



· · I·H·M·

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



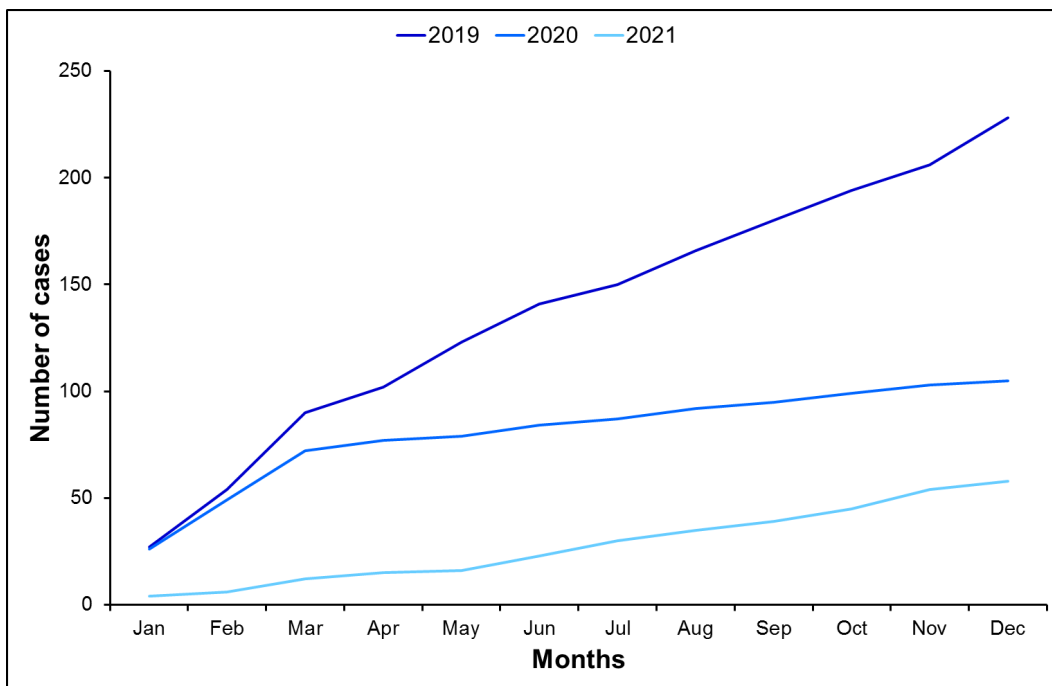
**Data of the laboratory surveillance of meningococci at the NRZMHi  
(2021)**

**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 2021, 119 samples from 109 individuals were submitted to the NRZMHi. *Neisseria meningitidis* was confirmed in samples of 85 patients, 58 of them were from primarily sterile compartments (latter figure corresponds to the number of cases with invasive disease). In 11 samples (19.0% out of 58) detection of meningococci was carried out exclusively by molecular methods. During the same period, 71 IMD cases were notified to the RKI (data as of 05.03.2022, SurvStat@RKI). Given that all IMD cases processed at the NRZMHi were notified retrospectively, one can assume a 81% coverage of IMD cases at the NRZMHi (77% in 2021).

In 2021, the incidence of IMD in Germany (0.09/100,000) was significantly lower than in 2020 (0.17/100,000) (data as of 05.03.2022, SurvStat@RKI). The ongoing measures to contain the COVID-19 pandemic, such as hand hygiene, wearing face masks and social distancing, were responsible for the reduction of infectious diseases, caused by i.e. meningococci and *Haemophilus influenzae*, in Germany and world-wide (EpiBull 2021;7:3-7; Brueggemann et al., Lancet Digit Health 2021 Jun;3(6):e360-e370).-7; Brueggemann et al., Lancet Digit Health 2021 Jun;3(6):e360-e370).

