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**National Reference Centre for
Meningococci and *Haemophilus influenzae*
(NRZMHi)**



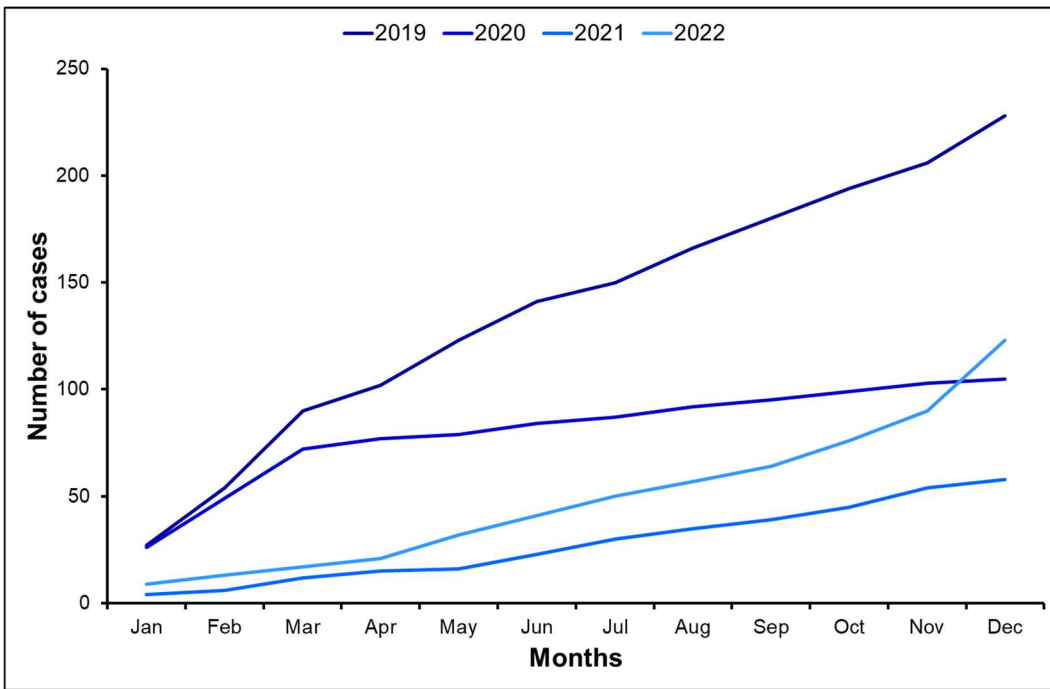
Data of the laboratory surveillance of meningococci (2022)

Introduction

The German National Reference Centre for Meningococci and *Haemophilus influenzae* (NRZMHi) has been assigned for the laboratory surveillance of invasive meningococcal disease (IMD) by the Robert Koch Institute (RKI). In 2022, 205 samples from 182 individuals were submitted to the NRZMHi. *Neisseria meningitidis* was confirmed in samples of 149 patients, 122 of them were from primarily sterile compartments (latter figure corresponds to the number of cases with IMD). In 26 samples (clinical samples and non-viable meningococci) detection of meningococci was carried out exclusively by molecular methods (21.3% out of 122). During the same period, 141 IMD cases were notified to the RKI (data as of 02.02.2023, SurvStat@RKI). Given that all IMD cases processed at the NRZMHi were notified retrospectively, a 87% coverage of IMD cases at the NRZMHi is assumed (81% in 2021).

In 2022, the incidence of IMD in Germany (0.17/100,000, data as of 02.02.2023, SurvStat@RKI) increased significantly (2021: 0.09/100,000) and is comparable to the data of 2020.

