Outbreak Reports

The First Case of Serogroup Y *Neisseria meningitidis* and An Expanded Investigation of Healthy Carriers — Shijiazhuang City, Hebei Province, China, 2023

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Summary

What is already known about this topic?

Neisseria meningitidis (Nm) is a bacterial pathogen that causes meningococcal disease. Serogroups A, B, C, W, X, and Y account for the vast majority of cases. However, invasive meningococcal disease (IMD) caused by NmY is rare in China and has been reported only in Tianjin, Guangdong, Shanghai, and Hunan provinces and cities.

What is added by this report?

This article reports the first case of *NmY*:cc23 meningococcal disease in Hebei Province, confirmed by metagenomic sequencing. We also present the results of expanded surveillance in the healthy population associated with the case.

What are the implications for public health practice?

NmY has caused multiple case reports across China, especially in southern cities. The first report of a serogroup Y case in Hebei Province, and the carriage rate in the healthy population, reminds us to increase public health attention on *Nm*. The results of this study suggest that surveillance of the *Nm* carriage rate among healthy carriers and serogroup changes in *Nm* should be strengthened.

On November 28, 2023, the Shijiazhuang CDC received a reported case of meningitis from the Hebei Provincial Chest Hospital. Preliminary investigations revealed the patient was a student with no travel history. Laboratory tests identified *Neisseria meningitidis* serogroup Y (NmY) in both the patient and the healthy population. Given the rarity of serogroup Y meningitis in China, and its absence in prior reports from Hebei Province, the Shijiazhuang CDC and Hebei Provincial CDC conducted an investigation of 166 healthy individuals. This paper summarizes our epidemiological and laboratory analyses of this event.

INVESTIGATION AND RESULTS

The patient, a 17-year-old male boarding school student, had been vaccinated with *Nm* A+C polysaccharide vaccine in 2009 and 2012. The onset was rapid, beginning with a high fever (40 °C) and severe headache on November 23, 2023. Other clinical symptoms included nausea, vomiting, neck stiffness, and altered consciousness. Kernig's sign and Brudzinski's sign were positive. A blood test revealed a leukocyte count of 15.21×10^9/L with 79% neutrophils. His cerebrospinal fluid (CSF) sample was turbid. Analysis showed a protein level of 2,410 mg/L, a white blood cell count of 1.978×10^4/L, a glucose level of 0.02 mmol/L, and a chloride level of 117 mmol/L. After admission, he received meropenem, vancomycin, and ganciclovir for combined anti-infective treatment. On November 27, a third-party mNGS report indicated the detection of *Nm* sequences in the patient's CSF. On November 28, the case was reported online as "meningitis, confirmed case, not classified." On December 29, the patient was discharged after clinical treatment, cured, and without sequelae.

On December 4, the patient's CSF *Nm* real-time PCR test for NmY was positive, though cultures were negative. Oropharyngeal swabs were then sampled from 166 healthy individuals, including 77 close contacts (Supplementary Table S1, available at https://weekly.chinacdc.cn/), and these samples underwent *N. meningitidis* culturing and real-time PCR testing. NmY strains were isolated from 18 samples (one per individual), with a total carriage rate of 10.84% (18/166). Among them, 7 strains were isolated from close contacts, with a carriage rate of 9.09% (7/77). Eleven strains were isolated from the other 89 individuals, with a carriage rate of 12.36% (11/89).

Epidemiological investigations revealed that the

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school operated under a closed boarding system with monthly holidays. The school had no vaccination requirements, and the patient had no travel history within two months and had not left the school within 15 days before disease onset. A total of nine other students shared a dormitory with the patient, and three of them experienced respiratory symptoms, including fever and rhinorrhea. All three recovered after receiving medication. The patient's class comprised 76 students, all of whom attended classes in the same classroom; no other students developed meningococcal disease. All healthy carriers of *NmY* had no history of leaving the school within one month before the case occurred. The patient was also diagnosed with malnutrition upon admission to the hospital. No other individuals were found to be malnourished. Following this case, during the month-end holiday, the school underwent terminal disinfection, and all students isolated at home for two weeks. No subsequent cases were identified in the follow-up epidemiological investigation.