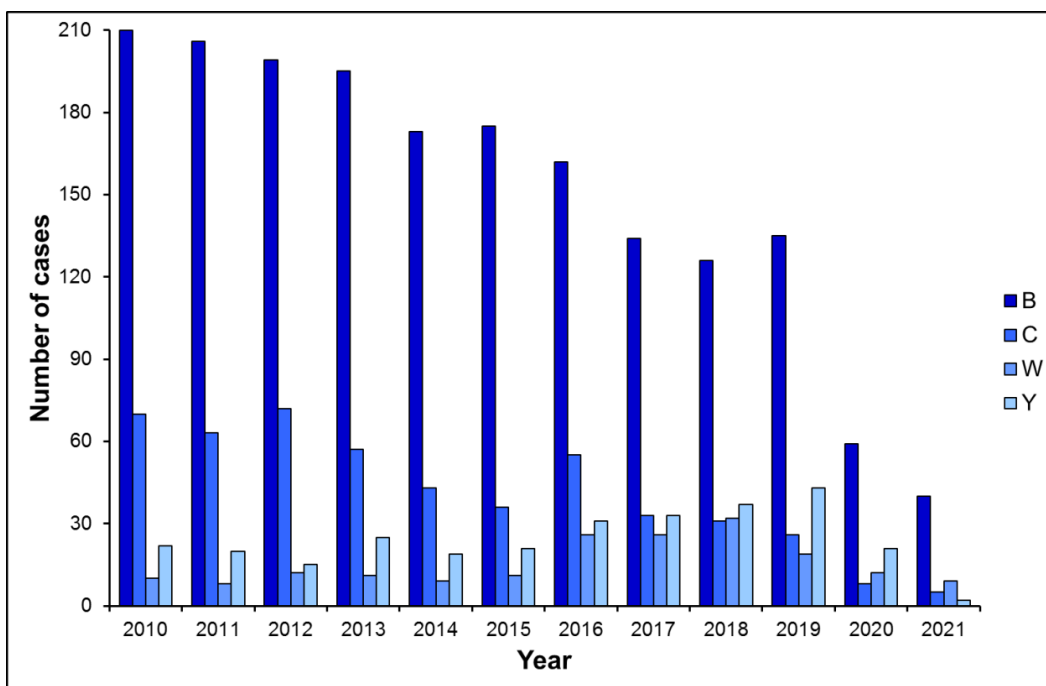
**Trend of IMD cases in the course of the COVID-19 pandemic 2020/2021**



*Cumulative graph of the number of IMD cases processed at the NRZMHi during the pandemic 2020 - 2021 in comparison to the number of IMD cases in 2019.*

Beginning in March 2020 with the first nation-wide lockdown the number of IMD cases submitted to the NRZMHi decreased dramatically in parallel with the notified cases at the RKI. This trend continued in 2021.

**Frequency of serogroups B, C, W and Y (2010-2021)**



Due to persisting infection control measures to combat the COVID-19 pandemic, once again less IMD cases occurred in all serogroups in comparison to the previous year.

### Serogroups according to federal states (2021)

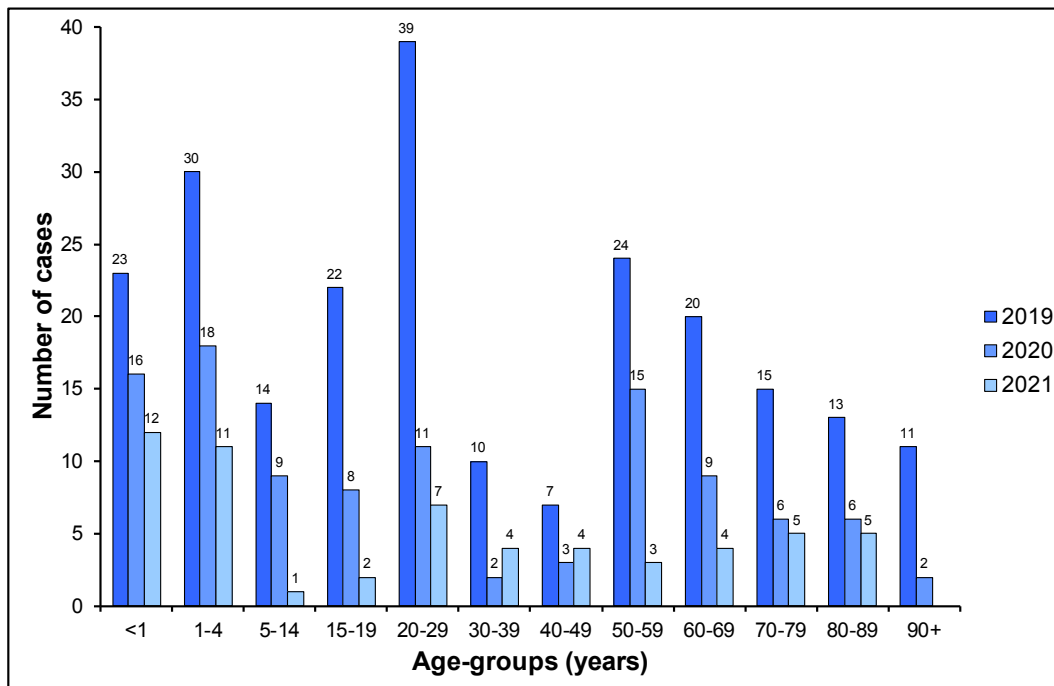
serogroup	BW	BY	BE	BB	HB	HH	HE	NI	NW	RP	ST	SH	TH	Unkn.
B	9	1	2	3	1	2	2	3	8	4	2	1	2	
C		1	1				1		2					
W	3						1	1	2			1		1
Y		1	1											
NG									1				1	
<b>IMD cases analysed at the NRZMHi</b>	12	3	4	3	1	2	4	4	13	4	2	2	3	1
<b>incidence/100.000</b>	0,11	0,05	0,11	0,12	0,29	0,11	0,08	0,09	0,09	0,12	0,18	0,03	0,09	

