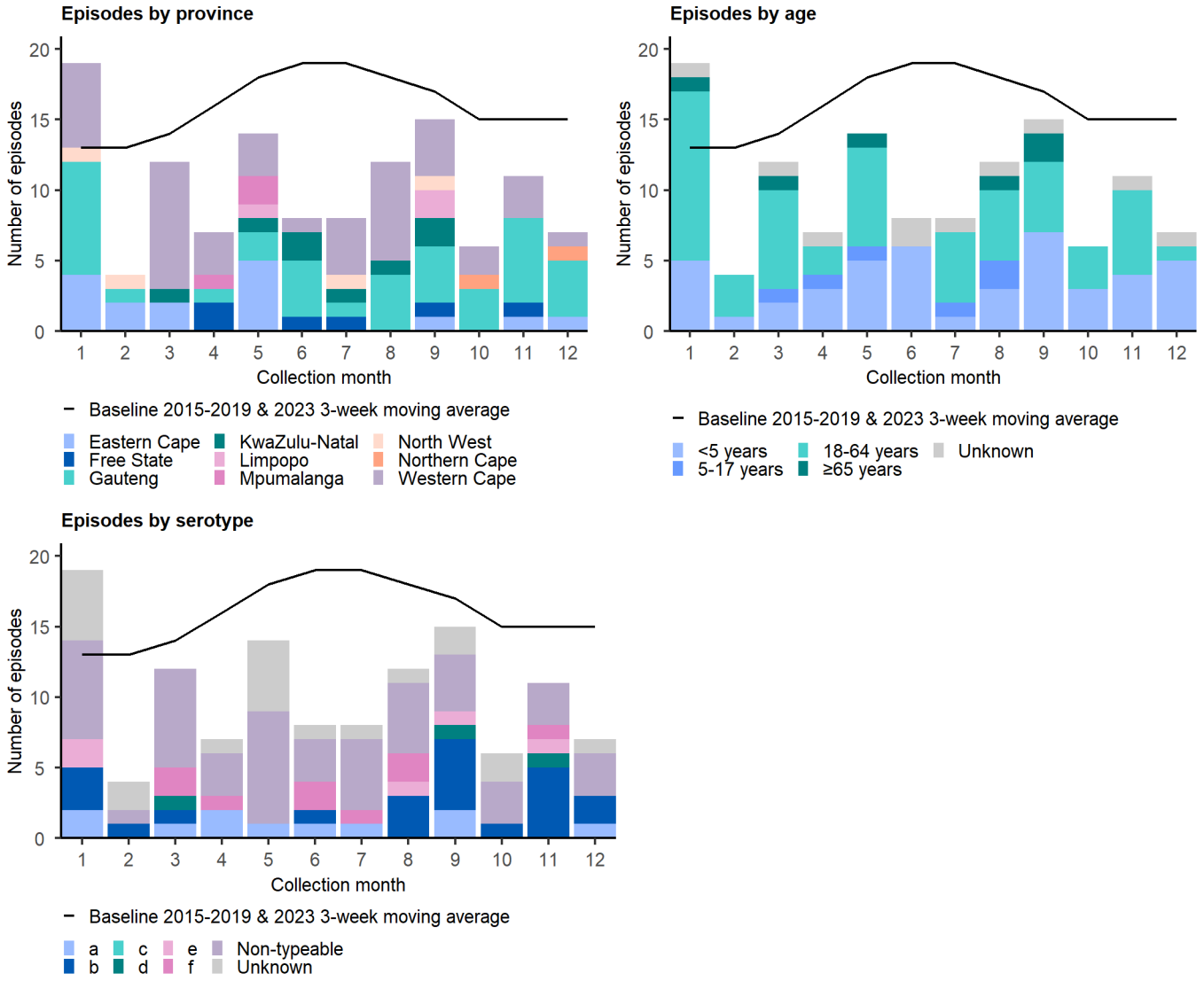

Figure 4: Disease episodes of invasive *Haemophilus influenzae* with viable isolates and those serotyped using molecular techniques, GERMS-SA laboratory-based surveillance, South Africa, 01 January 2024 to 31 December 2024. Unknown serotype: Characterisation pending, insufficient specimen for molecular assay or tested negative for all targets in molecular assay (cycle threshold too high).