A total of 18 carriers of group Y meningococcus were found across 8 classes. Eleven were boys living in building A (including 2 in the same class and dormitory as the case patient, and 2 in the same class but different dormitories). Seven were girls living in building B (including 3 in the same class as the case patient) (Figure 1).

Metagenomic next-generation sequencing (mNGS) of the patient's CSF was performed on the BGI G99 platform, yielding 242,348,594 reads with a Q30 of 93.92%. Reads were aligned to the reference genome of the case's *Nm* using BWA software, resulting in 541,066 *Nm* reads (0.22% of the total). The aligned data were assembled using the SPAdes genome assembler v3.15.5, generating 128 contigs with a total length of 2,031,385 bp (93.66% of the average length). This sequence was used for genomic comparison of all strains in this investigation.

All strains isolated in this incident underwent whole-genome sequencing on the BGI G99 and ONT platforms. Comparison with the database identified the pathogen as belonging to the CC23 clonal complex. As of 26 March 2024, the PubMLST *Neisseria* Database contained 2,368 *Neisseria meningitidis* serogroup Y (NmY) genomes (CC23) from at least 33 countries; these CC23 genomes were downloaded for comparison. A phylogenetic tree was constructed using whole-genome single nucleotide polymorphism (wgSNP) data. MUMmer3.23 software identified SNPs among all strains. To improve data quality, SNP positions within 5 bp of each other and those containing unspecified nucleotides ("N") were removed, resulting in a 15,413 SNP matrix. FastTree, using the maximum likelihood method, constructed the phylogenetic tree based on the wgSNP multiple sequence alignment (MSA). For further analysis, 52 representative genomes were selected, including NmY previously reported in China and global strains from 1966–2024 (Supplementary Table S2, available at https://weekly.chinacdc.cn/). The wgSNP-based phylogenetic tree revealed that the isolated strains clustered into two phylogenetic branches. The case sequence (Nm_23CSF) and six isolates from healthy individuals (Nm_1240, Nm_1241, Nm_1254, Nm_1266, Nm_1267, Nm_1269) belonged to the ST-18108 clonal complex (CC23). This group,

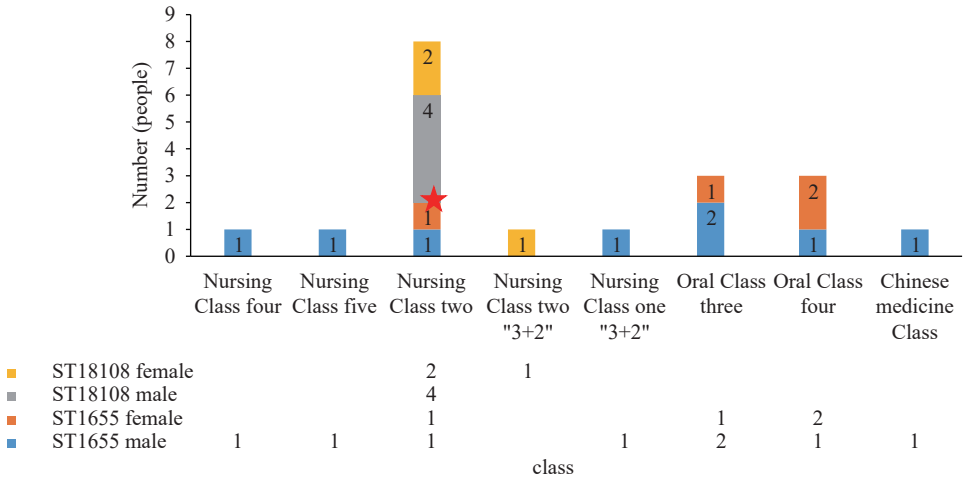

FIGURE 1. Class distribution of the patient and healthy carriers.
★ Remarked the case.

designated the close contact group, formed a distinct phylogenetic branch significantly divergent from other national strains. Twelve other isolates from healthy individuals (Nm_1253, Nm_1255, Nm_1256, Nm_1257, Nm_1258, Nm_1259, Nm_1260, Nm_1262, Nm_1263, Nm_1264, Nm_1265, Nm_1268) belonged to ST-1655 (CC23) and clustered into another phylogenetic branch most closely related to strains from Portugal, the USA, Japan, New Zealand, and Sweden (Figure 2).