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

No cases occurred in Mecklenburg-Western Pomerania, Saxony and Saarland.

For two invasive cases, the serogroup could not be determined (NG).

### IMD cases according to age groups (2019 - 2021)



At the NRZMHi, a further decrease of IMD cases was observed in almost all age-groups.

## Antimicrobial susceptibility of invasive meningococcal isolates

(according to EUCAST breakpoints 2021)

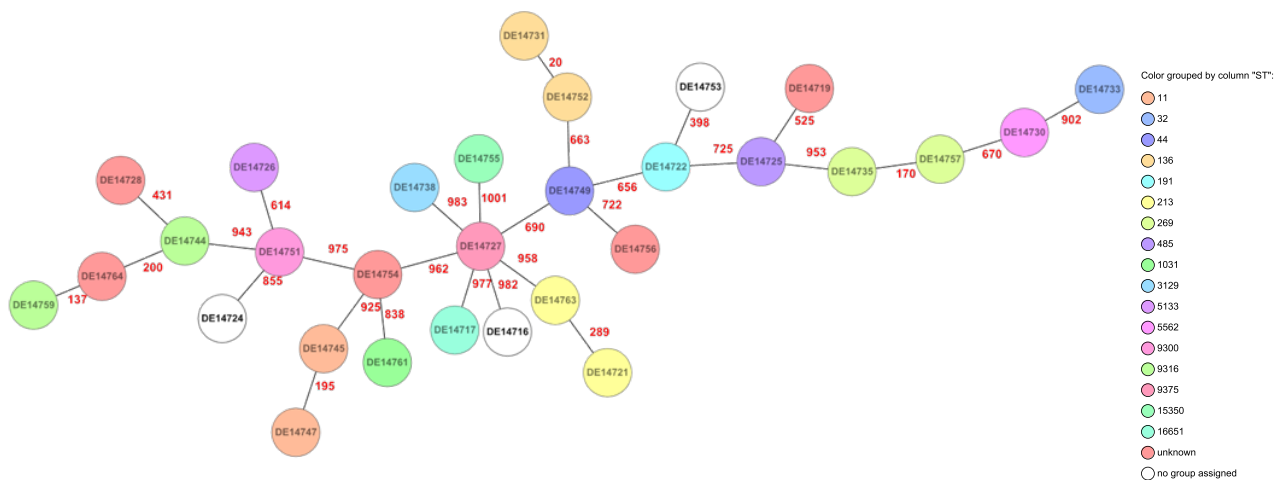
Antibiotics	susceptible	resistant
Penicillin	43	4 (8.5%)
Cefotaxime	46	1
Ciprofloxacin	46	1
Rifampicin	47	

In 2021, the EUCAST penicillin breakpoint was raised from 0.06µg/ml to 0.25µg/ml. Thus, the category intermediate susceptible is no longer applicable.

One meningococcal isolate stood-out with its unusual multi-resistance: PenR, CtxR, CipR. Typical mutations responsible for penicillin resistance were detected in penicillin binding protein 2 as well as a typical mutation in subunit A of the DNA gyrase associated with ciprofloxacin resistance.

## Meningococcal typing based on whole genome sequencing

Up to now, whole genome sequencing was applied to 29 of 47 meningococcal isolates (data as of 05.03.2022). Numerous allele differences were detected between the isolates. No fine-type occurred more than twice and no clusters have been detected yet, indicating that the IMD cases occurred sporadically.



The figure shows a minimum spanning tree based on the cgMLST scheme of Ridom SeqSphere+. Isolates with identical sequence types (ST) are labelled with identical colours. The red numbers indicate the number of different gene variants between the strains. It is assumed that strains belonging to a cluster differ in less than seven genes.

## 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.