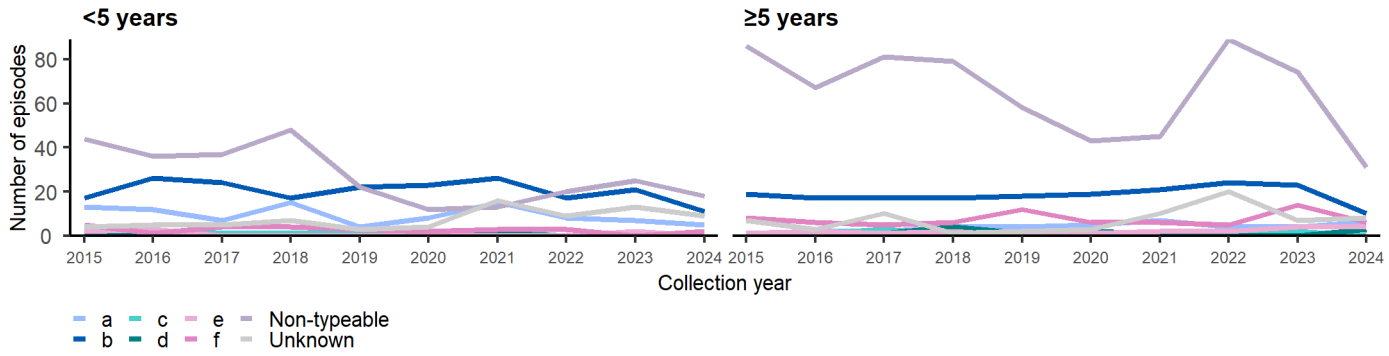

Figure 5: Serotypes identified in disease episodes of invasive *Haemophilus influenzae* by age and year with viable isolates and those serotyped using molecular techniques, GERMS-SA laboratory-based surveillance, South Africa, 01 January 2015 to 31 December 2024. Unknown serotype: Characterisation pending or tested negative for all targets in molecular assay (cycle threshold too high).

Data are provisional as on date data extracted. Episodes of disease are reported by date of specimen collection. Data cleaning is ongoing and this may result in some changes in subsequent reports.

Neisseria meningitidis

Table 9: Number of invasive *Neisseria meningitidis* disease episodes by viability, GERMS-SA laboratory-based surveillance, South Africa, 01 January 2015 to 31 December 2024.

	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024
Viable	80 (52)	62 (47)	70 (51)	49 (40)	43 (39)	23 (46)	13 (39)	29 (41)	41 (38)	59 (40)
Non-viable	52 (34)	57 (44)	43 (32)	53 (43)	52 (47)	17 (34)	20 (61)	32 (46)	59 (55)	56 (38)
Audit/missing	21 (14)	12 (9)	23 (17)	22 (18)	16 (14)	10 (20)	0 (0)	9 (13)	7 (7)	24 (16)
Viability unknown	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	8 (5)
Total	153	131	136	124	111	50	33	70	107	147

Viability unknown: Cases reported to CRDM, but viability unknown due to capturing delays.

Table 10: Number of invasive *Neisseria meningitidis* disease episodes by province, GERMS-SA laboratory-based surveillance, South Africa, 01 January 2015 to 31 December 2024.

	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024
Eastern Cape	27 (18)	15 (11)	18 (13)	26 (21)	12 (11)	6 (12)	5 (15)	5 (7)	12 (11)	25 (17)
Free State	9 (6)	2 (2)	8 (6)	2 (2)	3 (3)	0 (0)	0 (0)	3 (4)	4 (4)	5 (3)
Gauteng	45 (29)	36 (27)	42 (31)	37 (30)	37 (33)	10 (20)	8 (24)	23 (33)	32 (30)	38 (26)
KwaZulu-Natal	22 (14)	11 (8)	8 (6)	8 (6)	13 (12)	4 (8)	3 (9)	6 (9)	9 (8)	8 (5)
Limpopo	1 (1)	1 (1)	4 (3)	4 (3)	2 (2)	1 (2)	0 (0)	3 (4)	2 (2)	4 (3)
Mpumalanga	3 (2)	5 (4)	4 (3)	2 (2)	1 (1)	1 (2)	1 (3)	2 (3)	0 (0)	0 (0)
North West	2 (1)	5 (4)	5 (4)	6 (5)	4 (4)	1 (2)	1 (3)	2 (3)	2 (2)	2 (1)
Northern Cape	2 (1)	2 (2)	0 (0)	1 (1)	1 (1)	0 (0)	0 (0)	1 (1)	3 (3)	4 (3)
Western Cape	42 (27)	54 (41)	47 (35)	38 (31)	38 (34)	27 (54)	15 (45)	25 (36)	43 (40)	61 (41)
Total	153	131	136	124	111	50	33	70	107	147

Table 11: Number of invasive *Neisseria meningitidis* disease episodes by patient age, GERMS-SA laboratory-based surveillance, South Africa, 01 January 2015 to 31 December 2024.

	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024
<5 years	53 (35)	45 (34)	48 (35)	47 (38)	27 (24)	25 (50)	17 (52)	32 (46)	31 (29)	53 (36)
5-17 years	36 (24)	31 (24)	23 (17)	29 (23)	35 (32)	12 (24)	5 (15)	13 (19)	26 (24)	29 (20)
18-64 years	60 (39)	48 (37)	59 (43)	42 (34)	48 (43)	13 (26)	10 (30)	24 (34)	47 (44)	50 (34)
≥65 years	1 (1)	2 (2)	2 (1)	5 (4)	1 (1)	0 (0)	1 (3)	0 (0)	1 (1)	5 (3)
Unknown	3 (2)	5 (4)	4 (3)	1 (1)	0 (0)	0 (0)	0 (0)	1 (1)	2 (2)	10 (7)
Total	153	131	136	124	111	50	33	70	107	147

Table 12: Number of invasive *Neisseria meningitidis* disease episodes by serogroup, GERMS-SA laboratory-based surveillance, South Africa, 01 January 2015 to 31 December 2024.