We investigated these 18 serogroup Y strains by whole-genome sequencing and submitted the whole-genome data to the *Neisseria* spp. database at https://pubmlst.org/. Among these 18 isolates, all were characterized as Y:P1.5–1,10–1:F4-1:ST-1655 (CC23), but 7 ST-18108 sequences harbored a novel *gdh* allele (1349). This ST-18108 has not been reported internationally. All 18 isolates from the carriers shared identical *fHbp* allele 25, *porB* allele 3-117, and *nhba* allele 10, indicating considerable genetic similarity. The 18 strains were divided into 3 types according to the capsular A region, and 7 ST-18108 sequences possessed *csy* gene number 1 (Table 1). The novel *gdh* allele and the novel ST sequence type were not related to vaccine antigen sites.

DISCUSSION

Nm is responsible for IMD globally, presenting primarily as septicemia and meningitis (*1*).

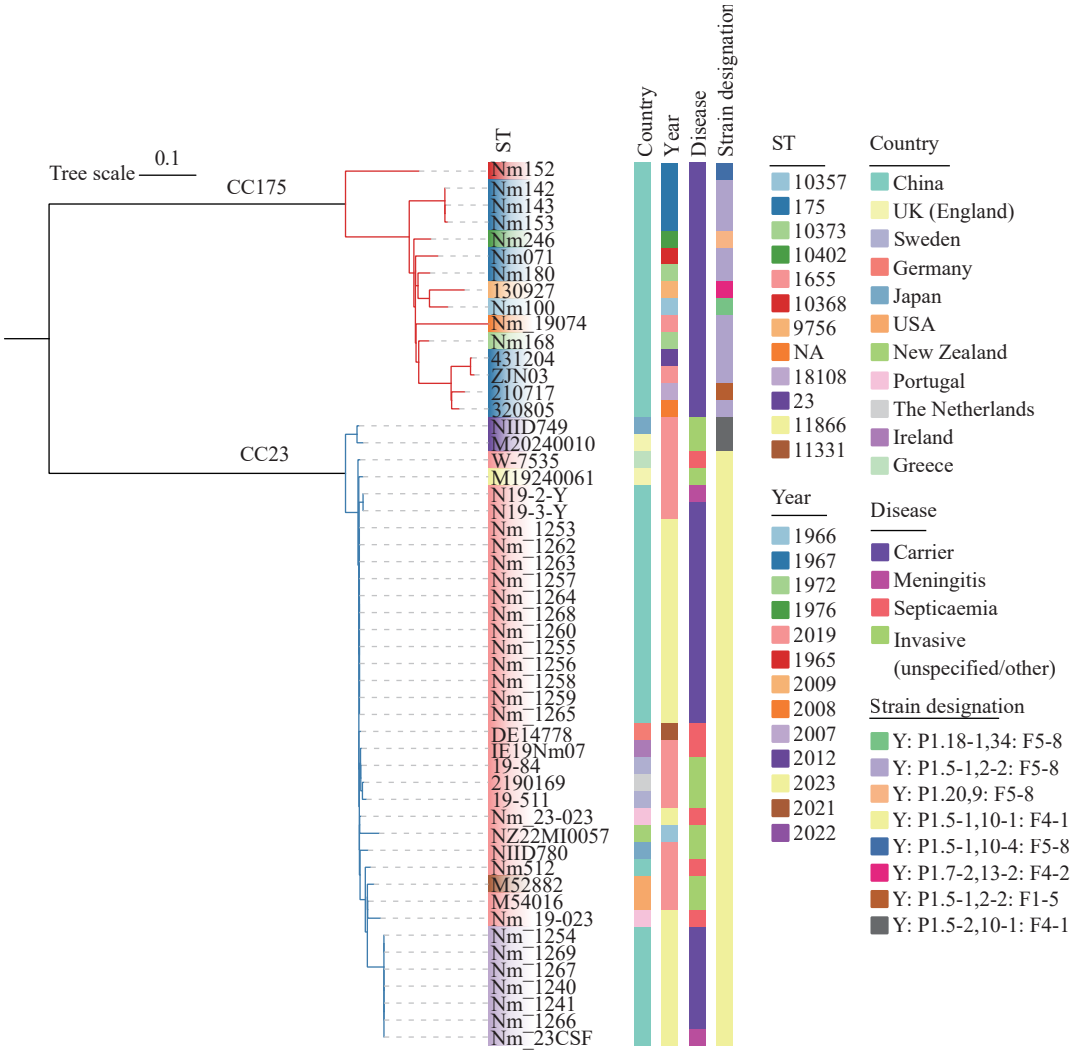

FIGURE 2. Phylogenies of lineages of *Neisseria meningitidis* serogroup Y strains by wgSNPs analysis.
Note: Phylogenetic analysis revealed that Nm_23CSF and six other strains were clustered into the CC23 cluster closest to the US and Portuguese strains, which were isolated from meningitis patients and healthy people. All strains' PorA genotypes were determined to be P1.5-1, and the *porB* and *fetA* alleles of these strains were 10-1 and F4–1, respectively.

TABLE 1. Molecular characteristics of serogroup Y *N. meningitidis* carriage isolates recovered in this study.

Isolate	Serogroup	MLST		Finetyping antigens				Peptide variant		Capsule region A					
		ST	CC	PorA_VR1	PorA_VR2	FetA_VR	porB	fHbp	NHBA	cssA	cssB	cssC	csy	cssF	ctrG