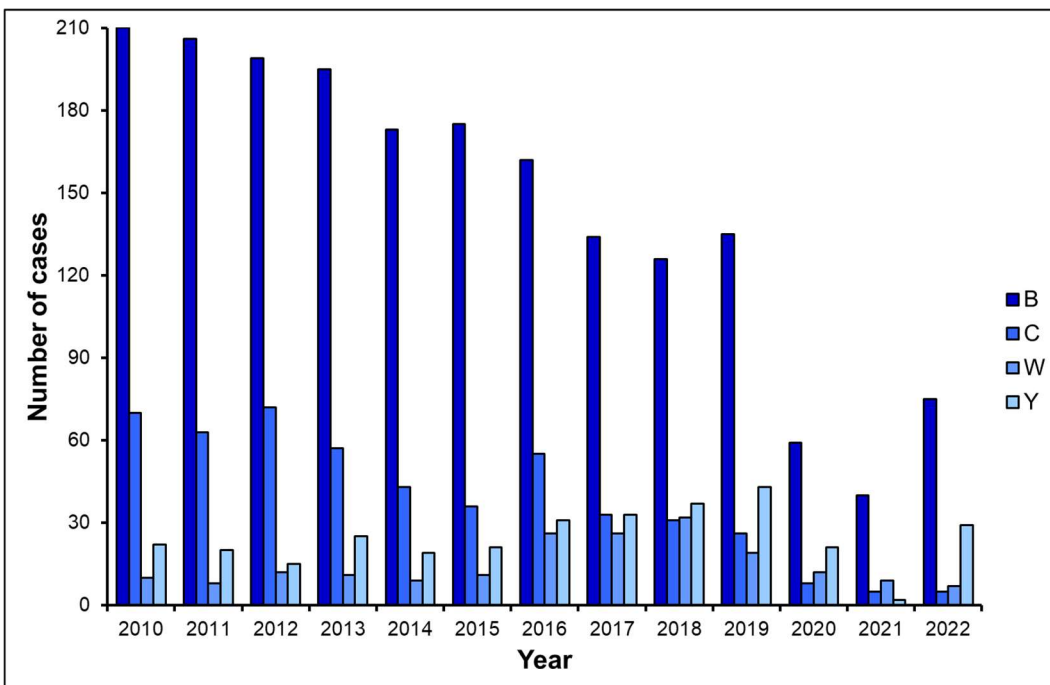
Trend of IMD cases 2019-2022



Cumulative graph of the number of IMD cases processed at the NRZMHi 2019 - 2022.

Beginning in March 2020 with the first nation-wide lockdown the number of IMD cases submitted to the NRZMHi decreased dramatically which continued until 2021. Since spring 2022, the number of IMD cases is increasing.

Frequency of serogroups B, C, W and Y (2010-2022)



In 2022, the number of serogroup Y cases increased considerably.

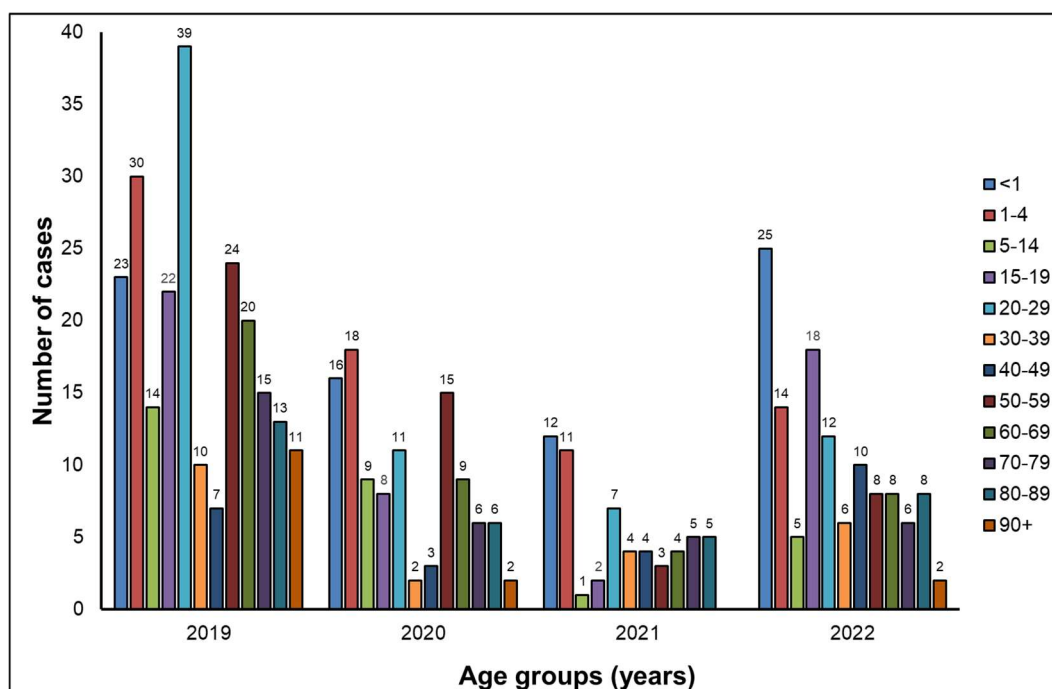
Serogroups according to federal states (2022)

serogroup	BW	BY	BE	BB	HB	HH	HE	MV	NI	NW	RP	SL	SN	ST	SH	TH	unkn
B	8	11	6	5	1	3	1	1	4	16	3	3	1	1	3	5	3
C	1	1	1						1	1							
W		1		1				1		4							
Y	3	13	1						2	2	1		1		2	2	2
others*		1								3	1						1
IMD cases analysed at the NRZMHi	12	27	8	6	1	3	1	2	7	26	5	3	2	1	5	7	6
incidence/100.000	0,13	0,24	0,24	0,28	0,15	0,16	0,1	0,31	0,12	0,17	0,1	0,2	0,07	0,09	0,17	0,38	

*others comprise serogroup E (n=1) and X (n=2) cases. Furthermore, one isolate was unencapsulated due to the capsule null locus (cni) and in two cases the serogroup could not be determined.