	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024
B	49 (32)	48 (37)	45 (33)	42 (34)	36 (32)	26 (52)	14 (42)	15 (21)	44 (41)	33 (22)
C	11 (7)	15 (11)	14 (10)	11 (9)	5 (5)	2 (4)	1 (3)	3 (4)	10 (9)	9 (6)
W	42 (27)	30 (23)	27 (20)	24 (19)	25 (23)	7 (14)	4 (12)	11 (16)	15 (14)	23 (16)
Y	24 (16)	20 (15)	21 (15)	21 (17)	27 (24)	3 (6)	4 (12)	16 (23)	11 (10)	26 (18)
Other	1 (1)	1 (1)	0 (0)	0 (0)	1 (1)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)
Non-groupable	1 (1)	3 (2)	1 (1)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	3 (3)	3 (2)
Unknown	25 (16)	14 (11)	28 (21)	26 (21)	17 (15)	12 (24)	10 (30)	25 (36)	24 (22)	53 (36)
Total	153	131	136	124	111	50	33	70	107	147

Other: Serogroup A, E, X or Z. Unknown: Characterisation pending, no isolate/specimen available, insufficient specimen for molecular assay or tested negative for all targets in molecular assay (cycle threshold too high).

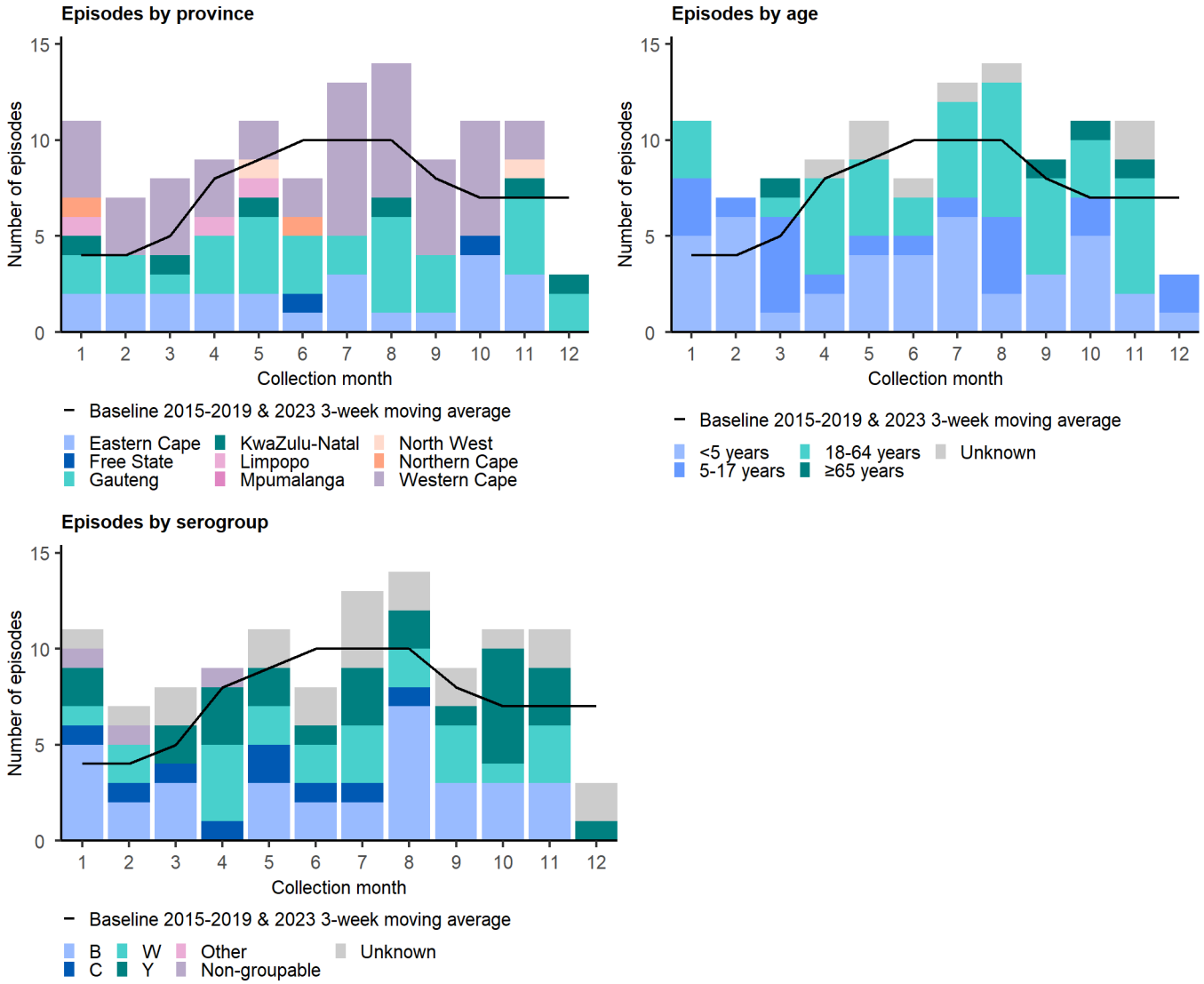

Figure 6: Disease episodes of invasive *Neisseria meningitidis* with viable isolates and those serogrouped using molecular techniques, GERMS-SA laboratory-based surveillance, South Africa, 01 January 2024 to 31 December 2024. Other serogroup: Serogroup A, E, X or Z. Unknown serogroup: Characterisation pending, insufficient specimen for molecular assay or tested negative for all targets in molecular assay (cycle threshold too high.