Nm_23CSF, Nm_1240, Nm_1241, Nm_1254, Nm_1266, Nm_1267, Nm_1269	Y	18108	23	5-1	10-1	F4-1	3-117	25	10	2	1	4	1	2	20
Nm_1253, Nm_1255, Nm_1256, Nm_1258, Nm_1262, Nm_1263, Nm_1265	Y	1655	23	5-1	10-1	F4-1	3-117	25	10	2	1	4	22	2	20
Nm_1257, Nm_1259, Nm_1260, Nm_1264, Nm_1268	Y	1655	23	5-1	10-1	F4-1	3-117	25	10	95	1	4	22	2	20

Asymptomatic nasopharyngeal carriage occurs in up to 35% of individuals at any given time (*2*–*3*), but prevalence in the general population is highly variable by region, ranging from 10% to 35% (*4*). *Nm* serogroups are defined by their capsular polysaccharides, with A, B, C, W, and Y being the most pathogenic. Over the last two decades, serogroup Y IMD has increased in Europe and the United States (*5*–*6*). For example, serogroup Y was the most prevalent cause of IMD in Sweden in 2015, representing 53% of all cases (*7*). Recent IMD cases in China have been caused mainly by serogroups C, A, B, and W (*8*); serogroup Y IMD is rare. To date, only 9 cases of serogroup Y IMD have been reported in China (Table 2): 1 in Tianjin in 2015 (*9*), 2 in Guangdong in 2019 (*10*–*11*), 1 in Hunan (*12*), 1 in Shanghai (*13*), 1 in Hunan in 2020 (*12*), 1 in Guangdong in 2021 (*14*), 1 in Zhejiang in 2021 (*15*), and 1 in Guangdong in 2023 (*16*). These Chinese serogroup Y cases were the internationally common ST-1655 or ST-23 types, both belonging to the CC23 complex. The case in this paper is the only NmY case reported in Hebei Province in the past 10 years. Previous continuous surveillance of meningococcal infection identified serogroup B as the predominant strain, although serogroups W and Y were occasionally isolated from throat swab samples of healthy individuals.