BW: Baden-Wuerttemberg, BY: Bavaria, BE: Berlin, BB: Brandenburg, HB Bremen, HH: Hamburg, HE: Hesse, MV: Mecklenburg-Western Pomerania, NI: Lower Saxony, NW: North Rhine-Westphalia, RP: Rhineland-Palatinate, SL: Saarland, SN: Saxony, ST: Saxony-Anhalt, SH: Schleswig-Holstein, TH: Thuringia, unkn: unknown

IMD cases according to age groups (2019 - 2022)



A marked increase in cases was observed in 2022 among infants, 15-19-year-olds, and 40-49-year-olds, which almost reached pre-pandemic numbers.

Antimicrobial susceptibility of invasive meningococcal isolates

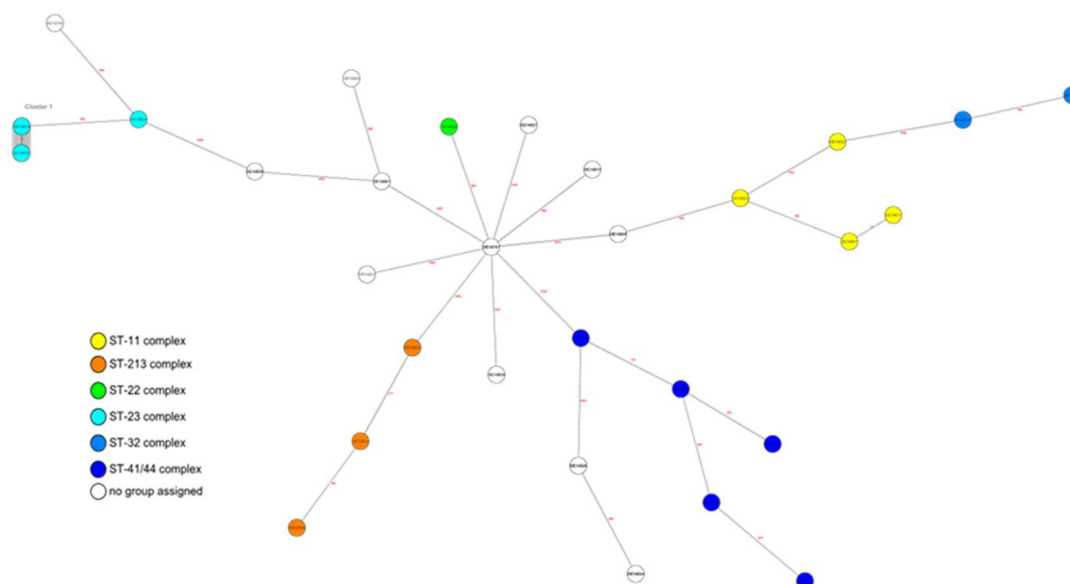
(According to EUCAST breakpoints 2022)

Antibiotics	susceptible	resistant
Penicillin	89	7(7.2%)
Cefotaxime	94	2
Ciprofloxacin	93	3
Rifampicin	96	

The proportion of penicillin-resistant isolates is comparable to 2021 (8.2%) Once again a meningococcal isolate with an unusual multi-resistance (Pen^R, Ctx^R, Cip^R) occurred.

Meningococcal typing based on whole genome sequencing

Up to now, whole genome sequencing was applied to the meningococcal isolates (n=30) of the first half of 2022 (data as of 25.04.2023). A cluster (Y: P1.5-1,2-2:F5-8) with two isolates was identified, which differed by only two alleles.



The figure shows a minimum spanning tree of the genome data based on the cgMLST scheme of Ridom SeqSphere+.

Isolates assigned to identical clonal complexes are labelled by identical colours. It is assumed that strains belonging to a cluster (shaded in grey) differ in six or less alleles.

Disclaimer

The above data were generated with federal funds (RKI). Scientific use is prohibited without prior written consent by the NRZMHi or the RKI. Commercial use is strictly prohibited. Inclusion of figures or tables in talks or oral presentations is not allowed.