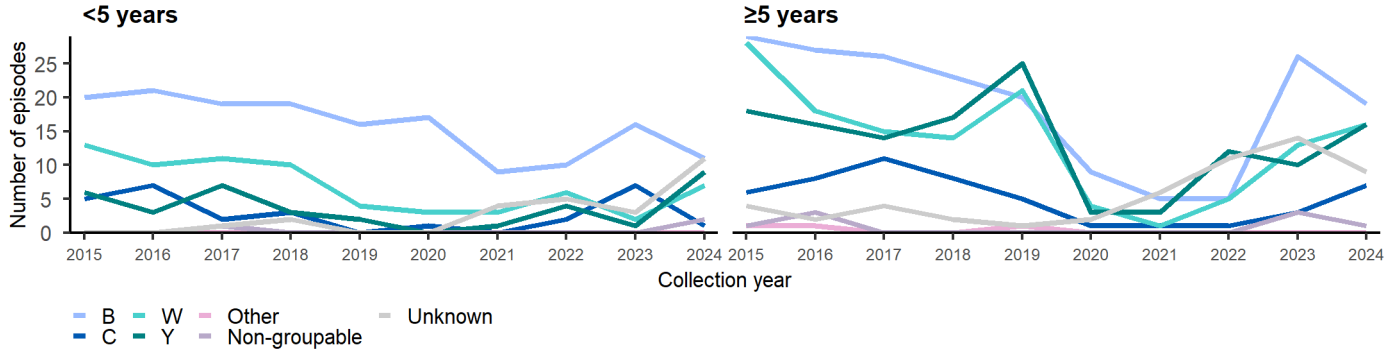

Figure 7: Serogroups identified in disease episodes of invasive *Neisseria meningitidis* by age and year with viable isolates and those serogrouped using molecular techniques, GERMS-SA laboratory-based surveillance, South Africa, 01 January 2015 to 31 December 2024. Other serogroup: Serogroup A, E, X or Z. Unknown serogroup: Characterisation pending, insufficient specimen for molecular assay or tested negative for all targets in molecular assay (cycle threshold too high).

Data are provisional as on date data extracted. Episodes of disease are reported by date of specimen collection. Data cleaning is ongoing and this may result in some changes in subsequent reports.

Streptococcus agalactiae (Group B Streptococcus)

Table 13: Number of invasive *Streptococcus agalactiae* disease episodes by viability, GERMS-SA laboratory-based surveillance, South Africa, 01 January 2019 to 31 December 2024.

	2019	2020	2021	2022	2023	2024
Viable	338 (34)	353 (46)	469 (38)	420 (38)	420 (42)	188 (23)
Non-viable	17 (2)	20 (3)	36 (3)	40 (4)	16 (2)	17 (2)
Audit/missing	636 (64)	402 (52)	714 (59)	632 (58)	566 (56)	454 (55)
Viability unknown	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	167 (20)
Total	991	775	1219	1092	1002	826

Viability unknown: Cases reported to CRDM, but viability unknown due to capturing delays.

Table 14: Number of invasive *Streptococcus agalactiae* disease episodes by province, GERMS-SA laboratory-based surveillance, South Africa, 01 January 2019 to 31 December 2024.

	2019	2020	2021	2022	2023	2024
Eastern Cape	64 (6)	49 (6)	71 (6)	55 (5)	54 (5)	52 (6)
Free State	30 (3)	25 (3)	43 (4)	41 (4)	39 (4)	38 (5)
Gauteng	421 (42)	337 (43)	595 (49)	475 (43)	479 (48)	351 (42)
KwaZulu-Natal	199 (20)	133 (17)	216 (18)	236 (22)	181 (18)	150 (18)
Limpopo	36 (4)	27 (3)	52 (4)	39 (4)	29 (3)	38 (5)
Mpumalanga	37 (4)	20 (3)	56 (5)	64 (6)	36 (4)	23 (3)
North West	12 (1)	6 (1)	14 (1)	16 (1)	24 (2)	24 (3)
Northern Cape	7 (1)	6 (1)	3 (0)	4 (0)	5 (0)	6 (1)
Western Cape	185 (19)	172 (22)	169 (14)	162 (15)	155 (15)	144 (17)
Total	991	775	1219	1092	1002	826

Table 15: Number of invasive *Streptococcus agalactiae* disease episodes by patient age, GERMS-SA laboratory-based surveillance, South Africa, 01 January 2019 to 31 December 2024.

	2019	2020	2021	2022	2023	2024
<5 years	591 (60)	498 (64)	779 (64)	648 (59)	539 (54)	442 (54)
5-17 years	19 (2)	14 (2)	21 (2)	12 (1)	16 (2)	18 (2)
18-64 years	286 (29)	161 (21)	333 (27)	350 (32)	342 (34)	263 (32)
≥65 years	58 (6)	40 (5)	47 (4)	29 (3)	40 (4)	43 (5)
Unknown	37 (4)	62 (8)	39 (3)	53 (5)	65 (6)	60 (7)
Total	991	775	1219	1092	1002	826

Table 16: Number of invasive *Streptococcus agalactiae* disease episodes by serotype, GERMS-SA laboratory-based surveillance, South Africa, 01 January 2019 to 31 December 2024.