Laboratory testing identified this case as the first serogroup Y *Nm* case in Hebei Province, caused by a novel sequence type (ST) within CC23. This ST represents the first reported instance of this NmY CC23 in China. Epidemiological investigation indicated this was a sporadic, locally acquired case, with no other similar cases identified during this period. While the reported NmY carriage rate among healthy individuals in China is 0.01% (*17*), this investigation identified 18 asymptomatic carriers among 166 individuals, resulting in a carriage rate of 10.84% (18/166). Epidemiological findings suggest that this strain established a transmission vector within the school, potentially posing a challenge to local invasive meningococcal disease (IMD) prevention and control. Increased international travel elevates the risk of NmY importation into China, potentially altering the dominant circulating strains.

Although failure to isolate the *Nm* strain from the patient's CSF was likely due to the delay between sampling and testing, *Nm* DNA fragments were identified in the CSF, and the complete *Nm* genome was assembled using mNGS. Integrating sequencing data from carriers ensured the integrity and accuracy of the laboratory data.

In Europe, the age of *Neisseria meningitidis* serogroup Y cases exhibits a bimodal distribution. In addition to the commonly reported adolescents and young adults aged 15 to 20 years, 50% of patients are between 45 and 88 years old (*6*). The patient in Hebei Province was 17 years old, within the high-incidence age range.

Genetic analysis revealed that the serogroup Y *N. meningitidis* strains prevalent in this school belonged to two phylogenetic branches. Similar cases involving other serogroups have been occasionally reported (*18*). Serogroup Y Nm ST-18108, belonging to CC23, was identified in this meningitis case and has not been previously reported. Phylogenetic analysis demonstrated that ST-18108 has a distant genetic relationship with NmY cases reported in China and other countries. Within the contact group, 5 classmates (Nm_1240, Nm_1241, Nm_1266, Nm_1267, and Nm_1269) were all close contacts of the patient. Only 1 student (Nm_1254), with whom the patient had contact, did not meet the definition of close contact. The patient's malnutrition may have contributed to lowered immunity (*19*), predisposing them to disease.

The clustering results, based on MLST, further demonstrate that the CC23 identified in this study is distinct from previously isolated strains. This suggests

TABLE 2. Summary of serogroup Y *Nm* isolated from cases and healthy people in China, 2013–2023.