	2019	2020	2021	2022	2023	2024
Ia	95 (10)	92 (12)	130 (11)	126 (12)	136 (14)	0 (0)
Ib	24 (2)	23 (3)	27 (2)	29 (3)	36 (4)	0 (0)
II	27 (3)	29 (4)	27 (2)	22 (2)	39 (4)	0 (0)
III	136 (14)	164 (21)	192 (16)	157 (14)	141 (14)	0 (0)
IV	9 (1)	4 (1)	12 (1)	18 (2)	12 (1)	0 (0)
V	46 (5)	39 (5)	74 (6)	55 (5)	43 (4)	0 (0)
VI	0 (0)	0 (0)	0 (0)	0 (0)	1 (0)	0 (0)
VIII	1 (0)	0 (0)	2 (0)	4 (0)	2 (0)	0 (0)
IX	0 (0)	0 (0)	2 (0)	4 (0)	3 (0)	0 (0)
Non-typeable	0 (0)	0 (0)	3 (0)	0 (0)	0 (0)	0 (0)
Unknown	653 (66)	424 (55)	750 (62)	677 (62)	589 (59)	826 (100)
Total	991	775	1219	1092	1002	826

Unknown: Characterisation pending or no isolate available.

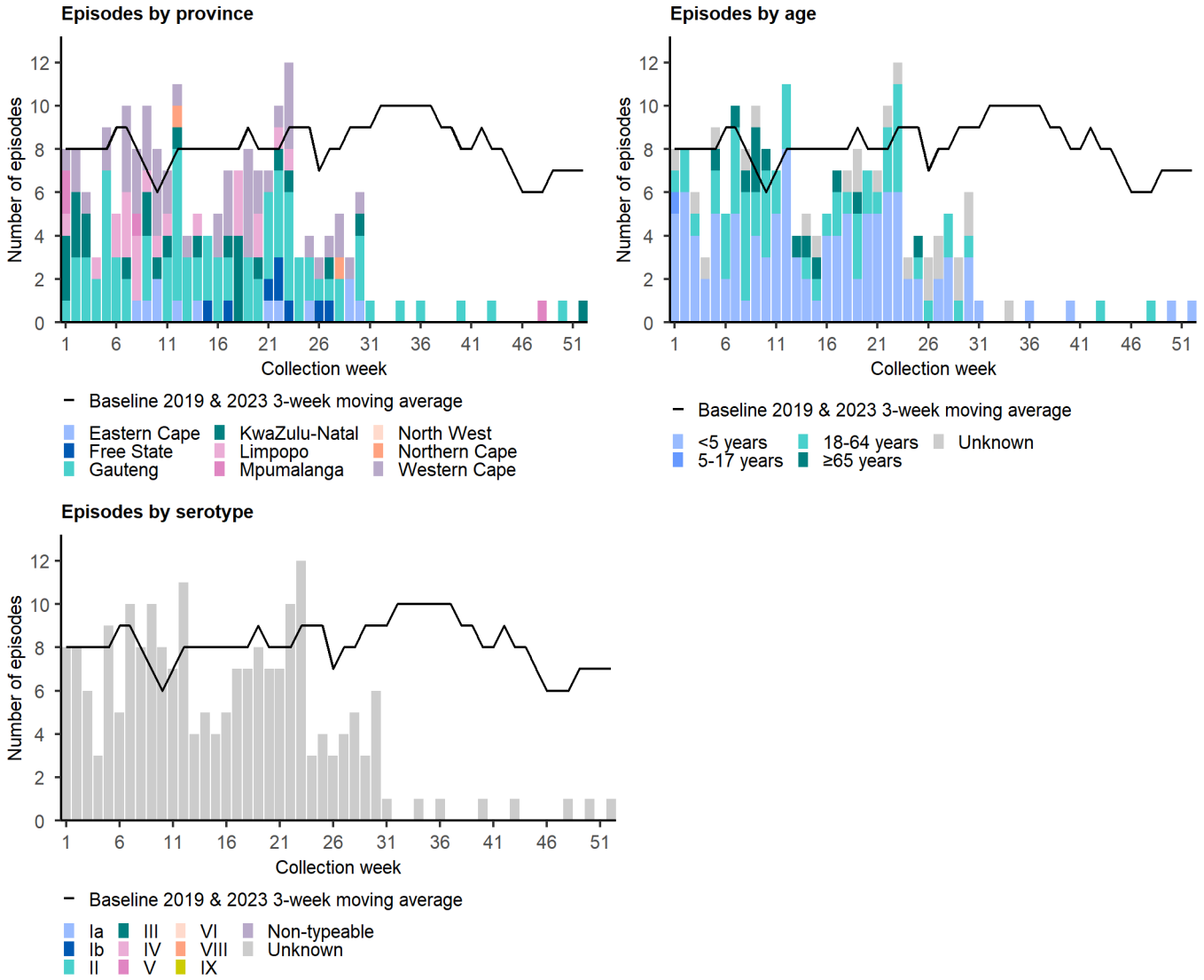

Figure 8: Disease episodes of invasive *Streptococcus agalactiae* with viable isolates, GERMS-SA laboratory-based surveillance, South Africa, 01 January 2024 to 31 December 2024. Unknown serotype: Characterisation pending

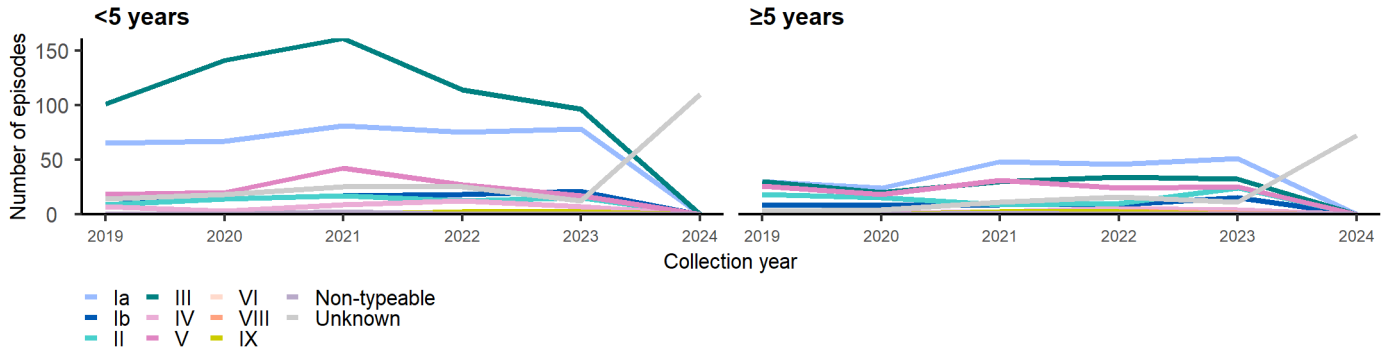

Figure 9: Serotypes identified in disease episodes of invasive *Streptococcus agalactiae* by age and year with viable isolates, GERMS-SA laboratory-based surveillance, South Africa, 01 January 2019 to 31 December 2024. Unknown serotype: Characterisation pending.

Data are provisional as on date data extracted. Episodes of disease are reported by date of specimen collection. Data cleaning is ongoing and this may result in some changes in subsequent reports.

Streptococcus pyogenes (Group A Streptococcus)

Table 17: Number of *Streptococcus pyogenes* disease episodes by viability, GERMS-SA laboratory-based surveillance, South Africa, 01 January 2019 to 31 December 2024.

	2019	2020	2021	2022	2023	2024
Viable	350 (36)	268 (52)	404 (54)	466 (50)	511 (56)	201 (29)
Non-viable	12 (1)	7 (1)	22 (3)	20 (2)	13 (1)	11 (2)
Audit/missing	608 (63)	237 (46)	322 (43)	449 (48)	394 (43)	309 (45)
Viability unknown	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	161 (24)
Total	970	512	748	935	918	682

Prior to 2024 case definition included detection from a non-sterile site with an accompanying diagnosis of septic shock, necrotising fasciitis, or necrotic tissue.
Viability unknown: Cases reported to CRDM, but viability unknown due to capturing delays.

Table 18: Number of *Streptococcus pyogenes* disease episodes by province, GERMS-SA laboratory-based surveillance, South Africa, 01 January 2019 to 31 December 2024.

	2019	2020	2021	2022	2023	2024
Eastern Cape	143 (15)	71 (14)	151 (20)	120 (13)	75 (8)	72 (11)
Free State	22 (2)	11 (2)	21 (3)	35 (4)	26 (3)	31 (5)
Gauteng	200 (21)	95 (19)	174 (23)	259 (28)	328 (36)	233 (34)
KwaZulu-Natal	162 (17)	49 (10)	92 (12)	96 (10)	72 (8)	81 (12)
Limpopo	7 (1)	5 (1)	10 (1)	19 (2)	25 (3)	14 (2)
Mpumalanga	11 (1)	9 (2)	23 (3)	20 (2)	19 (2)	16 (2)
North West	2 (0)	3 (1)	9 (1)	10 (1)	11 (1)	10 (1)
Northern Cape	7 (1)	7 (1)	3 (0)	2 (0)	6 (1)	1 (0)
Western Cape	416 (43)	262 (51)	265 (35)	374 (40)	356 (39)	224 (33)
Total	970	512	748	935	918	682

Prior to 2024 case definition included detection from a non-sterile site with an accompanying diagnosis of septic shock, necrotising fasciitis, or necrotic tissue.
Unknown: Characterisation pending or no isolate available.

Table 19: Number of *Streptococcus pyogenes* disease episodes by patient age, GERMS-SA laboratory-based surveillance, South Africa, 01 January 2019 to 31 December 2024.

	2019	2020	2021	2022	2023	2024
<5 years	139 (14)	52 (10)	102 (14)	122 (13)	128 (14)	102 (15)
5-17 years	69 (7)	31 (6)	51 (7)	57 (6)	63 (7)	45 (7)
18-64 years	627 (65)	327 (64)	498 (67)	632 (68)	565 (62)	407 (60)
≥65 years	106 (11)	68 (13)	68 (9)	90 (10)	93 (10)	67 (10)
Unknown	29 (3)	34 (7)	29 (4)	34 (4)	69 (8)	61 (9)
Total	970	512	748	935	918	682

Prior to 2024 case definition included detection from a non-sterile site with an accompanying diagnosis of septic shock, necrotising fasciitis, or necrotic tissue.
Unknown: Characterisation pending or no isolate available.