Number	Isolate	Age	Gender	Source	Year	Province	City	Sample	Culture	Serogroup	ST	CC	Reference
Case 0	Nm-TJ	17 years	Male	IMD	2015	−	Tianjin	Blood	Positive	Y	175	175	(*9*)
Case 1	N19-2-Y	16 years	Male	IMD	2019	Guangdong	Dongguan	CSF	Positive	Y	1655	23	(*10*)
Carrier 0	N19-3-Y	−	−	Carrier	2019	Guangdong	Dongguan	Swab	Positive	Y	1655	23	(*10*)
Case 2	−	5 months	Male	IMD	2019	Guangdong	Shantou	Blood	Positive	Y	1655	23	(*11*)
Case 3	2019B22	9 years	Male	IMD	2019	Hunan	Yongzhou	Blood	Positive	Y	1655	23	(*12*)
Case 4	Nm512	35 months	Male	Septicaemia	2019	−	Shanghai	Blood	Positive	Y	1655	23	(*13*)
Case 5	2020B22	45 years	Male	IMD	2020	Hunan	Yueyang	CSF	Positive	Y	1655	23	(*12*)
Case 6	106308	65 years	Male	Respiratory failure	2021	Guangdong	Guangzhou	Blood	Positive	Y	1655	23	(*14*)
Case 7	−	−	−	IMD	2021	Zhejiang	−	−	−	Y	1655	23	(*15*)
Case 8	−	16 years	−	IMD	2023	Guangdong	Guangzhou	Blood	Negative	Y	1655	23	(*16*)
Case 9	Nm-23CSF	17 years	Male	IMD	2023	Hebei	Shijiazhuang	CSF	Negative	Y	18108	23	This study
Carrier 1	Nm-1240	15 years	Male	Carrier	2023	Hebei	Shijiazhuang	Swab	Positive	Y	18108	23	This study
Carrier 2	Nm-1241	16 years	Male	Carrier	2023	Hebei	Shijiazhuang	Swab	Positive	Y	18108	23	This study
Carrier 3	Nm-1254	15 years	Female	Carrier	2023	Hebei	Shijiazhuang	Swab	Positive	Y	18108	23	This study
Carrier 4	Nm-1266	15 years	Female	Carrier	2023	Hebei	Shijiazhuang	Swab	Positive	Y	18108	23	This study
Carrier 5	Nm-1267	15 years	Female	Carrier	2023	Hebei	Shijiazhuang	Swab	Positive	Y	18108	23	This study
Carrier 6	Nm-1269	15 years	Male	Carrier	2023	Hebei	Shijiazhuang	Swab	Positive	Y	18108	23	This study
Carrier 7	Nm-1253	16 years	Male	Carrier	2023	Hebei	Shijiazhuang	Swab	Positive	Y	1655	23	This study
Carrier 8	Nm-1255	16 years	Male	Carrier	2023	Hebei	Shijiazhuang	Swab	Positive	Y	1655	23	This study
Carrier 9	Nm-1256	16 years	Male	Carrier	2023	Hebei	Shijiazhuang	Swab	Positive	Y	1655	23	This study
Carrier 10	Nm-1257	16 years	Male	Carrier	2023	Hebei	Shijiazhuang	Swab	Positive	Y	1655	23	This study
Carrier 11	Nm-1258	16 years	Male	Carrier	2023	Hebei	Shijiazhuang	Swab	Positive	Y	1655	23	This study
Carrier 12	Nm-1259	15 years	Female	Carrier	2023	Hebei	Shijiazhuang	Swab	Positive	Y	1655	23	This study
Carrier 13	Nm-1260	15 years	Male	Carrier	2023	Hebei	Shijiazhuang	Swab	Positive	Y	1655	23	This study
Carrier 14	Nm-1262	15 years	Female	Carrier	2023	Hebei	Shijiazhuang	Swab	Positive	Y	1655	23	This study
Carrier 15	Nm-1263	15 years	Female	Carrier	2023	Hebei	Shijiazhuang	Swab	Positive	Y	1655	23	This study
Carrier 16	Nm-1264	15 years	Male	Carrier	2023	Hebei	Shijiazhuang	Swab	Positive	Y	1655	23	This study
Carrier 17	Nm-1265	17 years	Female	Carrier	2023	Hebei	Shijiazhuang	Swab	Positive	Y	1655	23	This study
Carrier 18	Nm-1268	16 years	Male	Carrier	2023	Hebei	Shijiazhuang	Swab	Positive	Y	1655	23	This study

Note: "−" means unknown.

the emergence of a novel clone group in Hebei Province. The initial appearance of this clone group resulted in cases that rapidly spread on a small scale within the population, leading to widespread carriage. This indicates potentially greater pathogenicity and transmissibility of this NmY clone group compared to previous NmY strains, warranting further investigation. Host factors may also have contributed to the invasiveness of the infection. Given the increasing incidence of *N. meningitidis* serogroup Y cases reported both domestically and internationally, enhanced surveillance of NmY is crucial. Immunization strategies should be adjusted accordingly to prevent outbreaks of serogroup Y meningococcal disease in key settings such as schools and to reduce the incidence of fatal cases.

Conflicts of interest: No conflicts of interest.

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SUPPLEMENTARY MATERIAL

SUPPLEMENTARY TABLE S1. Information of 166 healthy people and the patient in this investigation.