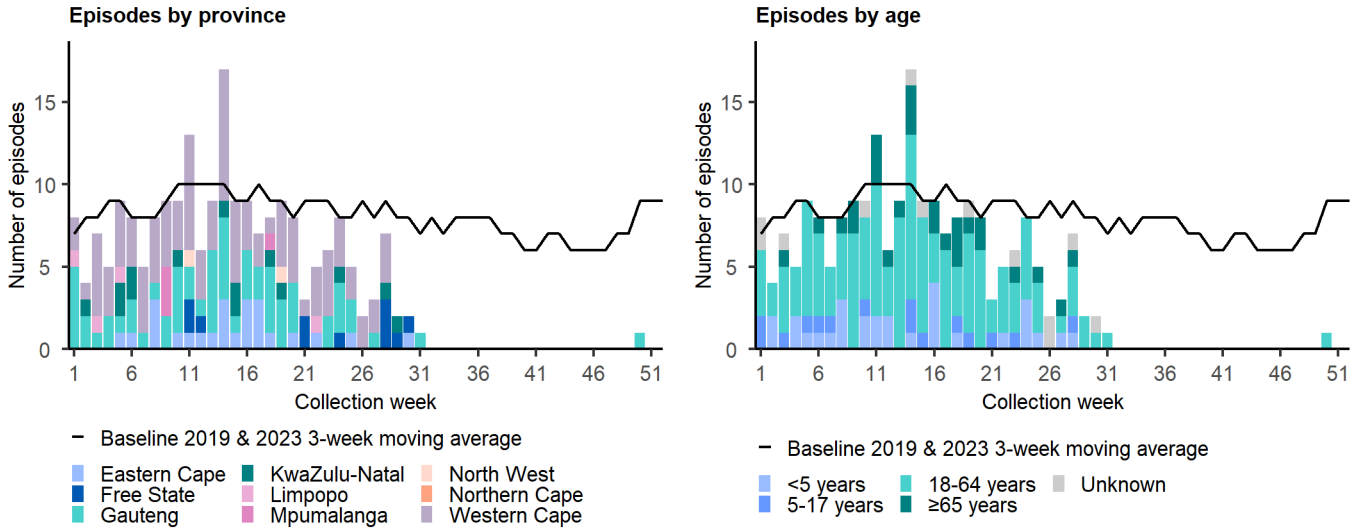

Figure 10: Disease episodes of *Streptococcus pyogenes* with viable isolates and those confirmed using molecular techniques, GERMS-SA laboratory-based surveillance, South Africa, 01 January 2024 to 31 December 2024. Prior to 2024 case definition included detection from a non-sterile site with an accompanying diagnosis of septic shock, necrotising fasciitis, or necrotic tissue.

Data are provisional as on date data extracted. Episodes of disease are reported by date of specimen collection. Data cleaning is ongoing and this may result in some changes in subsequent reports.

Methods

GERMS-SA is a national, active, laboratory-based surveillance system initiated in 2003 in which public and private laboratories send reports and isolates. As part of GERMS-SA, laboratories at the National Institute for Communicable Diseases (NICD) receive clinical isolates and specimens from both private and public laboratories across South Africa, based on specified case definitions. Duplicate results from the same patient within a 21-day period were excluded through matching of patient demographics. In addition to the specimens received at NICD, the Surveillance Data Warehouse (SDW) of the National Health Laboratory Service (NHLS) was searched for any positive laboratory result for pathogens under surveillance to identify any cases not reported to NICD. These cases, referred to as "Audit" cases would not have any serotyping data available.

Case definitions:

Streptococcus pneumoniae, *Haemophilus influenzae*, and *Neisseria meningitidis*: culture and/or PCR positive OR culture negative but latex antigen positive, corresponding Gram stain and/or PCR from any normally sterile body site. *Streptococcus agalactiae*: culture and/or PCR positive from any normally sterile body site OR non-sterile body site specimen obtained from patient with intrauterine sepsis (uterine tissue, endocervical tissue/fallopian tubes/placenta/ products of conception/ foetus). *Streptococcus pyogenes*: culture and/or PCR positive from any normally sterile body site. Prior to 2024 the case definition included detection from a non-sterile site with an accompanying diagnosis of septic shock, necrotising fasciitis, or necrotic tissue.

Serotyping of *Streptococcus pneumoniae*:

Pneumococcal isolates were serotyped by Quellung reaction using specific antisera (2003-2016: Statens Serum Institute, Copenhagen, Denmark; 2017 onwards: SSI Diagnostica, Copenhagen, Denmark). Culture-negative/bacterial antigen detection test positive clinical specimens, or isolates that lost viability were confirmed positive using real-time PCR (Wang *et al.* 2012) and serotyped using an adaption from methods described previously (Azzari *et al.* 2010 and Pimenta *et al.* 2013). This molecular assay includes targets for 38 serotypes (42 serotypes prior to 2014) and covers all serotypes included in PCV13. Only samples with an initial lytA PCR ct value of ≤35 were included. Where ct value was ≤35 but no serotype could be identified by including the 38 targets (42 targets prior to 2014), serotype was classified as non-vaccine type. Where lytA PCR ct value was ≥36, serotype was classified as unknown and was not included in graphs. Where the PCR target could not distinguish between vaccine and non-vaccine serotype, serotype was classified as unknown and not included in the figures (targets: 18ABC, 18ABCF, 7AF, 9ALVN and 9AV). From the 1st January 2023, the pneumococcal molecular serotyping method changed to the use of a TaqMan Array card (Spn TAC). The TaqMan Array Card (TAC) system, designed and validated by the United States Centers for Disease Control and Prevention (CDC) (Atlanta, USA) and manufactured by Life Technologies (New York, USA), is a semi-quantitative multi-target real-time PCR platform for the simultaneous detection of a range of targets (be it multiple pathogens or multiple serotypes) in a single specimen (Pholwat *et al.* 2016). The cards consist of multiple singleplex and/or duplex PCR reactions in 1 µl reaction wells pre-spotted with the target-specific primers and probes on a 384-well array card. Nucleic acids and reagents are mixed and loaded onto the card through individual sample ports, centrifuged at high speed for distribution of the reaction mix into reaction wells and then loaded onto a dedicated block on a ViiA7 or QS7 real-time PCR instrument (Life Technologies). The TAC system was pioneered by the CDC and has subsequently been used in a number of studies for screening a variety of pathogens (Pholwat *et al.* 2016). The Spn TAC card has 95 targets. The targets are able to identify *S. pneumoniae* (lytA and piaB) and 99 *S. pneumoniae* serotypes.

Serotyping of *Haemophilus influenzae*:

Isolates were serotyped by slide agglutination to detect serotypes a, b, c, d, e, f using antisera from Remel, Biotech Limited, Dartford, United Kingdom (prior to December 2023) and Mast Group Limited, Merseyside, United Kingdom (December 2023 onwards). Non-reactive isolates were classified as non-typeable. PCR serotyping was also performed on all isolates and clinical specimens to detect serotypes a, b, c, d, e and f using a method was developed by the (CDC) (Atlanta, USA) (unpublished) and implemented in Nov 2019 (NIC1188). Prior to 2019 PCR serotyping was performed according to methods adapted from Maaroufi *et al.* (2007) and Sandstedt *et al.* (2008) (NIC0598).

Serogrouping of *Neisseria meningitidis*:
Isolate serogroups were determined by slide agglutination using polyclonal antiserum followed by capsule-specific monoclonal antiserum (Remel, Biotech Limited, Dartford, United Kingdom) against serogroups A, C, X, Y, Z, and W, and monoclonal antibodies to polysaccharide B (Remel, Biotech Limited, Dartford, United Kingdom). Non-reactive isolates were classified as non-groupable (NG). Genogroup for cultures and clinical specimens was also determined using PCR by detection of csaB, csb, csc, csw, csxB, and csy genes, corresponding to serogroups A, B, C, W, X, and Y, respectively (Wang *et al.* 2012).

Serotyping of *Streptococcus agalactiae*:
Capsular serotyping of isolates was determined by slide agglutination using ImmulexTM Group B Streptococcus antisera (SSI Diagnostica, Denmark) for serotypes Ia, Ib, II, III, IV, V, VI, VII, VIII and IX as previously described (Slotved *et al.* 2003). Isolates that were non-reactive to all the type-specific antisera were classified serologically as non-typeable.

References:

- Azzari C, Moriondo M, Indolfi G, Cortimiglia M, Canessa C, Becciolini L, et al. Realtime PCR Is More Sensitive than Multiplex PCR for Diagnosis and Serotyping in Children with Culture Negative Pneumococcal Invasive Disease. PLoS One. 2010;5(2):e9282.
- Maaroufi Y, De Bruyne JM, Heymans C, Crokaert F. Real-time PCR for determining capsular serotypes of *Haemophilus influenzae*. J Clin Microbiol. 2007;45(7):2305-8.
- Pimenta FC, Roundtree A, Soysal A, Bakir M, du PM, Wolter N, et al. Sequential triplex real-time PCR assay for detecting 21 pneumococcal capsular serotypes that account for a high global disease burden. JClinMicrobiol. 2013;51(2):647-52.
- Pholwat S, Sakai F, Turner P, Vidal JE, Houpt ER. Development of a TaqMan Array Card for Pneumococcal Serotyping on Isolates and Nasopharyngeal Samples. J Clin Microbiol. 2016;54(7):1842-50
- Sandstedt SA, Zhang L, Patel M, McCrea KW, Qin Z, Marrs CF, et al. Comparison of laboratory-based and phylogenetic methods to distinguish between *Haemophilus influenzae* and H. haemolyticus. J Microbiol Methods. 2008;75(2):369-71.
- Slotved HC, Elliott J, Thompson T, Konradsen HB. Latex assay for serotyping of group B Streptococcus isolates. J Clin Microbiol. 2003;41(9):4445-7.
- Wang X, Theodore MJ, Mair R, Trujillo-Lopez E, du Plessis M, Wolter N, et al. Clinical validation of multiplex real-time PCR assays for detection of bacterial me**ningitis pathogens. J Clin Microbiol. 2012;50(3):702-8.