Characteristic	Sample No.	Age (years)	Gender		Sample name	N.m positive Culture	Dormitory number			NmY culture positive rate, %
			Female	Male			NmY ST18108	NmY ST1655	NmB	
Sample type										
Patient	1	17		1	CSF	0	6328 (1)	–	–	–
Healthy										
Close contact	77	13–34	57	20	Swab	7	6328 (2), 6218 (1), 5316 (1), 5317 (1)	6325 (1), 5314 (1)	–	9.09
Other individuals	89	14–44	50	39	Swab (86), blood (3)	NmY (11), NmB (1)	5306 (1)	6123 (1), 6127 (1), 6218 (2), 6229 (1), 6323 (1), 6331 (1), 5111 (1), 5118 (1), 5120 (1)	6128 (1)	12.36
Occupation										
Student										
Nursing Class two	73	13–18	53	20	Swab (72), CSF (1)	7	6328 (3), 6218 (1), 5316 (1), 5317 (1)	6325 (1), 5314 (1)	–	4.22
Chinese medicine Class	7	15–16	3	4	Swab	1	–	6123 (1)	–	0.60
Comprehensive Class	7	15–16	5	2	Swab	0	–	–	–	–
Nursing Class five	7	15–16	5	2	Swab	1	–	6229 (1)	–	0.60
Nursing Class four	7	16–17	4	3	Swab	1	–	6323 (1)	–	0.60
Nursing Class one	8	15–16	5	3	Swab	0	–	–	–	–
Nursing Class one “3+2”	7	15–16	5	2	Swab	1	–	6331 (1)	–	0.60
Nursing Class three	7	15–17	4	3	Swab	0	–	–	–	–
Nursing Class two “3+2”	7	15–16	4	3	Swab	1	5306 (1)	–	–	0.60
Oral Class four	7	15–16	4	3	Swab	3	–	5118 (1), 5120 (1)	6128 (1)	1.20
Oral Class one	7	15–18	3	4	Swab	0	–	–	–	–
Oral Class three	7	14–16	4	3	Swab	3	–	5111 (1), 6218 (2)	–	1.81
Oral Class two	7	15–16	3	4	Swab	0	–	–	–	–
Teacher	6	23–34	4	2	Swab	0	–	–	–	–
Others	3	23–44	1	2	blood	0	–	–	–	–

Note: “–”means not applicable.

SUPPLEMENTARY TABLE S2. Strain information for cluster analysis during 1966-2024.

Id	Isolate	Country	Year	Disease	Strain designation	ST	CC
26604	Nm100	China	1966	Carrier	Y: P1.18-1,34: F5-8	10357	175
26611	Nm143	China	1967	Carrier	Y: P1.5-1,2-2: F5-8	175	175
26620	Nm168	China	1972	Carrier	Y: P1.5-1,2-2: F5-8	10373	175
26650	Nm246	China	1976	Carrier	Y: P1.20,9: F5-8	10402	175
46123	N19-2-Y	China	2019	Meningitis	Y: P1.5-1,10-1: F4-1	1655	23
46127	N19-3-Y	China	2019	Carrier	Y: P1.5-1,10-1: F4-1	1655	23
52305	Nm071	China	1965	Carrier	Y: P1.5-1,2-2: F5-8	175	175
52313	Nm142	China	1967	Carrier	Y: P1.5-1,2-2: F5-8	175	175
52315	Nm153	China	1967	Carrier	Y: P1.5-1,2-2: F5-8	175	175
52323	Nm180	China	1972	Carrier	Y: P1.5-1,2-2: F5-8	175	175
52511	Nm152	China	1967	Carrier	Y: P1.5-1,10-4: F5-8	10368	175
71401	Nm512	China	2019	Septicemia	Y: P1.5-1,10-1: F4-1	1655	23
89150	130927	China	2009	Carrier	Y: P1.7-2,13-2: F4-2	9756	175
89151	320805	China	2008	Carrier	Y: P1.5-1,2-2: F5-8	175	175
89156	210717	China	2007	Carrier	Y: P1.5-1,2-2: F1-5	175	175
89157	431204	China	2012	Carrier	Y: P1.5-1,2-2: F5-8	175	175
96187	ZJN03	China	2019	Carrier	Y: P1.5-1,2-2: F5-8	175	175
Nm_19074	Nm_19074	China	2019	Carrier	Y: P1.5-1,2-2: F5-8	NA	175
Nm_23CSF	Nm_23CSF	China	2023	Meningitis	Y: P1.5-1,10-1: F4-1	18108	23
Nm_1240	Nm_1240	China	2023	Carrier	Y: P1.5-1,10-1: F4-1	18108	23
Nm_1241	Nm_1241	China	2023	Carrier	Y: P1.5-1,10-1: F4-1	18108	23
Nm_1253	Nm_1253	China	2023	Carrier	Y: P1.5-1,10-1: F4-1	1655	23
Nm_1254	Nm_1254	China	2023	Carrier	Y: P1.5-1,10-1: F4-1	18108	23
Nm_1255	Nm_1255	China	2023	Carrier	Y: P1.5-1,10-1: F4-1	1655	23
Nm_1256	Nm_1256	China	2023	Carrier	Y: P1.5-1,10-1: F4-1	1655	23
Nm_1257	Nm_1257	China	2023	Carrier	Y: P1.5-1,10-1: F4-1	1655	23
Nm_1258	Nm_1258	China	2023	Carrier	Y: P1.5-1,10-1: F4-1	1655	23
Nm_1259	Nm_1259	China	2023	Carrier	Y: P1.5-1,10-1: F4-1	1655	23
Nm_1260	Nm_1260	China	2023	Carrier	Y: P1.5-1,10-1: F4-1	1655	23
Nm_1262	Nm_1262	China	2023	Carrier	Y: P1.5-1,10-1: F4-1	1655	23
Nm_1263	Nm_1263	China	2023	Carrier	Y: P1.5-1,10-1: F4-1	1655	23
Nm_1264	Nm_1264	China	2023	Carrier	Y: P1.5-1,10-1: F4-1	1655	23
Nm_1265	Nm_1265	China	2023	Carrier	Y: P1.5-1,10-1: F4-1	1655	23
Nm_1266	Nm_1266	China	2023	Carrier	Y: P1.5-1,10-1: F4-1	18108	23
Nm_1267	Nm_1267	China	2023	Carrier	Y: P1.5-1,10-1: F4-1	18108	23
Nm_1268	Nm_1268	China	2023	Carrier	Y: P1.5-1,10-1: F4-1	1655	23
Nm_1269	Nm_1269	China	2023	Carrier	Y: P1.5-1,10-1: F4-1	18108	23
80101	M20 240010	UK [England]	2019	invasive (unspecified/other)	Y: P1.5-2,10-1: F4-1	23	23
85273	19-84	Sweden	2019	invasive (unspecified/other)	Y: P1.5-1,10-1: F4-1	1655	23
94395	M19 240061	UK [England]	2019	invasive (unspecified/other)	Y: P1.5-1,10-1: F4-1	11866	23
111311	DE14778	Germany	2021	Septicemia	Y: P1.5-1,10-1: F4-1	1655	23
120575	NIID749	Japan	2019	invasive (unspecified/other)	Y: P1.5-2,10-1: F4-1	23	23

Continued

Id	Isolate	Country	Year	Disease	Strain designation	ST	CC
120597	NIID780	Japan	2019	invasive (unspecified/other)	Y: P1.5-1,10-1: F4-1	1655	23
124932	M54016	USA	2019	invasive (unspecified/other)	Y: P1.5-1,10-1: F4-1	1655	23
124999	M52882	USA	2019	invasive (unspecified/other)	Y: P1.5-1,10-1: F4-1	11331	23
132452	NZ22MI0057	New Zealand	2022	invasive (unspecified/other)	Y: P1.5-1,10-1: F4-1	1655	23
138759	Nm_19-023	Portugal	2023	Septicemia	Y: P1.5-1,10-1: F4-1	1655	23
86972	2190169	The Netherlands	2019	invasive (unspecified/other)	Y: P1.5-1,10-1: F4-1	1655	23
91878	19-511	Sweden	2019	invasive (unspecified/other)	Y: P1.5-1,10-1: F4-1	1655	23
93967	IE19Nm07	Ireland	2019	Septicemia	Y: P1.5-1,10-1: F4-1	1655	23
72868	W-7535	Greece	2019	Septicemia	Y: P1.5-1,10-1: F4-1	1655	23
138762	Nm_23-023	Portugal	2023	Septicemia	Y: P1.5-1,10-1: F4-1	1655	23